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(54) Title: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY OF HEMATOLOGICAL MALIGNANCIES

(57) Abstract: Disclosed are compositions and methods for the diagnosis and therapy of hematological malignancies, and in particular, human leukemias and lymphomas of the follicular, Hodgkin's and non-Hodgkin's type. In particular embodiments, the invention provides new, effective methods, compositions and kits for eliciting immune and T cell response to specific malignancy-related antigenic polypeptides and antigenic polypeptide fragments thereof. Also disclosed are compositions and methods for use in the identification of cells and biological samples containing one or more hematological malignancy-related compositions, and methods for the detection and diagnosis of such diseases and affected cell types. Also disclosed are diagnostic and therapeutic kits, as well as uses for such kits and the disclosed polynucleotide, polypeptide, peptide, and antibody compositions in the preparation of medica-
ments suitable for therapy and/or prevention of a variety of leukemias and lymphomas.

DESCRIPTION

COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY OF HEMATOLOGICAL MALIGNANCIES

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1. BACKGROUND OF THE INVENTION

The present application claims priority to United States Provisional Patent Applications Serial No 60/186,126, filed March 1, 2000; Serial No. 60/190,479, filed March 17, 2000; Serial No. 60/200,545, filed April 27, 2000; Serial No. 60/200,303, filed April 28,
10 2000; Serial No. 60/200,779, filed April 28, 2000; Serial No. 60/200,999; filed May 1, 2000; Serial No. 60/202,084, filed May 4, 2000; Serial No. 60/206,201, filed May 22, 2000; Serial No. 60/218,950, filed July 14, 2000; Serial No. 60/222,903, filed August 3, 2000; Serial No. 60/223,416, filed August 4, 2000; and Serial No. 60/223,378, filed August 7, 2000; the entire specification, claims and figures of each of which is specifically incorporated herein by
15 reference in its entirety without disclaimer.

1.1 FIELD OF THE INVENTION

The present invention relates generally to the fields of cancer diagnosis and therapy. More particularly, it concerns the surprising discovery of compositions and methods for the
20 detection and immunotherapy of hematological malignancies, and particularly, leukemias, and lymphomas of the follicular, Hodgkin's and T cell and B cell Non-Hodgkin's types. The invention provides new, effective methods, compositions and kits for eliciting immune and T-cell response to antigenic polypeptides, and antigenic peptide fragments isolated therefrom, and methods for the use of such compositions for diagnosis, detection, treatment,
25 monitoring, and/or prevention of various types of human hematological malignancies. In particular, the invention provides polypeptide, peptide, antibody, antigen binding fragment, hybridoma, host cell, vector, and polynucleotide compounds and compositions for use in identification and discrimination between various types of hematological malignancies, and

methods for the detection, diagnosis, prognosis, monitoring, and therapy of such conditions in an affected animal.

1.2 DESCRIPTION OF RELATED ART

5 1.2.1 HEMATOLOGICAL MALIGNANCIES

Hematological malignancies, such as leukemias and lymphomas, are conditions characterized by abnormal growth and maturation of hematopoietic cells. Leukemias are generally neoplastic disorders of hematopoietic stem cells, and include adult and pediatric acute myeloid leukemia (AML), chronic myeloid leukemia (CML), acute lymphocytic
10 leukemia (ALL), chronic lymphocytic leukemia (CLL) and secondary leukemia. Among lymphomas, there are two distinct groups: non-Hodgkin's lymphoma (NHL) and Hodgkin's disease. NHLs are the result of a clonal expansion of B- or T-cells, but the molecular pathogenesis of Hodgkin's disease, including lineage derivation and clonality, remains obscure. Other hematological malignancies include myelodysplastic syndromes (MDS),
15 myeloproliferative syndromes (MPS) and myeloma. Hematological malignancies are generally serious disorders, resulting in a variety of symptoms, including bone marrow failure and organ failure.

NHLs are the sixth most common cause of cancer related deaths in the United States. Only prostate, breast, lung, colorectal and bladder cancer currently exceed lymphoma in
20 annual incidence. In 1995, more than 45,000 new NHLs were diagnosed, and over 21,000 patients died of these diseases. The average age of lymphoma patients is relatively young (42 years), and the resulting number of years of life lost to these diseases renders NHLs fourth in economic impact among cancers in the United States. In the past 15 years, the American Cancer Society reported a 50% increase in the incidence of NHLs, one of the
25 largest increases for any cancer group. Much of this increase has been attributed to the development of lymphomas in younger men who have acquired AIDS. Lymphomas are also the third most common childhood malignancy and account for approximately 10% of cancers in children. The survival rate (all ages) varies from 73% (low risk) to 26% (high risk).

1.3 DEFICIENCIES IN THE PRIOR ART

Treatment for many hematological malignancies, including leukemias and lymphomas, remains difficult, and existing therapies are not universally effective. While treatments involving specific immunotherapy appear to have considerable potential, such treatments have been limited by the small number of known malignancy-associated antigens. Moreover the ability to detect such hematological malignancies in their early stages can be quite difficult depending upon the particular malady. The lack of a sufficient number of specific diagnostic and prognostic markers of the diseases, and identification of cells and tissues that can be affected, has significantly limited the field of oncology.

Accordingly, there remains a need in the art for improved methods for detecting, screening, diagnosis and treatment of hematological malignancies such as Hodgkin's disease, chronic lymphocytic leukemia, as well as follicular and non-Hodgkin's lymphomas. The present invention fulfills these and other inherent needs in the field, and provides significant advantages in the detection of cells, and cell types that express one or more polypeptides that have been shown to be over-expressed in one or more of such hematological malignancies.

2. SUMMARY OF THE INVENTION

The present invention addresses the foregoing long-felt need and other deficiencies in the art by identifying new and effective strategies for the identification, detection, screening, diagnosis, prognosis, prophylaxis, therapy, and immunomodulation of one or more hematological malignancies, and in particular, leukemias such as chronic lymphocytic leukemia, and lymphomas, such as those of the follicular, Hodgkin's and non-Hodgkin's types.

The present invention is based, in part, upon the surprising and unexpected discovery that certain previously unknown or unidentified human polypeptides, peptides, and antigenic fragments derived therefrom have now been identified that are overexpressed in one or more types of hematological malignancies. The genes encoding several of these polypeptides are now identified and obtained in isolated form, and have been characterized using a series of molecular biology methodologies including subtractive library analysis, microarray screening, polynucleotide sequencing, peptide and epitopic identification and characterization, as well as expression profiling, and *in vitro* whole gene cell priming. A set

of these polynucleotides, and the polypeptides, peptides, and antigenic fragments they encode are now identified and implicated in the complex processes of hematological malignancy disease onset, progression, and/or outcome, and in particular, diseases such as leukemias and lymphomas.

5 The inventors have further demonstrated that a number of these polynucleotides, and their encoded polypeptides, as well as antibodies, antigen presenting cells, T cells, and the antigen binding fragments derived from such antibodies are useful in the development of particularly advantageous compositions and methods for the detection, diagnosis, prognosis, prophylaxis and/or therapy of one or more of these diseases, and particularly those conditions
10 that are characterized by (a) an increased, altered, elevated, or sustained expression of one or more polynucleotides that comprise at least a first sequence region that comprises a nucleic acid sequence as disclosed in any one of SEQ ID NO:1 through SEQ ID NO:278, or (b) an increased, altered, elevated, or sustained biological activity of one or more polypeptides that comprise at least a first sequence region that comprises an amino acid sequence as disclosed
15 in any one of SEQ ID NO:669 through SEQ ID NO:2532.

 The present invention also provides methods and uses for one or more of the disclosed peptide, polypeptide, antibody, antigen binding fragment, and polynucleotide compositions of the present invention in generating an immune response or in generating a T-cell response in an animal, and in particular in a mammal such as a human. The invention
20 also provides methods and uses for one or more of these compositions in the identification, detection, and quantitation of hematological malignancy compositions in clinical samples, isolated cells, whole tissues, and even affected individuals. The compositions and methods disclosed herein also may be used in the preparation of one or more diagnostic reagents, assays, medicaments, or therapeutics, for diagnosis and/or therapy of such diseases.

25 In a first important embodiment, there is provided a composition comprising at least a first isolated peptide or polypeptide comprising at least a first isolated coding region that comprises an amino acid sequence that is at least about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about
30 98%, or about 99% identical to the amino acid sequence of any one of SEQ ID NO:669 to

SEQ ID NO:2532. Exemplary preferred sequences are those that comprise at least a first coding region that comprises an amino acid sequence that is at least about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, or about 94% identical to the amino acid sequence of any one of SEQ ID NO:669 to SEQ ID NO:2532, with those sequences that comprise at least a first coding region that comprises an amino acid sequence that is at least about 95%, about 96%, about 97%, about 98%, or about 99% identical to the amino acid sequence of any one of SEQ ID NO:669 to SEQ ID NO:2532 being examples of particularly preferred sequences in the practice of the present invention. Likewise, peptide and polypeptide compounds and compositions are also provided that comprise, consist essentially of, or consist of the amino acid sequence of any one of SEQ ID NO:669 to SEQ ID NO:2532.

In particular embodiments relating to compositions and methods for the detection, diagnosis, prognosis, prophylaxis, treatment, and therapy of Hodgkin's lymphoma, exemplary preferred peptide and polypeptide compositions have been provided herein. These include, but are not limited to, those peptide and polypeptide compounds and compositions that comprise at least a first isolated peptide or polypeptide comprising at least a first isolated coding region that comprises an amino acid sequence that is at least about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, or about 99% identical to the amino acid sequence of any one of SEQ ID NO:669 to SEQ ID NO:1380, and those that comprise at least a first coding region that comprises an amino acid sequence that is at least about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, or about 94% identical to the amino acid sequence of any one of SEQ ID NO:669 to SEQ ID NO:1380, and even those sequences that comprise at least a first coding region that comprises an amino acid sequence that is at least about 95%, about 96%, about 97%, about 98%, or about 99% identical to the amino acid sequence of any one of SEQ ID NO:669 to SEQ ID NO:1380.

Likewise, in particular embodiments relating to compositions and methods for the detection, diagnosis, prognosis, prophylaxis, treatment, and therapy of follicular lymphoma,

exemplary preferred peptide and polypeptide compositions have also been provided herein. These include, but are not limited to, those peptide and polypeptide compounds and compositions that comprise at least a first isolated peptide or polypeptide comprising at least a first isolated coding region that comprises an amino acid sequence that is at least about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, or about 99% identical to the amino acid sequence of any one of SEQ ID NO:1381 to SEQ ID NO:1859, and those that comprise at least a first coding region that comprises an amino acid sequence that is at least about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, or about 94% identical to the amino acid sequence of any one of SEQ ID NO:1381 to SEQ ID NO:1859, and even those sequences that comprise at least a first coding region that comprises an amino acid sequence that is at least about 95%, about 96%, about 97%, about 98%, or about 99% identical to the amino acid sequence of any one of SEQ ID NO:1381 to SEQ ID NO:1859.

In a similar fashion, there are also embodiments disclosed herein that provide compositions and methods for the detection, diagnosis, prognosis, prophylaxis, treatment, and therapy of B cell non-Hodgkin's lymphoma. Exemplary preferred peptide and polypeptide compounds and compositions relating to this aspect of the invention include, but are not limited to, those peptide and polypeptide compounds or compositions that comprise at least a first isolated peptide or polypeptide comprising at least a first isolated coding region that comprises an amino acid sequence that is at least about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, or about 99% identical to the amino acid sequence of any one of SEQ ID NO:1860 to SEQ ID NO:2105, and those that comprise at least a first coding region that comprises an amino acid sequence that is at least about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, or about 94% identical to the amino acid sequence of any one of SEQ ID NO:1860 to SEQ ID NO:2105, and even those sequences that comprise at least a first coding region that comprises an amino acid

sequence that is at least about 95%, about 96%, about 97%, about 98%, or about 99% identical to the amino acid sequence of any one of SEQ ID NO:1860 to SEQ ID NO:2105.

In those embodiments relating to compositions and methods for the detection, diagnosis, prognosis, prophylaxis, treatment, and therapy of T cell non-Hodgkin's lymphoma, exemplary preferred peptide and polypeptide compositions include those
5 compositions that comprise at least a first isolated peptide or polypeptide comprising at least a first isolated coding region that comprises an amino acid sequence that is at least about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about
10 95%, about 96%, about 97%, about 98%, or about 99% identical to the amino acid sequence of any one of SEQ ID NO:2106 to SEQ ID NO:2375, and those that comprise at least a first coding region that comprises an amino acid sequence that is at least about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, or about 94% identical to the amino acid sequence of any one of SEQ ID NO:2106 to SEQ ID
15 NO:2375, and even those sequences that comprise at least a first coding region that comprises an amino acid sequence that is at least about 95%, about 96%, about 97%, about 98%, or about 99% identical to the amino acid sequence of any one of SEQ ID NO:2106 to SEQ ID NO:2375.

In those embodiments relating to compositions and methods for the detection,
20 diagnosis, prognosis, prophylaxis, treatment, and therapy of lymphoma, exemplary preferred peptide and polypeptide compositions include those compositions that comprise at least a first isolated peptide or polypeptide comprising at least a first isolated coding region that comprises an amino acid sequence that is at least about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%,
25 about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, or about 99% identical to the amino acid sequence of any one of SEQ ID NO:2376 to SEQ ID NO:2352, and those that comprise at least a first coding region that comprises an amino acid sequence that is at least about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, or about 94% identical to the amino
30 acid sequence of any one of SEQ ID NO:2376 to SEQ ID NO:2352, and even those

sequences that comprise at least a first coding region that comprises an amino acid sequence that is at least about 95%, about 96%, about 97%, about 98%, or about 99% identical to the amino acid sequence of any one of SEQ ID NO:2376 to SEQ ID NO:2352.

Exemplary peptides of the present invention may be of any suitable length,
5 depending upon the particular application thereof, and encompass those peptides that are about 10, about 15, about 20, about 25, about 30, about 35, about 40, about 45, about 50, about 55, about 60, about 65, about 70, about 75, about 80, about 85, about 90, about 95, or about 100 or so amino acids in length. Of course, the peptides of the invention may also encompass any intermediate lengths or integers within the stated ranges.

10 Exemplary polypeptides and proteins of the present invention may be of any suitable length, depending upon the particular application thereof, and encompass those polypeptides and proteins that are about 100, about 150, about 200, about 250, about 300, about 350, about 400, about 450, about 500, about 550, about 600, about 650, about 700, about 750, about 800, about 850, about 900, about 950, or about 1000 or so amino acids in
15 length, as well as longer polypeptides and proteins that are about 1000, about 1050, about 1100, about 1200, about 1250, about 1300, about 1350, about 1400, about 1450, about 1500, about 1600, about 1700, about 1800, about 1900, about 2000, about 2500, about 3000, about 3500, about 4000, about 4500, or even about 5000 or so amino acids in length. Of course, the polypeptides and proteins of the invention may also encompass any intermediate lengths
20 or integers within the stated ranges.

The peptides, polypeptides, proteins, antibodies, and antigen binding fragments of the present invention will preferably comprise at least a first isolated coding region that comprises a sequence of at least about 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95 or 100 contiguous amino acids from any one of SEQ ID NO:669 to SEQ ID NO:1380, SEQ ID
25 NO:1381 to SEQ ID NO:1859, SEQ ID NO:1860 to SEQ ID NO:2105, SEQ ID NO:2106 to SEQ ID NO:2375 or SEQ ID NO:2376 to SEQ ID NO:2532.

Furthermore, the polypeptides, proteins, antibodies, and antigen binding fragments of the present invention will even more preferably comprise at least a first isolated coding region that comprises a sequence of at least about 100, 110, 120, 130, 140, 150, 160, 170,
30 180, 190, or 200 contiguous amino acids from any one of SEQ ID NO:669 to SEQ ID

NO:1380, SEQ ID NO:1381 to SEQ ID NO:1859, SEQ ID NO:1860 to SEQ ID NO:2105, SEQ ID NO:2106 to SEQ ID NO:2375 or SEQ ID NO:2376 to SEQ ID NO:2532.

Likewise, the polypeptides, proteins, antibodies, and antigen binding fragments of the present invention may comprise at least a first isolated coding region that comprises a substantially longer sequence, such as for example, one of at least about 200, 220, 240, 260, 280, or 300 or more contiguous amino acids from any one of SEQ ID NO:669 to SEQ ID NO:1380, SEQ ID NO:1381 to SEQ ID NO:1859, SEQ ID NO:1860 to SEQ ID NO:2105, SEQ ID NO:2106 to SEQ ID NO:2375 or SEQ ID NO:2376 to SEQ ID NO:2532.

In illustrative embodiments, and particularly in those embodiments concerning methods and compositions relating to Hodgkin's lymphoma, the polypeptides of the invention comprise at least a first isolated coding region that (a) comprises, (b) consists essentially of, or (c) consists of, the amino acid sequence of SEQ ID NO:669, SEQ ID NO:670, SEQ ID NO:671, SEQ ID NO:672, SEQ ID NO:673, SEQ ID NO:674, SEQ ID NO:675, SEQ ID NO:676, SEQ ID NO:677, SEQ ID NO:678, SEQ ID NO:679, SEQ ID NO:680, SEQ ID NO:681, SEQ ID NO:682, SEQ ID NO:683, SEQ ID NO:684, SEQ ID NO:685, SEQ ID NO:686, SEQ ID NO:687, SEQ ID NO:688, SEQ ID NO:689, SEQ ID NO:690, SEQ ID NO:691, SEQ ID NO:692, SEQ ID NO:693, SEQ ID NO:694, SEQ ID NO:695, SEQ ID NO:696, SEQ ID NO:697, SEQ ID NO:698, SEQ ID NO:699, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703, SEQ ID NO:704, SEQ ID NO:705, SEQ ID NO:706, SEQ ID NO:707, SEQ ID NO:708, SEQ ID NO:709, SEQ ID NO:710, SEQ ID NO:711, SEQ ID NO:712, SEQ ID NO:713, SEQ ID NO:714, SEQ ID NO:715, SEQ ID NO:716, SEQ ID NO:717, SEQ ID NO:718, SEQ ID NO:719, SEQ ID NO:720, SEQ ID NO:721, SEQ ID NO:722, SEQ ID NO:723, SEQ ID NO:724, SEQ ID NO:725, SEQ ID NO:726, SEQ ID NO:727, SEQ ID NO:728, SEQ ID NO:729, SEQ ID NO:730, SEQ ID NO:731, SEQ ID NO:732, SEQ ID NO:733, SEQ ID NO:734, SEQ ID NO:735, SEQ ID NO:736, SEQ ID NO:737, SEQ ID NO:738, SEQ ID NO:739, SEQ ID NO:740, SEQ ID NO:741, SEQ ID NO:742, SEQ ID NO:743, SEQ ID NO:744, SEQ ID NO:745, SEQ ID NO:746, SEQ ID NO:747, SEQ ID NO:748, SEQ ID NO:749, SEQ ID NO:750, SEQ ID NO:751, SEQ ID NO:752, SEQ ID NO:753, SEQ ID NO:754, SEQ ID NO:755, SEQ ID NO:756, SEQ ID NO:757, SEQ ID NO:758, SEQ ID NO:759, SEQ ID

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In illustrative embodiments, and particularly in those embodiments concerning methods and compositions relating to B cell non-Hodgkin's lymphoma, the polypeptides of 30 the invention comprise at least a first isolated coding region that (a) comprises, (b) consists

essentially of, or (c) consists of, the amino acid sequence of SEQ ID NO:1860, SEQ ID NO:1861, SEQ ID NO:1862, SEQ ID NO:1863, SEQ ID NO:1864, SEQ ID NO:1865, SEQ ID NO:1866, SEQ ID NO:1867, SEQ ID NO:1868, SEQ ID NO:1869, SEQ ID NO:1870, SEQ ID NO:1871, SEQ ID NO:1872, SEQ ID NO:1873, SEQ ID NO:1874, SEQ ID NO:1875, SEQ ID NO:1876, SEQ ID NO:1877, SEQ ID NO:1878, SEQ ID NO:1879, SEQ ID NO:1880, SEQ ID NO:1881, SEQ ID NO:1882, SEQ ID NO:1883, SEQ ID NO:1884, SEQ ID NO:1885, SEQ ID NO:1886, SEQ ID NO:1887, SEQ ID NO:1888, SEQ ID NO:1889, SEQ ID NO:1890, SEQ ID NO:1891, SEQ ID NO:1892, SEQ ID NO:1893, SEQ ID NO:1894, SEQ ID NO:1895, SEQ ID NO:1896, SEQ ID NO:1897, SEQ ID NO:1898, SEQ ID NO:1899, SEQ ID NO:1900, SEQ ID NO:1901, SEQ ID NO:1902, SEQ ID NO:1903, SEQ ID NO:1904, SEQ ID NO:1905, SEQ ID NO:1906, SEQ ID NO:1907, SEQ ID NO:1908, SEQ ID NO:1909, SEQ ID NO:1910, SEQ ID NO:1911, SEQ ID NO:1912, SEQ ID NO:1913, SEQ ID NO:1914, SEQ ID NO:1915, SEQ ID NO:1916, SEQ ID NO:1917, SEQ ID NO:1918, SEQ ID NO:1919, SEQ ID NO:1920, SEQ ID NO:1921, SEQ ID NO:1922, SEQ ID NO:1923, SEQ ID NO:1924, SEQ ID NO:1925, SEQ ID NO:1926, SEQ ID NO:1927, SEQ ID NO:1928, SEQ ID NO:1929, SEQ ID NO:1930, SEQ ID NO:1931, SEQ ID NO:1932, SEQ ID NO:1933, SEQ ID NO:1934, SEQ ID NO:1935, SEQ ID NO:1936, SEQ ID NO:1937, SEQ ID NO:1938, SEQ ID NO:1939, SEQ ID NO:1940, SEQ ID NO:1941, SEQ ID NO:1942, SEQ ID NO:1943, SEQ ID NO:1944, SEQ ID NO:1945, SEQ ID NO:1946, SEQ ID NO:1947, SEQ ID NO:1948, SEQ ID NO:1949, SEQ ID NO:1950, SEQ ID NO:1951, SEQ ID NO:1952, SEQ ID NO:1953, SEQ ID NO:1954, SEQ ID NO:1955, SEQ ID NO:1956, SEQ ID NO:1957, SEQ ID NO:1958, SEQ ID NO:1959, SEQ ID NO:1960, SEQ ID NO:1961, SEQ ID NO:1962, SEQ ID NO:1963, SEQ ID NO:1964, SEQ ID NO:1965, SEQ ID NO:1966, SEQ ID NO:1967, SEQ ID NO:1968, SEQ ID NO:1969, SEQ ID NO:1970, SEQ ID NO:1971, SEQ ID NO:1972, SEQ ID NO:1973, SEQ ID NO:1974, SEQ ID NO:1975, SEQ ID NO:1976, SEQ ID NO:1977, SEQ ID NO:1978, SEQ ID NO:1979, SEQ ID NO:1980, SEQ ID NO:1981, SEQ ID NO:1982, SEQ ID NO:1983, SEQ ID NO:1984, SEQ ID NO:1985, SEQ ID NO:1986, SEQ ID NO:1987, SEQ ID NO:1988, SEQ ID NO:1989, SEQ ID NO:1990, SEQ ID NO:1991, SEQ ID NO:1992, SEQ ID NO:1993, SEQ ID NO:1994, SEQ ID NO:1995, SEQ ID NO:1996,

SEQ ID NO:1997, SEQ ID NO:1998, SEQ ID NO:1999, SEQ ID NO:2000, SEQ ID NO:2001, SEQ ID NO:2002, SEQ ID NO:2003, SEQ ID NO:2004, SEQ ID NO:2005, SEQ ID NO:2006, SEQ ID NO:2007, SEQ ID NO:2008, SEQ ID NO:2009, SEQ ID NO:2010, SEQ ID NO:2011, SEQ ID NO:2012, SEQ ID NO:2013, SEQ ID NO:2014, SEQ ID NO:2015, SEQ ID NO:2016, SEQ ID NO:2017, SEQ ID NO:2018, SEQ ID NO:2019, SEQ ID NO:2020, SEQ ID NO:2021, SEQ ID NO:2022, SEQ ID NO:2023, SEQ ID NO:2024, SEQ ID NO:2025, SEQ ID NO:2026, SEQ ID NO:2027, SEQ ID NO:2028, SEQ ID NO:2029, SEQ ID NO:2030, SEQ ID NO:2031, SEQ ID NO:2032, SEQ ID NO:2033, SEQ ID NO:2034, SEQ ID NO:2035, SEQ ID NO:2036, SEQ ID NO:2037, SEQ ID NO:2038, SEQ ID NO:2039, SEQ ID NO:2040, SEQ ID NO:2041, SEQ ID NO:2042, SEQ ID NO:2043, SEQ ID NO:2044, SEQ ID NO:2045, SEQ ID NO:2046, SEQ ID NO:2047, SEQ ID NO:2048, SEQ ID NO:2049, SEQ ID NO:2050, SEQ ID NO:2051, SEQ ID NO:2052, SEQ ID NO:2053, SEQ ID NO:2054, SEQ ID NO:2055, SEQ ID NO:2056, SEQ ID NO:2057, SEQ ID NO:2058, SEQ ID NO:2059, SEQ ID NO:2060, SEQ ID NO:2061, SEQ ID NO:2062, SEQ ID NO:2063, SEQ ID NO:2064, SEQ ID NO:2065, SEQ ID NO:2066, SEQ ID NO:2067, SEQ ID NO:2068, SEQ ID NO:2069, SEQ ID NO:2070, SEQ ID NO:2071, SEQ ID NO:2072, SEQ ID NO:2073, SEQ ID NO:2074, SEQ ID NO:2075, SEQ ID NO:2076, SEQ ID NO:2077, SEQ ID NO:2078, SEQ ID NO:2079, SEQ ID NO:2080, SEQ ID NO:2081, SEQ ID NO:2082, SEQ ID NO:2083, SEQ ID NO:2084, SEQ ID NO:2085, SEQ ID NO:2086, SEQ ID NO:2087, SEQ ID NO:2088, SEQ ID NO:2089, SEQ ID NO:2090, SEQ ID NO:2091, SEQ ID NO:2092, SEQ ID NO:2093, SEQ ID NO:2094, SEQ ID NO:2095, SEQ ID NO:2096, SEQ ID NO:2097, SEQ ID NO:2098, SEQ ID NO:2099, SEQ ID NO:2100, SEQ ID NO:2101, SEQ ID NO:2102, SEQ ID NO:2103, SEQ ID NO:2104, or SEQ ID NO:2105.

Further, in a variety of illustrative embodiments, and particularly in those embodiments concerning methods and compositions relating to T cell non-Hodgkin's lymphoma, the polypeptides of the invention comprise at least a first isolated coding region that (a) comprises, (b) consists essentially of, or (c) consists of, the amino acid sequence of SEQ ID NO:2106, SEQ ID NO:2107, SEQ ID NO:2108, SEQ ID NO:2109, SEQ ID NO:2110, SEQ ID NO:2111, SEQ ID NO:2112, SEQ ID NO:2113, SEQ ID NO:2114, SEQ

ID NO:2115, SEQ ID NO:2116, SEQ ID NO:2117, SEQ ID NO:2118, SEQ ID NO:2119,
SEQ ID NO:2120, SEQ ID NO:2121, SEQ ID NO:2122, SEQ ID NO:2123, SEQ ID
NO:2124, SEQ ID NO:2125, SEQ ID NO:2126, SEQ ID NO:2127, SEQ ID NO:2128, SEQ
ID NO:2129, SEQ ID NO:2130, SEQ ID NO:2131, SEQ ID NO:2132, SEQ ID NO:2133,
5 SEQ ID NO:2134, SEQ ID NO:2135, SEQ ID NO:2136, SEQ ID NO:2137, SEQ ID
NO:2138, SEQ ID NO:2139, SEQ ID NO:2140, SEQ ID NO:2141, SEQ ID NO:2142, SEQ
ID NO:2143, SEQ ID NO:2144, SEQ ID NO:2145, SEQ ID NO:2146, SEQ ID NO:2147,
SEQ ID NO:2148, SEQ ID NO:2149, SEQ ID NO:2150, SEQ ID NO:2151, SEQ ID
NO:2152, SEQ ID NO:2153, SEQ ID NO:2154, SEQ ID NO:2155, SEQ ID NO:2156, SEQ
10 ID NO:2157, SEQ ID NO:2158, SEQ ID NO:2159, SEQ ID NO:2160, SEQ ID NO:2161,
SEQ ID NO:2162, SEQ ID NO:2163, SEQ ID NO:2164, SEQ ID NO:2165, SEQ ID
NO:2166, SEQ ID NO:2167, SEQ ID NO:2168, SEQ ID NO:2169, SEQ ID NO:2170, SEQ
ID NO:2171, SEQ ID NO:2172, SEQ ID NO:2173, SEQ ID NO:2174, SEQ ID NO:2175,
SEQ ID NO:2176, SEQ ID NO:2177, SEQ ID NO:2178, SEQ ID NO:2179, SEQ ID
15 NO:2180, SEQ ID NO:2181, SEQ ID NO:2182, SEQ ID NO:2183, SEQ ID NO:2184, SEQ
ID NO:2185, SEQ ID NO:2186, SEQ ID NO:2187, SEQ ID NO:2188, SEQ ID NO:2189,
SEQ ID NO:2190, SEQ ID NO:2191, SEQ ID NO:2192, SEQ ID NO:2193, SEQ ID
NO:2194, SEQ ID NO:2195, SEQ ID NO:2196, SEQ ID NO:2197, SEQ ID NO:2198, SEQ
ID NO:2199, SEQ ID NO:2200, SEQ ID NO:2201, SEQ ID NO:2202, SEQ ID NO:2203,
20 SEQ ID NO:2204, SEQ ID NO:2205, SEQ ID NO:2206, SEQ ID NO:2207, SEQ ID
NO:2208, SEQ ID NO:2209, SEQ ID NO:2210, SEQ ID NO:2211, SEQ ID NO:2212, SEQ
ID NO:2213, SEQ ID NO:2214, SEQ ID NO:2215, SEQ ID NO:2216, SEQ ID NO:2217,
SEQ ID NO:2218, SEQ ID NO:2219, SEQ ID NO:2220, SEQ ID NO:2221, SEQ ID
NO:2222, SEQ ID NO:2223, SEQ ID NO:2224, SEQ ID NO:2225, SEQ ID NO:2226, SEQ
25 ID NO:2227, SEQ ID NO:2228, SEQ ID NO:2229, SEQ ID NO:2230, SEQ ID NO:2231,
SEQ ID NO:2232, SEQ ID NO:2233, SEQ ID NO:2234, SEQ ID NO:2235, SEQ ID
NO:2236, SEQ ID NO:2237, SEQ ID NO:2238, SEQ ID NO:2239, SEQ ID NO:2240, SEQ
ID NO:2241, SEQ ID NO:2242, SEQ ID NO:2243, SEQ ID NO:2244, SEQ ID NO:2245,
SEQ ID NO:2246, SEQ ID NO:2247, SEQ ID NO:2248, SEQ ID NO:2249, SEQ ID
30 NO:2250, SEQ ID NO:2251, SEQ ID NO:2252, SEQ ID NO:2253, SEQ ID NO:2254, SEQ

ID NO:2255, SEQ ID NO:2256, SEQ ID NO:2257, SEQ ID NO:2258, SEQ ID NO:2259,
SEQ ID NO:2260, SEQ ID NO:2261, SEQ ID NO:2262, SEQ ID NO:2263, SEQ ID
NO:2264, SEQ ID NO:2265, SEQ ID NO:2266, SEQ ID NO:2267, SEQ ID NO:2268, SEQ
ID NO:2269, SEQ ID NO:2270, SEQ ID NO:2271, SEQ ID NO:2272, SEQ ID NO:2273,
5 SEQ ID NO:2274, SEQ ID NO:2275, SEQ ID NO:2276, SEQ ID NO:2277, SEQ ID
NO:2278, SEQ ID NO:2279, SEQ ID NO:2280, SEQ ID NO:2281, SEQ ID NO:2282, SEQ
ID NO:2283, SEQ ID NO:2284, SEQ ID NO:2285, SEQ ID NO:2286, SEQ ID NO:2287,
SEQ ID NO:2288, SEQ ID NO:2289, SEQ ID NO:2290, SEQ ID NO:2291, SEQ ID
NO:2292, SEQ ID NO:2293, SEQ ID NO:2294, SEQ ID NO:2295, SEQ ID NO:2296, SEQ
10 ID NO:2297, SEQ ID NO:2298, SEQ ID NO:2299, SEQ ID NO:2300, SEQ ID NO:2301,
SEQ ID NO:2302, SEQ ID NO:2303, SEQ ID NO:2304, SEQ ID NO:2305, SEQ ID
NO:2306, SEQ ID NO:2307, SEQ ID NO:2308, SEQ ID NO:2309, SEQ ID NO:2310, SEQ
ID NO:2311, SEQ ID NO:2312, SEQ ID NO:2313, SEQ ID NO:2314, SEQ ID NO:2315,
SEQ ID NO:2316, SEQ ID NO:2317, SEQ ID NO:2318, SEQ ID NO:2319, SEQ ID
15 NO:2320, SEQ ID NO:2321, SEQ ID NO:2322, SEQ ID NO:2323, SEQ ID NO:2324, SEQ
ID NO:2325, SEQ ID NO:2326, SEQ ID NO:2327, SEQ ID NO:2328, SEQ ID NO:2329,
SEQ ID NO:2330, SEQ ID NO:2331, SEQ ID NO:2332, SEQ ID NO:2333, SEQ ID
NO:2334, SEQ ID NO:2335, SEQ ID NO:2336, SEQ ID NO:2337, SEQ ID NO:2338, SEQ
ID NO:2339, SEQ ID NO:2340, SEQ ID NO:2341, SEQ ID NO:2342, SEQ ID NO:2343,
20 SEQ ID NO:2344, SEQ ID NO:2345, SEQ ID NO:2346, SEQ ID NO:2347, SEQ ID
NO:2348, SEQ ID NO:2349, SEQ ID NO:2350, SEQ ID NO:2351, SEQ ID NO:2352, SEQ
ID NO:2353, SEQ ID NO:2354, SEQ ID NO:2355, SEQ ID NO:2356, SEQ ID NO:2357,
SEQ ID NO:2358, SEQ ID NO:2359, SEQ ID NO:2360, SEQ ID NO:2361, SEQ ID
NO:2362, SEQ ID NO:2363, SEQ ID NO:2364, SEQ ID NO:2365, SEQ ID NO:2366, SEQ
25 ID NO:2367, SEQ ID NO:2368, SEQ ID NO:2369, SEQ ID NO:2370, SEQ ID NO:2371,
SEQ ID NO:2372, SEQ ID NO:2373, SEQ ID NO:2374, or SEQ ID NO:2375.

In additional illustrative embodiments, and particularly in those embodiments
concerning methods and compositions relating to lymphoma, the polypeptides of the
invention comprise at least a first isolated coding region that (a) comprises, (b) consists
30 essentially of, or (c) consists of, the amino acid sequence of SEQ ID NO:2376, SEQ ID

NO:2377, SEQ ID NO:2378, SEQ ID NO:2379, SEQ ID NO:2380, SEQ ID NO:2381, SEQ
ID NO:2382, SEQ ID NO:2383, SEQ ID NO:2384, SEQ ID NO:2385, SEQ ID NO:2386,
SEQ ID NO:2387, SEQ ID NO:2388, SEQ ID NO:2389, SEQ ID NO:2390, SEQ ID
NO:2391, SEQ ID NO:2392, SEQ ID NO:2393, SEQ ID NO:2394, SEQ ID NO:2395, SEQ
5 ID NO:2396, SEQ ID NO:2397, SEQ ID NO:2398, SEQ ID NO:2399, SEQ ID NO:2400,
SEQ ID NO:2401, SEQ ID NO:2402, SEQ ID NO:2403, SEQ ID NO:2404, SEQ ID
NO:2405, SEQ ID NO:2406, SEQ ID NO:2407, SEQ ID NO:2408, SEQ ID NO:2409, SEQ
ID NO:2410, SEQ ID NO:2411, SEQ ID NO:2412, SEQ ID NO:2413, SEQ ID NO:2414,
SEQ ID NO:2415, SEQ ID NO:2416, SEQ ID NO:2417, SEQ ID NO:2418, SEQ ID
10 NO:2419, SEQ ID NO:2420, SEQ ID NO:2421, SEQ ID NO:2422, SEQ ID NO:2423, SEQ
ID NO:2424, SEQ ID NO:2425, SEQ ID NO:2426, SEQ ID NO:2427, SEQ ID NO:2428,
SEQ ID NO:2429, SEQ ID NO:2430, SEQ ID NO:2431, SEQ ID NO:2432, SEQ ID
NO:2433, SEQ ID NO:2434, SEQ ID NO:2435, SEQ ID NO:2436, SEQ ID NO:2437, SEQ
ID NO:2438, SEQ ID NO:2439, SEQ ID NO:2440, SEQ ID NO:2441, SEQ ID NO:2442,
15 SEQ ID NO:2443, SEQ ID NO:2444, SEQ ID NO:2445, SEQ ID NO:2446, SEQ ID
NO:2447, SEQ ID NO:2448, SEQ ID NO:2449, SEQ ID NO:2450, SEQ ID NO:2451, SEQ
ID NO:2452, SEQ ID NO:2453, SEQ ID NO:2454, SEQ ID NO:2455, SEQ ID NO:2456,
SEQ ID NO:2457, SEQ ID NO:2458, SEQ ID NO:2459, SEQ ID NO:2460, SEQ ID
NO:2461, SEQ ID NO:2462, SEQ ID NO:2463, SEQ ID NO:2464, SEQ ID NO:2465, SEQ
20 ID NO:2466, SEQ ID NO:2467, SEQ ID NO:2468, SEQ ID NO:2469, SEQ ID NO:2470,
SEQ ID NO:2471, SEQ ID NO:2472, SEQ ID NO:2473, SEQ ID NO:2474, SEQ ID
NO:2475, SEQ ID NO:2476, SEQ ID NO:2477, SEQ ID NO:2478, SEQ ID NO:2479, SEQ
ID NO:2480, SEQ ID NO:2481, SEQ ID NO:2482, SEQ ID NO:2483, SEQ ID NO:2484,
SEQ ID NO:2485, SEQ ID NO:2486, SEQ ID NO:2487, SEQ ID NO:2488, SEQ ID
25 NO:2489, SEQ ID NO:2490, SEQ ID NO:2491, SEQ ID NO:2492, SEQ ID NO:2493, SEQ
ID NO:2494, SEQ ID NO:2495, SEQ ID NO:2496, SEQ ID NO:2497, SEQ ID NO:2498,
SEQ ID NO:2499, SEQ ID NO:2500, SEQ ID NO:2501, SEQ ID NO:2502, SEQ ID
NO:2503, SEQ ID NO:2504, SEQ ID NO:2505, SEQ ID NO:2506, SEQ ID NO:2507, SEQ
ID NO:2508, SEQ ID NO:2509, SEQ ID NO:2510, SEQ ID NO:2511, SEQ ID NO:2512,
30 SEQ ID NO:2513, SEQ ID NO:2514, SEQ ID NO:2515, SEQ ID NO:2516, SEQ ID

NO:2517, SEQ ID NO:2518, SEQ ID NO:2519, SEQ ID NO:2520, SEQ ID NO:2521, SEQ ID NO:2522, SEQ ID NO:2523, SEQ ID NO:2524, SEQ ID NO:2525, SEQ ID NO:2526, SEQ ID NO:2527, SEQ ID NO:2528, SEQ ID NO:2529, SEQ ID NO:2530, SEQ ID NO:2531, or SEQ ID NO:2532.

5 The polypeptides and proteins of the invention preferably comprise at least a first isolated coding region comprising an amino acid sequence that is encoded by at least a first nucleic acid segment that comprises an at least 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 contiguous nucleotide sequence of any one of SEQ ID NO:1 to SEQ ID NO:668.

 The polypeptides and proteins of the invention may also preferably comprise one or
10 more coding regions that comprise an amino acid sequence encoded by at least a first nucleic acid segment that comprises an at least about 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40 contiguous nucleotide sequence of any one of SEQ ID NO:1 to SEQ ID NO:668. The polypeptides and proteins of the invention may also preferably comprise one or more coding regions that comprise an amino acid sequence encoded by at least a first nucleic acid segment
15 that comprises an at least about 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 contiguous nucleotide sequence of any one of SEQ ID NO:1 to SEQ ID NO:668. The polypeptides and proteins of the invention may also preferably comprise one or more coding regions that comprise an amino acid sequence encoded by at least a first nucleic acid segment that comprises an at
least about 51, 52, 53, 54, 55, 56, 57, 58, 59, or 60 contiguous nucleotide sequence of any
20 one of SEQ ID NO:1 to SEQ ID NO:668. The polypeptides and proteins of the invention may also preferably comprise one or more coding regions that comprise an amino acid sequence encoded by at least a first nucleic acid segment that comprises an at least about 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100 contiguous nucleotide sequence of
25 any one of SEQ ID NO:1 to SEQ ID NO:668.

 Likewise, the polypeptides and proteins of the invention may also preferably comprise one or more coding regions that comprise an amino acid sequence encoded by at least a first nucleic acid segment that comprises an at least about 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 240, 260, 280, 300, 320, 340, 360, 380, 400, 420, 440, 460,

480, or 500 contiguous nucleotide sequence, even up to and including the entire sequence or the substantially entire sequence of any one of SEQ ID NO:1 to SEQ ID NO:668.

In a second important embodiment, there is provided a composition comprising at least a first isolated polynucleotide that comprises a nucleic acid sequence that is at least
5 about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, or about 99% identical to the nucleic acid sequence of any one of SEQ ID NO:1 to SEQ ID NO:668. Exemplary preferred sequences are those that comprise a nucleic acid sequence that is at least about 85%, about 86%, about
10 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, or about 94% identical to the nucleic acid sequence of any one of SEQ ID NO:1 to SEQ ID NO:668, with those sequences that comprise at least a nucleic acid sequence that is at least about 95%, about 96%, about 97%, about 98%, or about 99% identical to the nucleic acid sequence of any one of SEQ ID NO:1 to SEQ ID NO:668 being examples of particularly preferred
15 sequences in the practice of the present invention.

In embodiments that relate particularly to compositions and methods for the detection, diagnosis, prognosis, prophylaxis, treatment, and therapy of Hodgkin's lymphoma exemplary preferred polynucleotide compositions include those compositions that comprise at least a first isolated nucleic acid segment that comprises a sequence that is at least about
20 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, or about 99% identical to the nucleic acid sequence of any one of SEQ ID NO:1 to SEQ ID NO:278 and SEQ ID NO:667 to SEQ ID NO:668, and those that comprise at least a first isolated nucleic acid segment that comprises a
25 sequence that is at least about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, or about 94% identical to the nucleic acid sequence of any one of SEQ ID NO:1 to SEQ ID NO:278 and SEQ ID NO:667 to SEQ ID NO:668, and even those sequences that comprise at least a first isolated nucleic acid segment that comprises a sequence that is at least about 95%, about 96%, about 97%, about 98%, or about
30 99% identical to the nucleic acid sequence of any one of SEQ ID NO:1 to SEQ ID NO:278

and SEQ ID NO:667 to SEQ ID NO:668. Such polynucleotides will preferably comprise one or more isolated coding region, each of which may (a) comprise, (b) consist essentially of, or (c) consist of, the nucleic acid sequence of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID

NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, SEQ ID NO:242, SEQ ID NO:243, SEQ ID NO:244, SEQ ID NO:245, SEQ ID NO:246, SEQ ID NO:247, SEQ ID NO:248, SEQ ID NO:249, SEQ ID NO:250, SEQ ID NO:251, SEQ ID NO:252, SEQ ID NO:253, SEQ ID NO:254, SEQ ID NO:255, SEQ ID NO:256, SEQ ID NO:257, SEQ ID NO:258, SEQ ID NO:259, SEQ ID NO:260, SEQ ID NO:261, SEQ ID NO:262, SEQ ID NO:263, SEQ ID NO:264, SEQ ID NO:265, SEQ ID NO:266, SEQ ID NO:267, SEQ ID NO:268, SEQ ID NO:269, SEQ ID NO:270, SEQ ID NO:271, SEQ ID NO:272, SEQ ID NO:273, SEQ ID NO:274, SEQ ID NO:275, SEQ ID NO:276, SEQ ID NO:277, or SEQ ID NO:278.

In embodiments that relate particularly to compositions and methods for the detection, diagnosis, prognosis, prophylaxis, treatment, and therapy of follicular lymphoma, exemplary preferred polynucleotide compositions include those compositions that comprise

at least a first isolated nucleic acid segment that comprises a sequence that is at least about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, or about 99% identical to the nucleic acid sequence of any one of SEQ ID NO:279 to SEQ ID NO:436, and those that comprise at least a first isolated nucleic acid segment that comprises a sequence that is at least about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, or about 94% identical to the nucleic acid sequence of any one of SEQ ID NO:279 to SEQ ID NO:436, and even those sequences that comprise at least a first isolated nucleic acid segment that comprises a sequence that is at least about 95%, about 96%, about 97%, about 98%, or about 99% identical to the nucleic acid sequence of any one of SEQ ID NO:279 to SEQ ID NO:436. Such polynucleotides will preferably comprise one or more isolated coding region, each of which may (a) comprise, (b) consist essentially of, or (c) consist of, the nucleic acid sequence of SEQ ID NO:279, SEQ ID NO:280, SEQ ID NO:281, SEQ ID NO:282, SEQ ID NO:283, SEQ ID NO:284, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:287, SEQ ID NO:288, SEQ ID NO:289, SEQ ID NO:290, SEQ ID NO:291, SEQ ID NO:292, SEQ ID NO:293, SEQ ID NO:294, SEQ ID NO:295, SEQ ID NO:296, SEQ ID NO:297, SEQ ID NO:298, SEQ ID NO:299, SEQ ID NO:300, SEQ ID NO:301, SEQ ID NO:302, SEQ ID NO:303, SEQ ID NO:304, SEQ ID NO:305, SEQ ID NO:306, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:309, SEQ ID NO:310, SEQ ID NO:311, SEQ ID NO:312, SEQ ID NO:313, SEQ ID NO:314, SEQ ID NO:315, SEQ ID NO:316, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:319, SEQ ID NO:320, SEQ ID NO:321, SEQ ID NO:322, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:325, SEQ ID NO:326, SEQ ID NO:327, SEQ ID NO:328, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:331, SEQ ID NO:332, SEQ ID NO:333, SEQ ID NO:334, SEQ ID NO:335, SEQ ID NO:336, SEQ ID NO:337, SEQ ID NO:338, SEQ ID NO:339, SEQ ID NO:340, SEQ ID NO:341, SEQ ID NO:342, SEQ ID NO:343, SEQ ID NO:344, SEQ ID NO:345, SEQ ID NO:346, SEQ ID NO:347, SEQ ID NO:348, SEQ ID NO:349, SEQ ID NO:350, SEQ ID NO:351, SEQ ID NO:352, SEQ ID NO:353, SEQ ID NO:354, SEQ ID NO:355, SEQ ID NO:356, SEQ ID NO:357, SEQ ID NO:358, SEQ ID NO:359, SEQ ID NO:360, SEQ ID NO:361, SEQ ID NO:362, SEQ ID

NO:363, SEQ ID NO:364, SEQ ID NO:365, SEQ ID NO:366, SEQ ID NO:367, SEQ ID NO:368, SEQ ID NO:369, SEQ ID NO:370, SEQ ID NO:371, SEQ ID NO:372, SEQ ID NO:373, SEQ ID NO:374, SEQ ID NO:375, SEQ ID NO:376, SEQ ID NO:377, SEQ ID NO:378, SEQ ID NO:379, SEQ ID NO:380, SEQ ID NO:381, SEQ ID NO:382, SEQ ID NO:383, SEQ ID NO:384, SEQ ID NO:385, SEQ ID NO:386, SEQ ID NO:387, SEQ ID NO:388, SEQ ID NO:389, SEQ ID NO:390, SEQ ID NO:391, SEQ ID NO:392, SEQ ID NO:393, SEQ ID NO:394, SEQ ID NO:395, SEQ ID NO:396, SEQ ID NO:397, SEQ ID NO:398, SEQ ID NO:399, SEQ ID NO:400, SEQ ID NO:401, SEQ ID NO:402, SEQ ID NO:403, SEQ ID NO:404, SEQ ID NO:405, SEQ ID NO:406, SEQ ID NO:407, SEQ ID NO:408, SEQ ID NO:409, SEQ ID NO:410, SEQ ID NO:411, SEQ ID NO:412, SEQ ID NO:413, SEQ ID NO:414, SEQ ID NO:415, SEQ ID NO:416, SEQ ID NO:417, SEQ ID NO:418, SEQ ID NO:419, SEQ ID NO:420, SEQ ID NO:421, SEQ ID NO:422, SEQ ID NO:423, SEQ ID NO:424, SEQ ID NO:425, SEQ ID NO:426, SEQ ID NO:427, SEQ ID NO:428, SEQ ID NO:429, SEQ ID NO:430, SEQ ID NO:431, SEQ ID NO:432, SEQ ID NO:433, SEQ ID NO:434, SEQ ID NO:435, or SEQ ID NO:436.

In embodiments that relate particularly to compositions and methods for the detection, diagnosis, prognosis, prophylaxis, treatment, and therapy of B cell non-Hodgkin's lymphoma, exemplary preferred polynucleotide compositions include those compositions that comprise at least a first isolated nucleic acid segment that comprises a sequence that is at least about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, or about 99% identical to the nucleic acid sequence of any one of SEQ ID NO:437 to SEQ ID NO:528 and SEQ ID NO:665 to SEQ ID NO:668, and those that comprise at least a first isolated nucleic acid segment that comprises a sequence that is at least about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, or about 94% identical to the nucleic acid sequence of any one of SEQ ID NO:437 to SEQ ID NO:528 and SEQ ID NO:665 to SEQ ID NO:668, and even those sequences that comprise at least a first isolated nucleic acid segment that comprises a sequence that is at least about 95%, about 96%, about 97%, about 98%, or about 99% identical to the nucleic acid sequence of any one of SEQ ID NO:437 to

SEQ ID NO:528 and SEQ ID NO:665 to SEQ ID NO:668. Such polynucleotides will preferably comprise one or more isolated coding region, each of which may (a) comprise, (b) consist essentially of, or (c) consist of, the nucleic acid sequence of SEQ ID NO:437, SEQ ID NO:438, SEQ ID NO:439, SEQ ID NO:440, SEQ ID NO:441, SEQ ID NO:442, SEQ ID NO:443, SEQ ID NO:444, SEQ ID NO:445, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:449, SEQ ID NO:450, SEQ ID NO:451, SEQ ID NO:452, SEQ ID NO:453, SEQ ID NO:454, SEQ ID NO:455, SEQ ID NO:456, SEQ ID NO:457, SEQ ID NO:458, SEQ ID NO:459, SEQ ID NO:460, SEQ ID NO:461, SEQ ID NO:462, SEQ ID NO:463, SEQ ID NO:464, SEQ ID NO:465, SEQ ID NO:466, SEQ ID NO:467, SEQ ID NO:468, SEQ ID NO:469, SEQ ID NO:470, SEQ ID NO:471, SEQ ID NO:472, SEQ ID NO:473, SEQ ID NO:474, SEQ ID NO:475, SEQ ID NO:476, SEQ ID NO:477, SEQ ID NO:478, SEQ ID NO:479, SEQ ID NO:480, SEQ ID NO:481, SEQ ID NO:482, SEQ ID NO:483, SEQ ID NO:484, SEQ ID NO:485, SEQ ID NO:486, SEQ ID NO:487, SEQ ID NO:488, SEQ ID NO:489, SEQ ID NO:490, SEQ ID NO:491, SEQ ID NO:492, SEQ ID NO:493, SEQ ID NO:494, SEQ ID NO:495, SEQ ID NO:496, SEQ ID NO:497, SEQ ID NO:498, SEQ ID NO:499, SEQ ID NO:500, SEQ ID NO:501, SEQ ID NO:502, SEQ ID NO:503, SEQ ID NO:504, SEQ ID NO:505, SEQ ID NO:506, SEQ ID NO:507, SEQ ID NO:508, SEQ ID NO:509, SEQ ID NO:510, SEQ ID NO:511, SEQ ID NO:512, SEQ ID NO:513, SEQ ID NO:514, SEQ ID NO:515, SEQ ID NO:516, SEQ ID NO:517, SEQ ID NO:518, SEQ ID NO:519, SEQ ID NO:520, SEQ ID NO:521, SEQ ID NO:522, SEQ ID NO:523, SEQ ID NO:524, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, or SEQ ID NO:528.

In embodiments that relate particularly to compositions and methods for the detection, diagnosis, prognosis, prophylaxis, treatment, and therapy of T cell non-Hodgkin's lymphoma, exemplary preferred polynucleotide compositions include those compositions that comprise at least a first isolated nucleic acid segment that comprises a sequence that is at least about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, or about 99% identical to the nucleic acid sequence of any one of SEQ ID NO:529 to SEQ ID NO:610 and SEQ ID NO:665 or

SEQ ID NO:666, and those that comprise at least a first isolated nucleic acid segment that comprises a sequence that is at least about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, or about 94% identical to the nucleic acid sequence of any one of SEQ ID NO:529 to SEQ ID NO:610 and SEQ ID NO:665 or

5 SEQ ID NO:666, and even those sequences that comprise at least a first isolated nucleic acid segment that comprises a sequence that is at least about 95%, about 96%, about 97%, about 98%, or about 99% identical to the nucleic acid sequence of any one of SEQ ID NO:529 to SEQ ID NO:610 and SEQ ID NO:665 or SEQ ID NO:666. Such polynucleotides will preferably comprise one or more isolated coding region, each of which may (a) comprise, (b)

10 consist essentially of, or (c) consist of, the nucleic acid sequence of SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:540, SEQ ID NO:541, SEQ ID NO:542, SEQ ID NO:543, SEQ ID NO:544, SEQ ID NO:545, SEQ ID NO:546, SEQ ID NO:547, SEQ ID NO:548, SEQ ID NO:549, SEQ ID

15 NO:550, SEQ ID NO:551, SEQ ID NO:552, SEQ ID NO:553, SEQ ID NO:554, SEQ ID NO:555, SEQ ID NO:556, SEQ ID NO:557, SEQ ID NO:558, SEQ ID NO:559, SEQ ID NO:560, SEQ ID NO:561, SEQ ID NO:562, SEQ ID NO:563, SEQ ID NO:564, SEQ ID NO:565, SEQ ID NO:566, SEQ ID NO:567, SEQ ID NO:568, SEQ ID NO:569, SEQ ID NO:570, SEQ ID NO:571, SEQ ID NO:572, SEQ ID NO:573, SEQ ID NO:574, SEQ ID

20 NO:575, SEQ ID NO:576, SEQ ID NO:577, SEQ ID NO:578, SEQ ID NO:579, SEQ ID NO:580, SEQ ID NO:581, SEQ ID NO:582, SEQ ID NO:583, SEQ ID NO:584, SEQ ID NO:585, SEQ ID NO:586, SEQ ID NO:587, SEQ ID NO:588, SEQ ID NO:589, SEQ ID NO:590, SEQ ID NO:591, SEQ ID NO:592, SEQ ID NO:593, SEQ ID NO:594, SEQ ID NO:595, SEQ ID NO:596, SEQ ID NO:597, SEQ ID NO:598, SEQ ID NO:599, SEQ ID

25 NO:600, SEQ ID NO:601, SEQ ID NO:602, SEQ ID NO:603, SEQ ID NO:604, SEQ ID NO:605, SEQ ID NO:606, SEQ ID NO:607, SEQ ID NO:608, SEQ ID NO:609, or SEQ ID NO:610.

In embodiments that relate particularly to compositions and methods for the detection, diagnosis, prognosis, prophylaxis, treatment, and therapy of lymphoma, exemplary

30 preferred polynucleotide compositions include those compositions that comprise at least a

first isolated nucleic acid segment that comprises a sequence that is at least about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, or about 99% identical to the nucleic acid sequence of any one of SEQ ID NO:611 to SEQ ID NO:664, and those that comprise at least a first isolated nucleic acid segment that comprises a sequence that is at least about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, or about 94% identical to the nucleic acid sequence of any one of SEQ ID NO:611 to SEQ ID NO:664, and even those sequences that comprise at least a first isolated nucleic acid segment that comprises a sequence that is at least about 95%, about 96%, about 97%, about 98%, or about 99% identical to the nucleic acid sequence of any one of SEQ ID NO:611 to SEQ ID NO:664. Such polynucleotides will preferably comprise one or more isolated coding region, each of which may (a) comprise, (b) consist essentially of, or (c) consist of, the nucleic acid sequence of SEQ ID NO:611, SEQ ID NO:612, SEQ ID NO:613, SEQ ID NO:614, SEQ ID NO:615, SEQ ID NO:616, SEQ ID NO:617, SEQ ID NO:618, SEQ ID NO:619, SEQ ID NO:620, SEQ ID NO:621, SEQ ID NO:622, SEQ ID NO:623, SEQ ID NO:624, SEQ ID NO:625, SEQ ID NO:626, SEQ ID NO:627, SEQ ID NO:628, SEQ ID NO:629, SEQ ID NO:630, SEQ ID NO:631, SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:634, SEQ ID NO:635, SEQ ID NO:636, SEQ ID NO:637, SEQ ID NO:638, SEQ ID NO:639, SEQ ID NO:640, SEQ ID NO:641, SEQ ID NO:642, SEQ ID NO:643, SEQ ID NO:644, SEQ ID NO:645, SEQ ID NO:646, SEQ ID NO:647, SEQ ID NO:648, SEQ ID NO:649, SEQ ID NO:650, SEQ ID NO:651, SEQ ID NO:652, SEQ ID NO:653, SEQ ID NO:654, SEQ ID NO:655, SEQ ID NO:656, SEQ ID NO:657, SEQ ID NO:658, SEQ ID NO:659, SEQ ID NO:660, SEQ ID NO:661, SEQ ID NO:662, SEQ ID NO:663, or SEQ ID NO:664.

In embodiments that relate particularly to compositions and methods for the detection, diagnosis, prognosis, prophylaxis, treatment, and therapy of chronic lymphocytic leukemia, exemplary preferred polynucleotide compositions include those compositions that comprise at least a first isolated nucleic acid segment that comprises a sequence that is at least about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about

94%, about 95%, about 96%, about 97%, about 98%, or about 99% identical to the nucleic acid sequence of SEQ ID NO:665 or SEQ ID NO:666, and those that comprise at least a first isolated nucleic acid segment that comprises a sequence that is at least about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, or about 94% identical to the nucleic acid sequence of SEQ ID NO:665 or SEQ ID NO:666, and even those sequences that comprise at least a first isolated nucleic acid segment that comprises a sequence that is at least about 95%, about 96%, about 97%, about 98%, or about 99% identical to the nucleic acid sequence of SEQ ID NO:665 or SEQ ID NO:666.

Exemplary polynucleotides of the present invention may be of any suitable length, depending upon the particular application thereof, and encompass those polynucleotides that (a) are at least about, or (b) comprise at least a first isolated nucleic acid segment that is at least about 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 120, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 320, 340, 360, 380, 400, 420, 440, 460, 480, 500, 520, 540, 560, 580, 600, 625, 650, 675, 700, 750, 800, 850, 900, 950, or 1000 or so nucleic acids in length, as well as longer polynucleotides that (a) are at least about, or (b) comprise at least a first isolated nucleic acid segment that is at least about 1000, 1025, 1050, 1075, 1100, 1150, 1200, 1250, 1300, 1350, 1400, 1450, 1500, 1550, 1600, 1650, 1700, 1750, 1800, 1850, 1900, 1950, 2000, 2100, 2200, 2300, 2400, 2500, 2600, 2700, 2800, 2900, or 3000 or so nucleic acids in length, as well as substantially larger polynucleotides that (a) are at least about, or (b) comprise at least a first isolated nucleic acid segment that is at least about 3500, 4000, 4500, 5000, 5500, 6000, 6500, 7000, 7500, 8000, 8500, 9000, 9500 or 10,000 so nucleic acids in length. Of course, the polynucleotides and nucleic acid segments of the invention may also encompass any intermediate lengths or integers within the stated ranges.

The compositions of the present invention may comprise a single polypeptide or polynucleotide, or alternatively, may comprise two or more such hematological malignancy compounds, such as for example, two or more polypeptides, two or more polynucleotides, or even combinations of one or more peptides or polypeptides, along with one or more polynucleotides. When two or more polypeptides are contemplated for particular applications, the second and/or third and/or fourth, *etc.* isolated peptides and/or polypeptides

will preferably comprise at least one isolated coding region that comprises an amino acid sequence that is at least about 91%, 93%, 95%, 97%, or 99% identical to the amino acid sequence of any one of SEQ ID NO:669 to SEQ ID NO:2532. Alternatively, the polynucleotides of the invention may comprise one or more coding regions that encode a first
5 fusion protein or peptide, such as an adjuvant-coding region fused in correct reading frame to one or more of the disclosed hematological malignancy peptides or polypeptides. Alternatively, the fusion protein may comprise a hematological malignancy polypeptide or peptide fused, in correct reading frame, to a detectable protein or peptide, or to an immunostimulant protein or peptide, or other such construct. Fusion proteins such as these
10 are particularly useful in those embodiments relating to diagnosis, detection, and therapy of one or more of the hematological malignancies as discussed herein.

The invention also provides a composition comprising at least a first hybridoma cell line that produces a monoclonal antibody having immunospecificity for one or more of the peptides or polypeptides as disclosed herein, or at least a first monoclonal antibody, or an
15 antigen-binding fragment thereof, that has immunospecificity for such a peptide or polypeptide. The antigen binding fragments may comprise a light chain variable region, a heavy-chain variable region, a Fab fragment, a F(ab)₂ fragment, an Fv fragment, an scFv fragment, or an antigen-binding fragment of such an antibody.

The invention also provides a composition comprising at least a first isolated
20 antigen-presenting cell that expresses a peptide or polypeptide as disclosed herein, or a plurality of isolated T cells that specifically react with such a peptide or polypeptide. Such pluralities of isolated T cells may be stimulated or expanded by contacting the T cells with one or more peptides or polypeptides as described herein. The T cells may be cloned prior to expansion, and may be obtained from bone marrow, a bone marrow fraction, peripheral
25 blood, or a peripheral blood fraction from a healthy mammal, or from a mammal that is afflicted with at least a first hematological malignancy such as leukemia or lymphoma.

As described above, the isolated coding regions within the polypeptides of the invention may be on the order of from 25 to about 1000 amino acids in length, or alternatively, may be on the order of from 50 to about 900 amino acids in length, from 75 to

about 800 amino acids in length, from 100 to about 700 amino acids in length, or from 125 to about 600 amino acids in length, or any other such suitable range.

The isolated nucleic acid segments that encode such isolated coding regions may be on the order of from 50 to about 10,000 nucleotides in length, from 150 to about 8000
5 nucleotides in length, from 250 to about 6000 nucleotides in length, from 350 to about 4000 nucleotides in length, or from 450 to about 2000 nucleotides in length, or any other such suitable range.

The nucleic acid segment may be operably positioned under the control of at least a first heterologous, recombinant promoter, such as a tissue-specific, cell-specific, inducible, or
10 otherwise regulated promoter. Such promoters may be further controlled or regulated by the presence of one or more additional enhancers or regulatory regions depending upon the particular cell type in which expression of the polynucleotide is desired. The polynucleotides and nucleic acid segments of the invention may also be comprised within a vector, such as a plasmid, or viral vector. The polypeptides and polynucleotides of the invention may also be
15 comprised within a host cell, such as a recombinant host cell, or a human host cell such as a blood or bone marrow cell.

The polynucleotides of the invention may comprise at least a first isolated nucleic acid segment is operably attached, in frame, to at least a second isolated nucleic acid segment, such that the polynucleotide encodes a fusion protein in which the first peptide or
20 polypeptide is linked to the second peptide or polypeptide.

The polypeptides of the present invention may comprise a contiguous amino acid coding region of any suitable length, such as for example, those of about 2000, about 1900, about 1850, about 1800, about 1750, about 1700, about 1650, about 1600, about 1550, about 1500, about 1450, about 1400, about 1350, about 1300, about 1250, about 1200, about 1150,
25 about 1100 amino acids, or about 1000 or so amino acids in length. Likewise, the polypeptides and peptides of the present invention may comprise slightly shorter contiguous amino acid coding regions, such as for example, those of about 950, about 900, about 850, about 800, about 750, about 700, about 650, about 600, about 550, about 500, about 450, about 400, about 350, about 300, about 250, about 200, about 150, or even about 100 amino
30 acids or so in length.

In similar fashion, the polypeptides and peptides of the present invention may comprise even smaller contiguous amino acid coding regions, such as for example, those of about 95, about 90, about 85, about 80, about 75, about 70, about 65, about 60, about 55, about 50, about 45, about 40, about 35, about 30, about 25, about 20, or even about 15 amino acids or so in length.

In all such embodiments, those peptides and polypeptides having intermediate lengths including all integers within the preferred ranges (*e.g.*, those peptides and polypeptides that comprise at least a first coding region of at least about 94, about 93, about 92, about 91, about 89, about 88, about 87, about 86, about 84, about 83, about 82, about 81, about 79, about 78, about 77, about 76, about 74, about 73, about 72, about 71, about 69, about 68, about 67, about 66 or so amino acids in length, *etc.*) are all contemplated to fall within the scope of the present invention.

In particular embodiments, the peptides and polypeptides of the present invention may comprise at least a first coding region that comprises a sequence of at least about 9, or about 10, or about 11, or about 12, or about 13, or about 14, or about 15, or about 16, or about 17, or about 18, or about 19, or about 20, or about 21, or about 22, or about 23, or about 24, or about 25, or about 26, or about 27, or about 28, or about 29, or about 30, or about 31, or about 32, or about 33, or about 34, or about 35, or about 36, or about 37, or about 38, or about 39, or about 40, or about 41, or about 42, or about 43, or about 44, or about 45, or about 46, or about 47, or about 48, or about 49, or about 50 contiguous amino acids as disclosed in any one or more of SEQ ID NO:669 through SEQ ID NO:2532 herein.

In other embodiments, the peptides and polypeptides of the present invention may comprise at least a first coding region that comprises a sequence of at least about 51, or about 52, or about 53, or about 54, or about 55, or about 56, or about 57, or about 58, or about 59, or about 60, or about 61, or about 62, or about 63, or about 64, or about 65, or about 66, or about 67, or about 68, or about 69, or about 70, or about 71, or about 72, or about 73, or about 74, or about 75, or about 76, or about 77, or about 78, or about 79, or about 80, or about 81, or about 82, or about 83, or about 84, or about 85, or about 86, or about 87, or about 88, or about 89, or about 90, about 91, or about 92, or about 93, or about 94, or about

95, or about 96, or about 97, or about 98, or about 99, or 100 contiguous amino acids as disclosed in any one or more of SEQ ID NO:669 through SEQ ID NO:2532 herein.

In still other embodiments, the preferred peptides and polypeptides of the present invention comprise at least a first coding region that comprises a sequence of at least about
5 100, 125, 150, 175, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 525, 550, 575, 600, 625, 650, 675 or 700 or more contiguous amino acids as disclosed in any one or more of SEQ ID NO:669 through SEQ ID NO:2532 herein. The preferred peptides and polypeptides of the present invention may also comprise at least a first coding region that comprises a sequence of at least about 750, 775, 800, 825, 850, 875, 900, 925, 950, 975,
10 1000, 1025, 1050, 1075, 1100, 1125, 1150, 1175, 1200, 1225, 1250, 1275, 1300, 1325, 1350, 1375 or 1400 or more contiguous amino acids as disclosed in any one or more of SEQ ID NO:669 through SEQ ID NO:2532 herein. Likewise, in still other embodiments, the preferred peptides and polypeptides of the present invention comprise at least a first coding region that comprises a sequence of at least about 1500, 1525, 1550, 1575, 1600, 1625, 1650,
15 1675, 1700, 1725, 1750, 1775, 1800, 1825, 1850, 1875, 1900, 1925, 1950, 1975, or 2000 or more contiguous amino acids as disclosed in any one or more of SEQ ID NO:669 through SEQ ID NO:2532 herein.

The polypeptides of the invention typically will comprise at least a first contiguous amino acid sequence according to any one of SEQ ID NO:669 through SEQ ID NO:2532, but
20 may also, optionally comprise at least a second, at least a third, or even at least a fourth or greater contiguous amino acid sequence according to any one of SEQ ID NO:669 through SEQ ID NO:2532. A single polypeptide may contain only a single coding region, or alternatively, a single polypeptide may comprise a plurality of identical or distinctly different contiguous amino acid sequences in accordance with any one of SEQ ID NO:669 through
25 SEQ ID NO:2532. In fact, the polypeptide may comprise a plurality of the same contiguous amino acid sequences, or they may comprise one or more different contiguous amino acid sequences disclosed in SEQ ID NO:669 through SEQ ID NO:2532. For example, a single polypeptide can comprise a single contiguous amino acid sequence from one or more of SEQ ID NO:669 through SEQ ID NO:2532, or alternatively, may comprise two or more distinctly
30 different contiguous amino acid sequences from one or more of SEQ ID NO:669 through

SEQ ID NO:2532. In fact, the polypeptide may comprise 2, 3, 4, or even 5 distinct contiguous amino sequences as disclosed in any of SEQ ID NO:669 through SEQ ID NO:2532. Alternatively, a single polypeptide may comprise 2, 3, 4, or even 5 distinct coding regions. For example, a polypeptide may comprise at least a first coding region that comprises a first contiguous amino acid sequence as disclosed in any of SEQ ID NO:669 through SEQ ID NO:2532, and at least a second coding region that comprises a second contiguous amino acid sequence as disclosed in any of SEQ ID NO:669 through SEQ ID NO:2532. In contrast, a polypeptide may comprise at least a first coding region that comprises a first contiguous amino acid sequence as disclosed in any of SEQ ID NO:669 through SEQ ID NO:2532, and at least a second coding region that comprises a second distinctly different peptide or polypeptide, such as for example, an adjuvant or an immunostimulant peptide or polypeptide.

In such cases, the two coding regions may be separate on the same polypeptide, or the two coding regions may be operatively attached, each in the correct reading frame, such that a fusion polypeptide is produced, in which the first amino acid sequence of the first coding region is linked to the second amino acid sequence of the second coding region.

Throughout this disclosure, a phrase such as "a sequence as disclosed in SEQ ID NO:1 to SEQ ID NO:4" is intended to encompass any and all contiguous sequences disclosed by any one of these sequence identifiers. That is to say, "a sequence as disclosed in any of SEQ ID NO:1 through SEQ ID NO:4" means any sequence that is disclosed in any one of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, or SEQ ID NO:4. Likewise, "a sequence as disclosed in any of SEQ ID NOs:25 to 37" means any sequence that is disclosed in any one of SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, or SEQ ID NO:37, and so forth.

Likewise, "at least a first sequence from any one of SEQ ID NO:55 to SEQ ID NO:62" is intended to refer to a first sequence that is disclosed in any one of SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, or SEQ ID NO:62.

It will also be understood that the kits, and compositions of the present invention comprise in an overall and general sense at least one or more particular polynucleotides, polypeptides, and peptides that comprise one or more contiguous sequence regions from one or more of the nucleic acid sequences disclosed herein in SEQ ID NO:1 through SEQ ID NO:668 or from one or more of the amino acid sequences disclosed herein in SEQ ID NO:669 through SEQ ID NO:2532, and that such peptide, polypeptide and polynucleotide compositions may be used in one or more of the particular methods and uses disclosed herein for the diagnosis, detection, prophylaxis, and therapy of one or more hematological cancers, and in particular, lymphomas of a variety of specific types. It will also be understood to the skilled artisan having benefit of the teachings of the present Specification, that the peptide and polypeptide compositions may be used to generate a T cell or an immune response in an animal, and that such compositions may also be administered to an animal from which immunospecific antibodies and antigen binding fragments may be isolated or identified that specifically bind to such peptides or polypeptides. Such an artisan will also recognize that the polynucleotides identified by the present disclosure may be used to produce such peptides, polypeptides, antibodies, and antigen binding fragments, by recombinant protein production methodologies that are also within the capability of the skilled artisan having benefit of the specific amino acid and nucleic acid sequences provided herein.

Likewise, it will be understood by a skilled artisan in the field, that one or more of the disclosed compositions may used in one or more diagnostic or detection methodologies to identify certain antibodies, peptides, polynucleotides, or polypeptides in a biological sample, in a host cell, or even within the body or tissues of an animal. It will be understood by a skilled artisan in the field, that one or more of the disclosed nucleic acid or amino acid compositions may used in the preparation or manufacture of one or more medicaments for use in the diagnosis, detection, prognosis, prophylaxis, or therapy of one or more hematological malignancies in an animal, and particularly those malignant conditions disclosed and claimed herein.

It will also be readily apparent to those of skill in the art, that the methods, kits, and uses, of the present invention preferably employ one or more of the compounds and/or compositions disclosed herein that comprise one or more contiguous nucleotide sequences as

may be presented in SEQ ID NO:1 through SEQ ID NO:10 of the attached sequence listing, as well as those compounds and compositions that comprise one or more contiguous nucleotide sequences as may be presented in SEQ ID NO:21 through SEQ ID NO:30, SEQ ID NO:31 through SEQ ID NO:40, SEQ ID NO:41 through SEQ ID NO:50, SEQ ID NO:51 through SEQ ID NO:60, SEQ ID NO:61 through SEQ ID NO:70, SEQ ID NO:71 through SEQ ID NO:80, SEQ ID NO:81 through SEQ ID NO:90, SEQ ID NO:91 through SEQ ID NO:100, SEQ ID NO:101 through SEQ ID NO:110, SEQ ID NO:111 through SEQ ID NO:120, SEQ ID NO:121 through SEQ ID NO:130, SEQ ID NO:131 through SEQ ID NO:140, SEQ ID NO:141 through SEQ ID NO:150, SEQ ID NO:151 through SEQ ID NO:160, SEQ ID NO:161 through SEQ ID NO:170, SEQ ID NO:171 through SEQ ID NO:180, SEQ ID NO:181 through SEQ ID NO:190, SEQ ID NO:191 through SEQ ID NO:200, SEQ ID NO:201 through SEQ ID NO:210, SEQ ID NO:211 through SEQ ID NO:220, SEQ ID NO:221 through SEQ ID NO:230, SEQ ID NO:231 through SEQ ID NO:240, SEQ ID NO:241 through SEQ ID NO:250, SEQ ID NO:251 through SEQ ID NO:260, SEQ ID NO:261 through SEQ ID NO:270, SEQ ID NO:271 through SEQ ID NO:280, SEQ ID NO:281 through SEQ ID NO:290, SEQ ID NO:291 through SEQ ID NO:300, SEQ ID NO:301 through SEQ ID NO:310, SEQ ID NO:311 through SEQ ID NO:320, SEQ ID NO:321 through SEQ ID NO:330, SEQ ID NO:331 through SEQ ID NO:340, SEQ ID NO:341 through SEQ ID NO:350, SEQ ID NO:351 through SEQ ID NO:360, SEQ ID NO:361 through SEQ ID NO:370, SEQ ID NO:371 through SEQ ID NO:380, SEQ ID NO:381 through SEQ ID NO:390, SEQ ID NO:391 through SEQ ID NO:400, SEQ ID NO:401 through SEQ ID NO:410, SEQ ID NO:411 through SEQ ID NO:420, SEQ ID NO:421 through SEQ ID NO:430, SEQ ID NO:431 through SEQ ID NO:440, SEQ ID NO:441 through SEQ ID NO:450, SEQ ID NO:451 through SEQ ID NO:460, SEQ ID NO:461 through SEQ ID NO:470, SEQ ID NO:471 through SEQ ID NO:480, SEQ ID NO:481 through SEQ ID NO:490, SEQ ID NO:491 through SEQ ID NO:500, SEQ ID NO:501 through SEQ ID NO:510, SEQ ID NO:511 through SEQ ID NO:520, SEQ ID NO:521 through SEQ ID NO:530, SEQ ID NO:531 through SEQ ID NO:540, SEQ ID NO:541 through SEQ ID NO:550, SEQ ID NO:551 through SEQ ID NO:560, SEQ ID NO:561 through SEQ ID NO:570, SEQ ID NO:571 through SEQ ID

NO:580, SEQ ID NO:581 through SEQ ID NO:590, SEQ ID NO:591 through SEQ ID NO:600, SEQ ID NO:601 through SEQ ID NO:610, SEQ ID NO:611 through SEQ ID NO:620, SEQ ID NO:621 through SEQ ID NO:630, SEQ ID NO:631 through SEQ ID NO:640, SEQ ID NO:641 through SEQ ID NO:650, SEQ ID NO:651 through SEQ ID NO:660, and SEQ ID NO:661 through SEQ ID NO:669.

Likewise, it will also be readily apparent to those of skill in the art, that the methods, kits, and uses, of the present invention may also employ one or more of the compounds and compositions disclosed herein that comprise one or more contiguous amino acid sequences as may be presented in SEQ ID NO:669 through SEQ ID NO:678 of the attached sequence listing, as well as those compounds and compositions that comprise one or more contiguous amino acid sequences as may be presented in SEQ ID NO:679 through SEQ ID NO:688, SEQ ID NO:689 through SEQ ID NO:698, SEQ ID NO:699 through SEQ ID NO:708, SEQ ID NO:709 through SEQ ID NO:718, SEQ ID NO:719 through SEQ ID NO:728, SEQ ID NO:729 through SEQ ID NO:738, SEQ ID NO:739 through SEQ ID NO:748, SEQ ID NO:749 through SEQ ID NO:758, SEQ ID NO:759 through SEQ ID NO:768, SEQ ID NO:769 through SEQ ID NO:778, SEQ ID NO:779 through SEQ ID NO:788, SEQ ID NO:789 through SEQ ID NO:798, SEQ ID NO:799 through SEQ ID NO:808, SEQ ID NO:809 through SEQ ID NO:818, SEQ ID NO:819 through SEQ ID NO:828, SEQ ID NO:829 through SEQ ID NO:838, SEQ ID NO:839 through SEQ ID NO:848, SEQ ID NO:849 through SEQ ID NO:858, SEQ ID NO:859 through SEQ ID NO:868, SEQ ID NO:869 through SEQ ID NO:878, SEQ ID NO:879 through SEQ ID NO:888, SEQ ID NO:889 through SEQ ID NO:898, SEQ ID NO:899 through SEQ ID NO:908, SEQ ID NO:909 through SEQ ID NO:918, SEQ ID NO:919 through SEQ ID NO:928, SEQ ID NO:929 through SEQ ID NO:938, SEQ ID NO:939 through SEQ ID NO:948, SEQ ID NO:949 through SEQ ID NO:958, SEQ ID NO:959 through SEQ ID NO:968, SEQ ID NO:969 through SEQ ID NO:978, SEQ ID NO:979 through SEQ ID NO:988, SEQ ID NO:989 through SEQ ID NO:998, SEQ ID NO:999 through SEQ ID NO:1008, SEQ ID NO:1009 through SEQ ID NO:1018, SEQ ID NO:1019 through SEQ ID NO:1028, SEQ ID NO:1029 through SEQ ID NO:1038, SEQ ID NO:1039 through SEQ ID NO:1048, SEQ ID NO:1049 through SEQ ID NO:1058, SEQ ID NO:1059 through SEQ ID NO:1068, SEQ ID

NO:1069 through SEQ ID NO:1078, SEQ ID NO:1079 through SEQ ID NO:1088, SEQ ID
NO:1089 through SEQ ID NO:1098, SEQ ID NO:1099 through SEQ ID NO:1108, SEQ ID
NO:1109 through SEQ ID NO:1118, SEQ ID NO:1119 through SEQ ID NO:1128, SEQ ID
NO:1129 through SEQ ID NO:1138, SEQ ID NO:1139 through SEQ ID NO:1148, SEQ ID
5 NO:1149 through SEQ ID NO:1158, SEQ ID NO:1159 through SEQ ID NO:1168, SEQ ID
NO:1169 through SEQ ID NO:1178, SEQ ID NO:1179 through SEQ ID NO:1188, SEQ ID
NO:1189 through SEQ ID NO:1198, SEQ ID NO:1199 through SEQ ID NO:1208, SEQ ID
NO:1209 through SEQ ID NO:1218, SEQ ID NO:1219 through SEQ ID NO:1228, SEQ ID
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NO:1489 through SEQ ID NO:1498, SEQ ID NO:1499 through SEQ ID NO:1508, SEQ ID
NO:1509 through SEQ ID NO:1518, SEQ ID NO:1519 through SEQ ID NO:1528, SEQ ID
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NO:1569 through SEQ ID NO:1578, SEQ ID NO:1579 through SEQ ID NO:1588, SEQ ID
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5 NO:1749 through SEQ ID NO:1758, SEQ ID NO:1759 through SEQ ID NO:1768, SEQ ID
NO:1769 through SEQ ID NO:1778, SEQ ID NO:1779 through SEQ ID NO:1788, SEQ ID
NO:1789 through SEQ ID NO:1798, SEQ ID NO:1799 through SEQ ID NO:1808, SEQ ID
NO:1809 through SEQ ID NO:1818, SEQ ID NO:1819 through SEQ ID NO:1828, SEQ ID
NO:1829 through SEQ ID NO:1838, SEQ ID NO:1839 through SEQ ID NO:1848, SEQ ID
10 NO:1849 through SEQ ID NO:1858, SEQ ID NO:1859 through SEQ ID NO:1868, SEQ ID
NO:1869 through SEQ ID NO:1878, SEQ ID NO:1879 through SEQ ID NO:1888, SEQ ID
NO:1889 through SEQ ID NO:1898, SEQ ID NO:1899 through SEQ ID NO:1908, SEQ ID
NO:1909 through SEQ ID NO:1918, SEQ ID NO:1919 through SEQ ID NO:1928, SEQ ID
NO:1929 through SEQ ID NO:1938, SEQ ID NO:1939 through SEQ ID NO:1948, SEQ ID
15 NO:1949 through SEQ ID NO:1958, SEQ ID NO:1959 through SEQ ID NO:1968, SEQ ID
NO:1969 through SEQ ID NO:1978, SEQ ID NO:1979 through SEQ ID NO:1988, SEQ ID
NO:1989 through SEQ ID NO:1998, SEQ ID NO:1999 through SEQ ID NO:2008, SEQ ID
NO:2009 through SEQ ID NO:2018, SEQ ID NO:2019 through SEQ ID NO:2028, SEQ ID
NO:2029 through SEQ ID NO:2038, SEQ ID NO:2039 through SEQ ID NO:2048, SEQ ID
20 NO:2049 through SEQ ID NO:2058, SEQ ID NO:2059 through SEQ ID NO:2068, SEQ ID
NO:2069 through SEQ ID NO:2078, SEQ ID NO:2079 through SEQ ID NO:2088, SEQ ID
NO:2089 through SEQ ID NO:2098, SEQ ID NO:2099 through SEQ ID NO:2108, SEQ ID
NO:2109 through SEQ ID NO:2118, SEQ ID NO:2119 through SEQ ID NO:2128, SEQ ID
NO:2129 through SEQ ID NO:2138, SEQ ID NO:2139 through SEQ ID NO:2148, SEQ ID
25 NO:2149 through SEQ ID NO:2158, SEQ ID NO:2159 through SEQ ID NO:2168, SEQ ID
NO:2169 through SEQ ID NO:2178, SEQ ID NO:2179 through SEQ ID NO:2188, SEQ ID
NO:2189 through SEQ ID NO:2198, SEQ ID NO:2199 through SEQ ID NO:2208, SEQ ID
NO:2209 through SEQ ID NO:2218, SEQ ID NO:2219 through SEQ ID NO:2228, SEQ ID
NO:2229 through SEQ ID NO:2238, SEQ ID NO:2239 through SEQ ID NO:2248, SEQ ID
30 NO:2249 through SEQ ID NO:2258, SEQ ID NO:2259 through SEQ ID NO:2268, SEQ ID

NO:2269 through SEQ ID NO:2278, SEQ ID NO:2279 through SEQ ID NO:2288, SEQ ID NO:2289 through SEQ ID NO:2298, SEQ ID NO:2299 through SEQ ID NO:2308, SEQ ID NO:2309 through SEQ ID NO:2318, SEQ ID NO:2319 through SEQ ID NO:2328, SEQ ID NO:2329 through SEQ ID NO:2338, SEQ ID NO:2339 through SEQ ID NO:2348, SEQ ID NO:2349 through SEQ ID NO:2358, SEQ ID NO:2359 through SEQ ID NO:2368, SEQ ID NO:2369 through SEQ ID NO:2378, SEQ ID NO:2379 through SEQ ID NO:2388, SEQ ID NO:2389 through SEQ ID NO:2398, SEQ ID NO:2399 through SEQ ID NO:2408, SEQ ID NO:2409 through SEQ ID NO:2418, SEQ ID NO:2419 through SEQ ID NO:2428, SEQ ID NO:2429 through SEQ ID NO:2438, SEQ ID NO:2439 through SEQ ID NO:2448, SEQ ID NO:2449 through SEQ ID NO:2458, SEQ ID NO:2459 through SEQ ID NO:2468, SEQ ID NO:2469 through SEQ ID NO:2478, SEQ ID NO:2479 through SEQ ID NO:2488, SEQ ID NO:2489 through SEQ ID NO:2498, SEQ ID NO:2499 through SEQ ID NO:2508, SEQ ID NO:2509 through SEQ ID NO:2518, SEQ ID NO:2519 through SEQ ID NO:2532 of the attached sequence listing.

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3. BRIEF DESCRIPTION OF THE DRAWINGS AND THE APPENDICES

The invention may be understood by reference to the following description taken in conjunction with the accompanying drawings, in which like reference numerals identify like elements, and in which:

20 **FIG. 1** illustrates a schematic outline of the microarray chip technology approach used to identify the cDNA targets of the present invention as described Section 5.1;

FIG. 2 illustrates a schematic outline of the general protocol for in vitro whole gene CD8 T cell priming procedure used to generate antigen-specific lines and to identify clones of interest;

25 **FIG. 3** illustrates a schematic outline of the general protocol for in vitro whole gene CD4 T cell priming procedure used to generate antigen-specific lines and to identify clones of interest;

FIG. 4 illustrates the results of Coronin 1A mRNA expression in lymphoma patients and normal tissues as determined by real-time PCR.

30 **FIG. 5** illustrates the results of TCL extended normal panel.

4. DESCRIPTION OF ILLUSTRATIVE EMBODIMENTS

In order that the invention herein described may be more fully understood, the following description of various illustrative embodiments is set forth.

The present invention is generally directed to compositions and methods for the immunotherapy and diagnosis of Hematological malignancies, such as leukemias and lymphomas of the Hodgkin's and non-Hodgkin's type.

4.1 METHODS OF NUCLEIC ACID DELIVERY AND DNA TRANSFECTION

In certain embodiments, it is contemplated that one or more RNA or DNA and/or substituted polynucleotide compositions disclosed herein will be used to transfect an appropriate host cell. Technology for introduction of RNAs and DNAs, and vectors comprising them into suitable host cells is well known to those of skill in the art. In particular, such polynucleotides may be used to genetically transform one or more host cells, when therapeutic administration of one or more active peptides, compounds or vaccines is achieved through the expression of one or more polynucleotide constructs that encode one or more therapeutic compounds of interest.

A variety of means for introducing polynucleotides and/or polypeptides into suitable target cells is known to those of skill in the art. For example, when polynucleotides are contemplated for delivery to cells, several non-viral methods for the transfer of expression constructs into cultured mammalian cells are available to the skilled artisan for his use. These include, for example, calcium phosphate precipitation (Graham and Van Der Eb, 1973; Chen and Okayama, 1987; Rippe *et al.*, 1990); DEAE-dextran precipitation (Gopal, 1985); electroporation (Wong and Neumann, 1982; Fromm *et al.*, 1985; Tur-Kaspa *et al.*, 1986; Potter *et al.*, 1984; Suzuki *et al.*, 1998; Vanbever *et al.*, 1998), direct microinjection (Capecchi, 1980; Harland and Weintraub, 1985), DNA-loaded liposomes (Nicolau and Sene, 1982; Fraley *et al.*, 1979; Takakura, 1998) and lipofectamine-DNA complexes, cell sonication (Fechheimer *et al.*, 1987), gene bombardment using high velocity microprojectiles (Yang *et al.*, 1990; Klein *et al.*, 1992), and receptor-mediated transfection (Curiel *et al.*, 1991; Wagner *et al.*, 1992; Wu and Wu, 1987; Wu and Wu, 1988). Some of these techniques may be successfully adapted for *in vivo* or *ex vivo* use.

A bacterial cell, a yeast cell, or an animal cell transformed with one or more of the disclosed expression vectors represent an important aspect of the present invention. Such transformed host cells are often desirable for use in the expression of the various DNA gene constructs disclosed herein. In some aspects of the invention, it is often desirable to modulate, regulate, or otherwise control the expression of the gene segments disclosed herein. Such methods are routine to those of skill in the molecular genetic arts. Typically, when increased or over-expression of a particular gene is desired, various manipulations may be employed for enhancing the expression of the messenger RNA, particularly by using an active promoter, and in particular, a tissue-specific promoter such as those disclosed herein, as well as by employing sequences, which enhance the stability of the messenger RNA in the particular transformed host cell.

Typically, the initiation and translational termination region will involve stop codon(s), a terminator region, and optionally, a polyadenylation signal. In the direction of transcription, namely in the 5' to 3' direction of the coding or sense sequence, the construct will involve the transcriptional regulatory region, if any, and the promoter, where the regulatory region may be either 5' or 3' of the promoter, the ribosomal binding site, the initiation codon, the structural gene having an open reading frame in phase with the initiation codon, the stop codon(s), the polyadenylation signal sequence, if any, and the terminator region. This sequence as a double strand may be used by itself for transformation of a microorganism or eukaryotic host, but will usually be included with a DNA sequence involving a marker, where the second DNA sequence may be joined to the expression construct during introduction of the DNA into the host.

Where no functional replication system is present, the construct will also preferably include a sequence of at least about 30 or about 40 or about 50 basepairs (bp) or so, preferably at least about 60, about 70, about 80, or about 90 to about 100 or so bp, and usually not more than about 500 to about 1000 or so bp of a sequence homologous with a sequence in the host. In this way, the probability of legitimate recombination is enhanced, so that the gene will be integrated into the host and stably maintained by the host. Desirably, the regulatory regions of the expression construct will be in close proximity to (and also operably positioned relative to) the selected therapeutic gene providing for complementation as well as the gene providing for

the competitive advantage. Therefore, in the event that the therapeutic gene is lost, the resulting organism will be likely to also lose the gene providing for the competitive advantage, so that it will be unable to compete in the environment with the gene retaining the intact construct.

The selected therapeutic gene can be introduced between the transcriptional and translational initiation region and the transcriptional and translational termination region, so as to be under the regulatory control of the initiation region. This construct may be included in a plasmid, which will include at least one replication system, but may include more than one, where one replication system is employed for cloning during the development of the plasmid and the second replication system is necessary for functioning in the ultimate host, in this case, a mammalian host cell. In addition, one or more markers may be present, which have been described previously. Where integration is desired, the plasmid will desirably include a sequence homologous with the host genome.

Genes or other nucleic acid segments, as disclosed herein, can be inserted into host cells using a variety of techniques that are well known in the art. Five general methods for delivering a nucleic segment into cells have been described: (1) chemical methods (Graham and VanDerEb, 1973); (2) physical methods such as microinjection (Capecchi, 1980), electroporation (U. S. Patent 5,472,869; Wong and Neumann, 1982; Fromm *et al.*, 1985), microprojectile bombardment (U. S. Patent 5,874,265, specifically incorporated herein by reference in its entirety), "gene gun" (Yang *et al.*, 1990); (3) viral vectors (Eglitis and Anderson, 1988); (4) receptor-mediated mechanisms (Curiel *et al.*, 1991; Wagner *et al.*, 1992); and (5) bacterial-mediated transformation.

4.2 HEMATOLOGICAL MALIGNANCY RELATED-SPECIFIC ANTIBODIES AND ANTIGEN-BINDING FRAGMENTS THEREOF

The present invention further provides antibodies and antigen-binding fragments thereof, that specifically bind to (or are immunospecific for) at least a first peptide or peptide variant as disclosed herein. As used herein, an antibody or an antigen-binding fragment is said to "specifically bind" to a peptide if it reacts at a detectable level (within, for example, an ELISA) with the peptide, and does not react detectably with unrelated peptides or proteins under similar conditions. As used herein, "binding" refers to a noncovalent association between two separate molecules such that a "complex" is formed. The ability to bind may be

evaluated by, for example, determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In the context of the present invention, in general, two compounds are said to "bind" when the binding constant for complex formation exceeds about 10^3 L/mol. The binding constant maybe determined using methods well known in the art.

Any agent that satisfies the above requirements may be a binding agent. In illustrative embodiments, a binding agent is an antibody or an antigen-binding fragment thereof. Such antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art (Harlow and Lane, 1988). In general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or *via* transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the peptide is initially injected into any of a wide variety of mammals (*e.g.*, mice, rats, rabbits, sheep or goats). In this step, the peptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short peptides, a superior immune response may be elicited if the peptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the peptide may then be purified from such antisera by, for example, affinity chromatography using the peptide coupled to a suitable solid support.

Monoclonal antibodies specific for the antigenic peptide of interest may be prepared, for example, using the technique of Kohler and Milstein (1976) and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.*, reactivity with the peptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the

spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks,
5 colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the peptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as
10 injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The peptides of this invention may be used in the purification process in, for example, an affinity chromatography
15 step.

Within certain embodiments, the use of antigen-binding fragments of antibodies may be preferred. Such fragments include Fab fragments, which may be prepared using standard techniques. Briefly, immunoglobulins may be purified from rabbit serum by affinity chromatography on Protein A bead columns (Harlow and Lane, 1988) and digested by papain
20 to yield Fab and Fc fragments. The Fab and Fc fragments may be separated by affinity chromatography on Protein A bead columns.

Monoclonal antibodies and fragments thereof may be coupled to one or more therapeutic agents. Suitable agents in this regard include radioactive tracers and chemotherapeutic agents, which may be used, for example, to purge autologous bone marrow *in vitro*). Representative therapeutic agents include radionuclides, differentiation inducers, drugs, toxins, and
25 derivatives thereof. Preferred radionuclides include ^{90}Y , ^{123}I , ^{125}I , ^{131}I , ^{186}Re , ^{188}Re , ^{211}At , and ^{212}Bi . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin,
30 and pokeweed antiviral protein. For diagnostic purposes, coupling of radioactive agents may

be used to facilitate tracing of metastases or to determine the location of hematological malignancy related-positive tumors.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, *via* a linker group). A direct reaction
5 between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

10 Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of
15 agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be affected, for example, through amino groups, carboxyl groups, and sulfhydryl groups
20 or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U. S. Patent No. 4,671,958.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group that is cleavable during or upon internalization into a cell. A number of different cleavable linker
25 groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (U. S. Patent No. 4,489,710), by irradiation of a photolabile bond (U. S. Patent No. 4,625,014), by hydrolysis of derivatized amino acid side chains (U. S. Patent No. 4,638,045), by serum complement-mediated hydrolysis (U. S. Patent No. 4,671,958), and acid-catalyzed hydrolysis
30 (U. S. Patent No. 4,569,789).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers that provide multiple sites for attachment can be used. Alternatively, a carrier can be used. A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (U. S. Patent No. 4,507,234), peptides and polysaccharides such as aminodextran (U. S. Patent No. 4,699,784). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (U. S. Patent No. 4,429,008 and U. S. Patent No. 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U. S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U. S. Patent No. 4,673,562 discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/ immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

Also provided herein are anti-idiotypic antibodies that mimic an immunogenic portion of hematological malignancy related. Such antibodies may be raised against an antibody, or an antigen-binding fragment thereof, that specifically binds to an immunogenic portion of hematological malignancy related, using well-known techniques. Anti-idiotypic antibodies that mimic an immunogenic portion of hematological malignancy related are those antibodies that bind to an antibody, or antigen-binding fragment thereof, that specifically binds to an immunogenic portion of hematological malignancy related, as described herein.

Irrespective of the source of the original hematological malignancy related peptide-specific antibody, the intact antibody, antibody multimers, or any one of a variety of functional, antigen-binding regions of the antibody may be used in the present invention. Exemplary functional regions include scFv, Fv, Fab', Fab and F(ab')₂ fragments of the hematological malignancy related peptide-specific antibodies. Techniques for preparing such constructs are well known to those in the art and are further exemplified herein.

The choice of antibody construct may be influenced by various factors. For example, prolonged half-life can result from the active readsorption of intact antibodies within the kidney, a property of the Fc piece of immunoglobulin. IgG based antibodies, therefore, are expected to exhibit slower blood clearance than their Fab' counterparts. However, Fab' fragment-based compositions will generally exhibit better tissue penetrating capability.

Antibody fragments can be obtained by proteolysis of the whole immunoglobulin by the non-specific thiol protease, papain. Papain digestion yields two identical antigen-binding fragments, termed "Fab fragments," each with a single antigen-binding site, and a residual "Fc fragment."

Papain should first be activated by reducing the sulphydryl group in the active site with cysteine, 2-mercaptoethanol or dithiothreitol. Heavy metals in the stock enzyme should be removed by chelation with EDTA (2 mM) to ensure maximum enzyme activity. Enzyme and substrate are normally mixed together in the ratio of 1:100 by weight. After incubation, the reaction can be stopped by irreversible alkylation of the thiol group with iodoacetamide or simply by dialysis. The completeness of the digestion should be monitored by SDS-PAGE and the various fractions separated by Protein A-Sepharose or ion exchange chromatography.

The usual procedure for preparation of F(ab')₂ fragments from IgG of rabbit and human origin is limited proteolysis by the enzyme pepsin. The conditions, 100x antibody excess wt./wt. in acetate buffer at pH 4.5, 37°C, suggest that antibody is cleaved at the C-terminal side of the inter-heavy-chain disulfide bond. Rates of digestion of mouse IgG may vary with subclass and it may be difficult to obtain high yields of active F(ab')₂ fragments without some undigested or completely degraded IgG. In particular, IgG_{2b} is highly susceptible to complete degradation. The other subclasses require different incubation conditions to produce optimal results, all of which is known in the art.

Pepsin treatment of intact antibodies yields an $F(ab')_2$ fragment that has two antigen-combining sites and is still capable of cross-linking antigen. Digestion of rat IgG by pepsin requires conditions including dialysis in 0.1 M acetate buffer, pH 4.5, and then incubation for four hrs with 1% wt./wt. pepsin; IgG₁ and IgG_{2a} digestion is improved if first dialyzed against
5 0.1 M formate buffer, pH 2.8, at 4°C, for 16 hrs followed by acetate buffer. IgG_{2b} gives more consistent results with incubation in staphylococcal V8 protease (3% wt./wt.) in 0.1 M sodium phosphate buffer, pH 7.8, for four hrs at 37°C.

A Fab fragment also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab' fragments differ from Fab fragments by the
10 addition of a few residues at the carboxyl terminus of the heavy chain CH1 domain including one or more cysteine(s) from the antibody hinge region. $F(ab')_2$ antibody fragments were originally produced as pairs of Fab' fragments that have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

The term "variable," as used herein in reference to antibodies, means that certain
15 portions of the variable domains differ extensively in sequence among antibodies, and are used in the binding and specificity of each particular antibody to its particular antigen. However, the variability is not evenly distributed throughout the variable domains of antibodies. It is concentrated in three segments termed "hypervariable regions," both in the light chain and the heavy chain variable domains.

20 The more highly conserved portions of variable domains are called the framework region (FR). The variable domains of native heavy and light chains each comprise four FRs (FR1, FR2, FR3 and FR4, respectively), largely adopting a β -sheet configuration, connected by three hypervariable regions, which form loops connecting, and in some cases, forming part of, the β -sheet structure.

25 The hypervariable regions in each chain are held together in close proximity by the FRs and, with the hypervariable regions from the other chain, contribute to the formation of the antigen-binding site of antibodies (Kabat *et al.*, 1991, specifically incorporated herein by reference). The constant domains are not involved directly in binding an antibody to an antigen, but exhibit various effector functions, such as participation of the antibody in antibody-
30 dependent cellular toxicity.

The term "hypervariable region," as used herein, refers to the amino acid residues of an antibody that are responsible for antigen-binding. The hypervariable region comprises amino acid residues from a "complementarity determining region" or "CDR" (*i.e.* residues 24-34 (L1), 50-56 (L2) and 89-97 (L3) in the light chain variable domain and 31-35 (H1), 50-56 (H2) and 95-102 (H3) in the heavy chain variable domain (Kabat *et al.*, 1991, specifically incorporated herein by reference) and/or those residues from a "hypervariable loop" (*i.e.*, residues 26-32 (L1), 50-52(L2) and 91-96 (L3) in the light chain variable domain and 26-32 (H1), 53-55 (H2) and 96-101 (H3) in the heavy chain variable domain). "Framework" or "FR" residues are those variable domain residues other than the hypervariable region residues as herein defined.

An "Fv" fragment is the minimum antibody fragment that contains a complete antigen-recognition and binding site. This region consists of a dimer of one heavy chain and one light chain variable domain in tight, con-covalent association. It is in this configuration that three hypervariable regions of each variable domain interact to define an antigen-binding site on the surface of the V_H - V_L dimer. Collectively, six hypervariable regions confer antigen-binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three hypervariable regions specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

"Single-chain Fv" or "sFv" antibody fragments comprise the V_H and V_L domains of antibody, wherein these domains are present in a single polypeptide chain. Generally, the Fv polypeptide further comprises a polypeptide linker between the V_H and V_L domains that enables the sFv to form the desired structure for antigen binding.

"Diabodies" are small antibody fragments with two antigen-binding sites, which fragments comprise a heavy chain variable domain (V_H) connected to a light chain variable domain (V_L) in the same polypeptide chain (V_H - V_L). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies are described in European Pat. Appl. No. EP 404,097 and Intl. Pat. Appl. Publ. No. WO 93/11161, each specifically incorporated herein by reference. "Linear antibodies", which can be bispecific or monospecific, comprise a pair of tandem Fd segments (V_H - C_H1 - V_H - C_H1) that

form a pair of antigen binding regions, as described in Zapata *et al.* (1995), specifically incorporated herein by reference.

Other types of variants are antibodies with improved biological properties relative to the parent antibody from which they are generated. Such variants, or second-generation
5 compounds, are typically substitutional variants involving one or more substituted hypervariable region residues of a parent antibody. A convenient way for generating such substitutional variants is affinity maturation using phage display.

In affinity maturation using phage display, several hypervariable region sites (*e.g.*, 6 to 7 sites) are mutated to generate all possible amino substitutions at each site. The antibody
10 variants thus generated are displayed in a monovalent fashion from filamentous phage particles as fusions to the gene III product of M13 packaged within each particle. The phage-displayed variants are then screened for their biological activity (*e.g.*, binding affinity) as herein disclosed. In order to identify candidate hypervariable region sites for modification, alanine-scanning mutagenesis can be performed on hypervariable region residues identified as contributing
15 significantly to antigen binding.

Alternatively, or in addition, the crystal structure of the antigen-antibody complex be delineated and analyzed to identify contact points between the antibody and target. Such contact residues and neighboring residues are candidates for substitution. Once such variants are generated, the panel of variants is subjected to screening, and antibodies with analogues but
20 different or even superior properties in one or more relevant assays are selected for further development.

In using a Fab' or antigen binding fragment of an antibody, with the attendant benefits on tissue penetration, one may derive additional advantages from modifying the fragment to increase its half-life. A variety of techniques may be employed, such as manipulation or
25 modification of the antibody molecule itself, and also conjugation to inert carriers. Any conjugation for the sole purpose of increasing half-life, rather than to deliver an agent to a target, should be approached carefully in that Fab' and other fragments are chosen to penetrate tissues. Nonetheless, conjugation to non-protein polymers, such PEG and the like, is contemplated.

Modifications other than conjugation are therefore based upon modifying the structure of the antibody fragment to render it more stable, and/or to reduce the rate of catabolism in the body. One mechanism for such modifications is the use of D-amino acids in place of L-amino acids. Those of ordinary skill in the art will understand that the introduction of such
5 modifications needs to be followed by rigorous testing of the resultant molecule to ensure that it still retains the desired biological properties. Further stabilizing modifications include the use of the addition of stabilizing moieties to either the N-terminal or the C-terminal, or both, which is generally used to prolong the half-life of biological molecules. By way of example only, one may wish to modify the termini by acylation or amination.

10 Moderate conjugation-type modifications for use with the present invention include incorporating a salvage receptor binding epitope into the antibody fragment. Techniques for achieving this include mutation of the appropriate region of the antibody fragment or incorporating the epitope as a peptide tag that is attached to the antibody fragment. Intl. Pat. Appl. Publ. No. WO 96/32478 is specifically incorporated herein by reference for the
15 purposes of further exemplifying such technology. Salvage receptor binding epitopes are typically regions of three or more amino acids from one or two loops of the Fc domain that are transferred to the analogous position on the antibody fragment. The salvage receptor-binding epitopes disclosed in Intl. Pat. Appl. Publ. No. WO 98/45331 are incorporated herein by reference for use with the present invention.

20 4.3 T CELL COMPOSITIONS SPECIFIC FOR HEMATOLOGICAL MALIGNANCY-RELATED PEPTIDES

Immunotherapeutic compositions may also, or alternatively, comprise T cells specific for hematological malignancy related. Such cells may generally be prepared *in vitro* or *ex*
25 *vivo*, using standard procedures. For example, T cells may be present within (or isolated from) bone marrow, peripheral blood or a fraction of bone marrow or peripheral blood of a mammal, such as a patient, using a commercially available cell separation system, such as the Isolex™ System, available from Nexell Therapeutics, Inc. (Irvine, CA; see also U. S. Patent No. 5,240,856; U. S. Patent No. 5,215,926; Intl. Pat. Appl. Publ. No. WO 89/06280;
30 Intl. Pat. Appl. Publ. No. WO 91/16116 and Intl. Pat. Appl. Publ. No. WO 92/07243).

Alternatively, T cells may be derived from related or unrelated humans, non-human mammals, cell lines or cultures.

T cells may be stimulated with hematological malignancy related peptide, polynucleotide encoding a hematological malignancy related peptide and/or an antigen-presenting cell (APC) that expresses a hematological malignancy related peptide. Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific for the hematological malignancy related peptide. Preferably, a hematological malignancy related peptide or polynucleotide is present within a delivery vehicle, such as a microsphere, to facilitate the generation of antigen-specific T cells. Briefly, T cells, which may be isolated from a patient or a related or unrelated donor by routine techniques (such as by Ficoll/Hypaque® density gradient centrifugation of peripheral blood lymphocytes), are incubated with hematological malignancy related peptide. For example, T cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with hematological malignancy related peptide (e.g., 5 to 25 µg/ml) or cells synthesizing a comparable amount of hematological malignancy related peptide. It may be desirable to incubate a separate aliquot of a T cell sample in the absence of hematological malignancy related peptide to serve as a control.

T cells are considered to be specific for a hematological malignancy related peptide if the T cells kill target cells coated with a hematological malignancy related peptide or expressing a gene encoding such a peptide. T cell specificity may be evaluated using any of a variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of more than two fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen *et al.* (1994). Alternatively, detection of the proliferation of T cells may be accomplished by a variety of known techniques. For example, T cell proliferation can be detected by measuring an increased rate of DNA synthesis (e.g., by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Other ways to detect T cell proliferation include measuring increases in interleukin-2 (IL-2) production, Ca²⁺ flux, or dye uptake, such as 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyl-tetrazolium. Alternatively,

synthesis of lymphokines (such as interferon-gamma) can be measured or the relative number of T cells that can respond to a hematological malignancy related peptide may be quantified. Contact with a hematological malignancy related peptide (200 ng/ml - 100 µg/ml, preferably 100 ng/ml - 25 µg/ml) for 3-7 days should result in at least a two-fold increase in proliferation of the T cells and/or contact as described above for 2-3 hrs should result in activation of the T cells, as measured using standard cytokine assays in which a two-fold increase in the level of cytokine release (*e.g.*, TNF or IFN-γ) is indicative of T cell activation (Coligan *et al.*, 1998). hematological malignancy related specific T cells may be expanded using standard techniques. Within preferred embodiments, the T cells are derived from a patient or a related or unrelated donor and are administered to the patient following stimulation and expansion.

T cells that have been activated in response to a hematological malignancy related peptide, polynucleotide or hematological malignancy related-expressing APC may be CD4⁺ and/or CD8⁺. Specific activation of CD4⁺ or CD8⁺ T cells may be detected in a variety of ways. Methods for detecting specific T cell activation include detecting the proliferation of T cells, the production of cytokines (*e.g.*, lymphokines), or the generation of cytolytic activity (*i.e.*, generation of cytotoxic T cells specific for hematological malignancy related). For CD4⁺ T cells, a preferred method for detecting specific T cell activation is the detection of the proliferation of T cells. For CD8⁺ T cells, a preferred method for detecting specific T cell activation is the detection of the generation of cytolytic activity.

For therapeutic purposes, CD4⁺ or CD8⁺ T cells that proliferate in response to the hematological malignancy related peptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be accomplished in a variety of ways. For example, the T cells can be re-exposed to hematological malignancy related peptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize a hematological malignancy related peptide. The addition of stimulator cells is preferred where generating CD8⁺ T cell responses. T cells can be grown to large numbers *in vitro* with retention of specificity in response to intermittent restimulation with hematological malignancy related peptide. Briefly, for the primary *in vitro* stimulation (IVS), large numbers of lymphocytes (*e.g.*,

greater than 4×10^7) may be placed in flasks with media containing human serum. hematological malignancy related peptide (*e.g.*, peptide at 10 $\mu\text{g/ml}$) may be added directly, along with tetanus toxoid (*e.g.*, 5 $\mu\text{g/ml}$). The flasks may then be incubated (*e.g.*, 37°C for 7 days). For a second IVS, T cells are then harvested and placed in new flasks with $2-3 \times 10^7$ irradiated peripheral blood mononuclear cells. hematological malignancy related peptide (*e.g.*, 10 $\mu\text{g/ml}$) is added directly. The flasks are incubated at 37°C for 7 days. On day 2 and day 4 after the second IVS, 2-5 units of interleukin-2 (IL-2) may be added. For a third IVS, the T cells may be placed in wells and stimulated with the individual's own EBV transformed B cells coated with the peptide. IL-2 may be added on days 2 and 4 of each cycle. As soon as the cells are shown to be specific cytotoxic T cells, they may be expanded using a 10-day stimulation cycle with higher IL-2 (20 units) on days 2, 4 and 6.

Alternatively, one or more T cells that proliferate in the presence of hematological malignancy related peptide can be expanded in number by cloning. Methods for cloning cells are well known in the art, and include limiting dilution. Responder T cells may be purified from the peripheral blood of sensitized patients by density gradient centrifugation and sheep red cell rosetting and established in culture by stimulating with the nominal antigen in the presence of irradiated autologous filler cells. In order to generate CD4⁺ T cell lines, hematological malignancy related peptide is used as the antigenic stimulus and autologous peripheral blood lymphocytes (PBL) or lymphoblastoid cell lines (LCL) immortalized by infection with Epstein Barr virus are used as antigen-presenting cells. In order to generate CD8⁺ T cell lines, autologous antigen-presenting cells transfected with an expression vector that produces hematological malignancy related peptide may be used as stimulator cells. Established T cell lines may be cloned 2-4 days following antigen stimulation by plating stimulated T cells at a frequency of 0.5 cells per well in 96-well flat-bottom plates with 1×10^6 irradiated PBL or LCL cells and recombinant interleukin-2 (rIL2) (50 U/ml). Wells with established clonal growth may be identified at approximately 2-3 weeks after initial plating and restimulated with appropriate antigen in the presence of autologous antigen-presenting cells, then subsequently expanded by the addition of low doses of rIL2 (10 U/ml) 2-3 days following antigen stimulation. T cell clones may be maintained in 24-well plates by periodic restimulation with antigen and rIL2 approximately

every two weeks. Cloned and/or expanded cells may be administered back to the patient as described, for example, by Chang *et al.*, (1996).

Within certain embodiments, allogeneic T-cells may be primed (*i.e.*, sensitized to hematological malignancy related) *in vivo* and/or *in vitro*. Such priming may be achieved by contacting T cells with a hematological malignancy related peptide, a polynucleotide encoding such a peptide or a cell producing such a peptide under conditions and for a time sufficient to permit the priming of T cells. In general, T cells are considered to be primed if, for example, contact with a hematological malignancy related peptide results in proliferation and/or activation of the T cells, as measured by standard proliferation, chromium release and/or cytokine release assays as described herein. A stimulation index of more than two fold increase in proliferation or lysis, and more than three fold increase in the level of cytokine, compared to negative controls indicates T-cell specificity. Cells primed *in vitro* may be employed, for example, within bone marrow transplantation or as donor lymphocyte infusion.

T cells specific for hematological malignancy related can kill cells that express hematological malignancy related protein. Introduction of genes encoding T-cell receptor (TCR) chains for hematological malignancy related are used as a means to quantitatively and qualitatively improve responses to hematological malignancy related bearing leukemia and cancer cells. Vaccines to increase the number of T cells that can react to hematological malignancy related positive cells are one method of targeting hematological malignancy related bearing cells. T cell therapy with T cells specific for hematological malignancy related is another method. An alternative method is to introduce the TCR chains specific for hematological malignancy related into T cells or other cells with lytic potential. In a suitable embodiment, the TCR alpha and beta chains are cloned out from a hematological malignancy related specific T cell line and used for adoptive T cell therapy, such as described in WO96/30516, incorporated herein by reference.

4.4 PHARMACEUTICAL COMPOSITIONS AND VACCINE FORMULATIONS

Within certain aspects, peptides, polynucleotides, antibodies and/or T cells may be incorporated into pharmaceutical compositions or immunogenic compositions (*i.e.*, vaccines). Alternatively, a pharmaceutical composition may comprise an antigen-presenting

cell (*e.g.*, a dendritic cell) transfected with a hematological malignancy related polynucleotide such that the antigen-presenting cell expresses a hematological malignancy related peptide. Pharmaceutical compositions comprise one or more such compounds or cells and a physiologically acceptable carrier or excipient. Vaccines may comprise one or more such compounds or cells and an immunostimulant, such as an adjuvant or a liposome (into which the compound is incorporated). An immunostimulant may be any substance that enhances or potentiates an immune response (antibody- and/or cell-mediated) to an exogenous antigen. Examples of immunostimulants include adjuvants, biodegradable microspheres (*e.g.*, polylactic galactide) and liposomes (into which the compound is incorporated) (U. S. Patent No. 4,235,877). Vaccine preparation is generally described in, for example, Powell and Newman (1995). Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, which may be biologically active or inactive. For example, one or more immunogenic portions of other tumor antigens may be present, either incorporated into a fusion peptide or as a separate compound, within the composition or vaccine.

Within certain embodiments, pharmaceutical compositions and vaccines are designed to elicit T cell responses specific for a hematological malignancy related peptide in a patient, such as a human. In general, T cell responses may be favored through the use of relatively short peptides (*e.g.*, comprising less than 23 consecutive amino acid residues of a native hematological malignancy related peptide, preferably 4-16 consecutive residues, more preferably 8-16 consecutive residues and still more preferably 8-10 consecutive residues). Alternatively, or in addition, a vaccine may comprise an immunostimulant that preferentially enhances a T cell response. In other words, the immunostimulant may enhance the level of a T cell response to a hematological malignancy related peptide by an amount that is proportionally greater than the amount by which an antibody response is enhanced. For example, when compared to a standard oil based adjuvant, such as CFA, an immunostimulant that preferentially enhances a T cell response may enhance a proliferative T cell response by at least two fold, a lytic response by at least 10%, and/or T cell activation by at least two fold compared to hematological malignancy related-negative control cell lines, while not detectably enhancing an antibody response. The amount by which a T cell or

antibody response to a hematological malignancy related peptide is enhanced may generally be determined using any representative technique known in the art, such as the techniques provided herein.

A pharmaceutical composition or vaccine may contain DNA encoding one or more of the peptides as described above, such that the peptide is generated *in situ*. As noted above, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacterial and viral expression systems and mammalian expression systems. Numerous gene delivery techniques are well known in the art (Rolland, 1998, and references cited therein). Appropriate nucleic acid expression systems contain the necessary DNA, cDNA or RNA sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the peptide on its cell surface or secretes such an epitope. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus (Fisher-Hoch *et al.*, 1989; Flexner *et al.*, 1989; Flexner *et al.*, 1990; U. S. Patent No. 4,603,112, U. S. Patent No. 4,769,330, U. S. Patent No. 5,017,487; Intl. Pat. Appl. Publ. No. WO 89/01973; U. S. Patent No. 4,777,127; Great Britain Patent No. GB 2,200,651; European Patent No. EP 0,345,242; Intl. Pat. Appl. Publ. No. WO 91/02805; Berkner, 1988; Rosenfeld *et al.*, 1991; Kolls *et al.*, 1994; Kass-Eisler *et al.*, 1993; Guzman *et al.*, 1993a; and Guzman *et al.*, 1993). Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in Ulmer *et al.* (1993) and reviewed by Cohen (1993). The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells. It will be apparent that a vaccine may comprise both a polynucleotide and a peptide component. Such vaccines may provide for an enhanced immune response.

As noted above, a pharmaceutical composition or vaccine may comprise an antigen-presenting cell that expresses a hematological malignancy related peptide. For therapeutic purposes, as described herein, the antigen-presenting cell is preferably an autologous

dendritic cell. Such cells may be prepared and transfected using standard techniques (Reeves *et al.*, 1996; Tuting *et al.*, 1998; and Nair *et al.*, 1998). Expression of a hematological malignancy related peptide on the surface of an antigen-presenting cell may be confirmed by *in vitro* stimulation and standard proliferation as well as chromium release assays, as described herein.

It will be apparent to those of ordinary skill in the art having the benefit of the present teachings that a vaccine may contain pharmaceutically acceptable salts of the polynucleotides and peptides provided herein. Such salts may be prepared from pharmaceutically acceptable non-toxic bases, including organic bases (*e.g.*, salts of primary, secondary and tertiary amines and basic amino acids) and inorganic bases (*e.g.*, sodium, potassium, lithium, ammonium, calcium and magnesium salts). The phrases "pharmaceutically or pharmacologically acceptable" refer to molecular entities and compositions that do not produce an adverse, allergic or other significant untoward reaction when administered to an animal, or a human, as appropriate. As used herein, "pharmaceutically acceptable carrier" includes any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents and the like. The use of such media and agents for pharmaceutical active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active ingredient, its use in the therapeutic compositions is contemplated. For human administration, preparations should meet sterility, pyrogenicity, and general safety and purity standards as required by the Food and Drug Administration Office of Biologics standards. Supplementary active ingredients can also be incorporated into the compositions.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous, intracranial, intraperitoneal, subcutaneous or intramuscular administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate,

may be employed. Biodegradable microspheres (*e.g.*, polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U. S. Patent Nos. 4,897,268; 5,075,109; 5,928,647; 5,811,128; 5,820,883; 5,853,763; 5,814,344 and 5,942,252. For
5 certain topical applications, formulation as a cream or lotion, using well-known components, is preferred.

Such compositions may also comprise buffers (*e.g.*, neutral buffered saline or phosphate buffered saline), carbohydrates (*e.g.*, glucose, mannose, sucrose or dextrans), mannitol, proteins, peptides or amino acids such as glycine, antioxidants, bacteriostats, chelating agents
10 such as EDTA or glutathione, adjuvants (*e.g.*, aluminum hydroxide), solutes that render the formulation isotonic, hypotonic or weakly hypertonic with the blood of a recipient, suspending agents, thickening agents and/or preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate, or formulated with one or more liposomes, microspheres, nanoparticles, or micronized delivery systems using well-known
15 technology.

Any of a variety of immunostimulants, such as adjuvants, may be employed in the preparation of vaccine compositions of this invention. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or
20 *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants are commercially available as, for example, alum-based adjuvants (*e.g.*, Alhydrogel, Rehydrigel, aluminum phosphate, Algamulin, aluminum hydroxide); oil based adjuvants (Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI), Specol, RIBI, TiterMax, Montanide ISA50 or Seppic MONTANIDE ISA 720); nonionic block copolymer-based adjuvants,
25 cytokines (*e.g.*, GM-CSF or Flt3-ligand); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and Quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or -
30 12, may also be used as adjuvants.

Hemocyanins and hemoerythrins may also be used in the invention. The use of hemocyanin from keyhole limpet (KLH) is particularly preferred, although other molluscan and arthropod hemocyanins and hemoerythrins may be employed. Various polysaccharide adjuvants may also be used. Polyamine varieties of polysaccharides are particularly preferred, such as chitin and chitosan, including deacetylated chitin.

A further preferred group of adjuvants are the muramyl dipeptide (MDP, N-acetylmuramyl-L-alanyl-D-isoglutamine) group of bacterial peptidoglycans. Derivatives of muramyl dipeptide, such as the amino acid derivative threonyl-MDP, and the fatty acid derivative MTPPE, are also contemplated.

U. S. Patent No. 4,950,645 describes a lipophilic disaccharide-tripeptide derivative of muramyl dipeptide that is proposed for use in artificial liposomes formed from phosphatidyl choline and phosphatidyl glycerol. It is said to be effective in activating human monocytes and destroying tumor cells, but is non-toxic in generally high doses. The compounds of U. S. Patent No. 4,950,645, and Intl. Pat. Appl. Publ. No. WO 91/16347 are also proposed for use in achieving particular aspects of the present invention.

BCG and BCG-cell wall skeleton (CWS) may also be used as adjuvants in the invention, with or without trehalose dimycolate. Trehalose dimycolate may be used itself. Azuma *et al.* (1988) show that trehalose dimycolate administration correlates with augmented resistance to influenza virus infection in mice. Trehalose dimycolate may be prepared as described in U. S. Patent No. 4,579,945.

Amphipathic and surface-active agents, *e.g.*, saponin and derivatives such as QS21 (Cambridge Biotech), form yet another group of preferred adjuvants for use with the immunogens of the present invention. Nonionic block copolymer surfactants (Rabinovich *et al.*, 1994; Hunter *et al.*, 1991) may also be employed. Oligonucleotides, as described by Yamamoto *et al.* (1988) are another useful group of adjuvants. Quil A and lentinen are also preferred adjuvants.

Superantigens are also contemplated for use as adjuvants in the present invention. "Superantigens" are generally bacterial products that stimulate a greater proportion of T lymphocytes than peptide antigens without a requirement for antigen processing (Mooney

et. al., 1994). Superantigens include *Staphylococcus* exoproteins, such as the α , β , γ and δ enterotoxins from *S. aureus* and *S. epidermidis*, and the α , β , γ and δ *E. coli* exotoxins.

Common *Staphylococcus* enterotoxins are known as staphylococcal enterotoxin A (SEA) and staphylococcal enterotoxin B (SEB), with enterotoxins through E (SEE) being
5 described (Rott *et. al.*, 1992). *Streptococcus pyogenes* B (SEB), *Clostridium perfringens* enterotoxin (Bowness *et. al.*, 1992), cytoplasmic membrane-associated protein (CAP) from *S. pyogenes* (Sato *et. al.*, 1994) and toxic shock syndrome toxin-1 (TSST-1) from *S. aureus* (Schwab *et. al.*, 1993) are further useful superantigens.

One group of adjuvants particularly preferred for use in the invention are the
10 detoxified endotoxins, such as the refined detoxified endotoxin of U. S. Patent No. 4,866,034. These refined detoxified endotoxins are effective in producing adjuvant responses in mammals.

The detoxified endotoxins may be combined with other adjuvants. Combination of detoxified endotoxins with trehalose dimycolate is contemplated, as described in U. S. Patent
15 No. 4,435,386. Combinations of detoxified endotoxins with trehalose dimycolate and endotoxic glycolipids is also contemplated (U. S. Patent No. 4,505,899), as is combination of detoxified endotoxins with cell wall skeleton (CWS) or CWS and trehalose dimycolate, as described in U. S. Patent Nos. 4,436,727, 4,436,728 and 4,505,900. Combinations of just CWS and trehalose dimycolate, without detoxified endotoxins are also envisioned to be
20 useful, as described in U. S. Patent No. 4,520,019.

MPL is currently one preferred immunopotentiating agent for use herein. References that concern the uses of MPL include Tomai *et al.* (1987), Chen *et al.* (1991) and Garg and Subbarao (1992), that each concern certain roles of MPL in the reactions of aging mice; Elliott *et al.* (1991), that concerns the D-galactosamine loaded mouse and its enhanced
25 sensitivity to lipopolysaccharide and MPL; Chase *et al.* (1986), that relates to bacterial infections; and Masihi *et al.* (1988), that describes the effects of MPL and endotoxin on resistance of mice to *Toxoplasma gondii*. Fitzgerald (1991) also reported on the use of MPL to up-regulate the immunogenicity of a syphilis vaccine and to confer significant protection against challenge infection in rabbits.

Thus MPL is known to be safe for use, as shown in the above model systems. Phase-I clinical trials have also shown MPL to be safe for use (Vosika *et al.*, 1984). Indeed, 100 $\mu\text{g}/\text{m}^2$ is known to be safe for human use, even on an outpatient basis (Vosika *et al.*, 1984).

5 MPL generally induces polyclonal B cell activation (Baker *et al.*, 1994), and has been shown to augment antibody production in many systems, for example, in immunologically immature mice (Baker *et al.*, 1988); in aging mice (Tomai and Johnson, 1989); and in nude and Xid mice (Madonna and Vogel, 1986; Myers *et al.*, 1995). Antibody production has been shown against erythrocytes (Hraba *et al.*, 1993); T cell dependent and independent
10 antigens; Pnu-immune vaccine (Garg and Subbarao, 1992); isolated tumor-associated antigens (U. S. Patent 4,877,611); against syngeneic tumor cells (Livingston *et al.*, 1985; Ravindranath *et al.*, 1994a;b); and against tumor-associated gangliosides (Ravindranath *et al.*, 1994a;b).

Another useful attribute of MPL is that it augments IgM responses, as shown by
15 Baker *et al.* (1988a), who describe the ability of MPL to increase antibody responses in young mice. This is a particularly useful feature of an adjuvant for use in certain embodiments of the present invention. Myers *et al.* (1995) recently reported on the ability of MPL to induce IgM antibodies, by virtue of T cell-independent antibody production.

In the Myers *et al.* (1995) studies, MPL was conjugated to the hapten, TNP. MPL
20 was proposed for use as a carrier for other haptens, such as peptides.

MPL also activates and recruits macrophages (Verma *et al.*, 1992). Tomai and Johnson (1989) showed that MPL-stimulated T cells enhance IL-1 secretion by macrophages. MPL is also known to activate superoxide production, lysozyme activity, phagocytosis, and killing of *Candida* in murine peritoneal macrophages (Chen *et al.*, 1991).

25 The effects of MPL on T cells include the endogenous production of cytotoxic factors, such as TNF, in serum of BCG-primed mice by MPL (Bennett *et al.*, 1988). Kovach *et al.* (1990) and Elliot *et al.* (1991) also show that MPL induces TNF activity. MPL is known to act with TNF- α to induce release of IFN- γ by NK cells. IFN- γ production by T cells in response to MPL was also documented by Tomai and Johnson (1989), and Odean
30 *et al.* (1990).

MPL is also known to be a potent T cell adjuvant. For example, MPL stimulates proliferation of melanoma-antigen specific CTLs (Mitchell *et al.*, 1988, 1993). Further, Baker *et al.* (1988b) showed that nontoxic MPL inactivated suppressor T cell activity. Naturally, in the physiological environment, the inactivation of T suppressor cells allows for increased benefit for the animal, as realized by, *e.g.*, increased antibody production. Johnson and Tomai (1988) have reported on the possible cellular and molecular mediators of the adjuvant action of MPL.

MPL is also known to induce aggregation of platelets and to phosphorylate a platelet protein prior to induction of serotonin secretion (Grabarek *et al.*, 1990). This study shows that MPL is involved in protein kinase C activation and signal transduction.

Many articles concern the structure and function of MPL include. These include Johnson *et al.* (1990), that describes the structural characterization of MPL homologs obtained from *Salmonella minnesota* Re595 lipopolysaccharide. The work of Johnson *et al.* (1990), in common with Grabarek *et al.* (1990), shows that the fatty acid moieties of MPL can vary, even in commercial species. In separating MPL into eight fractions by thin layer chromatography, Johnson *et al.* (1990) found that three were particularly active, as assessed using human platelet responses. The chemical components of the various MPL species were characterized by Johnson *et al.* (1990).

Baker *et al.* (1992) further analyzed the structural features that influence the ability of lipid A and its analogs to abolish expression of suppressor T cell activity. They reported that decreasing the number of phosphate groups in lipid A from two to one (*i.e.*, creating monophosphoryl lipid A, MPL) as well as decreasing the fatty acyl content, primarily by removing the residue at the 3 position, resulted in a progressive reduction in toxicity; however, these structural modifications did not influence its ability to abolish the expression of Ts function (Baker *et al.*, 1992). These types of MPL are ideal for use in the present invention.

Baker *et al.* (1992) also showed that reducing the fatty acyl content from five to four (lipid A precursor IV_A or I_b) eliminated the capacity to influence Ts function but not to induce polyclonal activation of B cells. These studies show that in order to be able to abolish the expression of Ts function, lipid A must be a glucosamine disaccharide; may have either one

or two phosphate groups; and must have at least five fatty acyl groups. Also, the chain length of the nonhydroxylated fatty acid, as well as the location of acyloxyacyl groups (2' versus 3' position), may play an important role (Baker *et al.*, 1992).

In examining the relationship between chain length and position of fatty acyl groups on the ability of lipid A to abolish the expression of suppressor T-cell (Ts) activity, Baker *et al.* (1994) found that fatty acyl chain lengths of C₁₂ to C₁₄ appeared to be optimal for bioactivity. Therefore, although their use is still possible, lipid A preparations with fatty acyl groups of relatively short chain length (C₁₀ to C₁₂ from *Pseudomonas aeruginosa* and *Chromobacterium violaceum*) or predominantly long chain length (C₁₈ from *Helicobacter pylori*) are less preferred for use in this invention.

Baker *et al.* (1994) also showed that the lipid A proximal inner core region oligosaccharides of some bacterial lipopolysaccharides increase the expression of Ts activity; due mainly to the capacity of such oligosaccharides, which are relatively conserved in structure among gram-negative bacterial, to enlarge or expand upon the population of CD8⁺ Ts generated during the course of a normal antibody response to unrelated microbial antigens. The minimal structure required for the expression of the added immunosuppression observed was reported to be a hexasaccharide containing one 2-keto-3-deoxyoctonate residue, two glucose residues, and three heptose residues to which are attached two pyrophosphorylethanolamine groups (Baker *et al.*, 1994). This information may be considered in utilizing or even designing further adjuvants for use in the invention.

In a generally related line of work, Tanamoto *et al.* (1994a;b; 1995) described the dissociation of endotoxic activities in a chemically synthesized Lipid A precursor after acetylation or succinylation. Thus, compounds such as "acetyl 406" and "succinyl 516" (Tanamoto *et al.*, 1994a;b; 1995) are also contemplated for use in the invention.

Synthetic MPLs form a particularly preferred group of antigens. For example, Brade *et al.* (1993) described an artificial glycoconjugate containing the bisphosphorylated glucosamine disaccharide backbone of lipid A that binds to anti-Lipid A MAbs. This is one candidate for use in certain aspects of the invention.

The MPL derivatives described in U. S. Patent No. 4,987,237 are particularly contemplated for use in the present invention. U. S. Patent No. 4,987,237 describes MPL

derivatives that contain one or more free groups, such as amines, on a side chain attached to the primary hydroxyl groups of the monophosphoryl lipid A nucleus through an ester group. The derivatives provide a convenient method for coupling the lipid A through coupling agents to various biologically active materials. The immunostimulant properties of lipid A are maintained. All MPL derivatives in accordance with U. S. Patent No. 4,987,237 are envisioned for use in the MPL adjuvant-incorporated cells of this invention.

Various adjuvants, even those that are not commonly used in humans, may still be employed in animals, where, for example, one desires to raise antibodies or to subsequently obtain activated T cells. The toxicity or other adverse effects that may result from either the adjuvant or the cells, *e.g.*, as may occur using non-irradiated tumor cells, is irrelevant in such circumstances.

Within the vaccines provided herein, the adjuvant composition is preferably designed to induce an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (*e.g.*, IFN- γ , TNF α , IL-2 and IL-12) tend to favor the induction of cell-mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (*e.g.*, IL-4, IL-5, IL-6 and IL-10) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines see *e.g.*, Mosmann and Coffman (1989).

Preferred adjuvants for use in eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt. MPL adjuvants are available from Corixa Corporation (Seattle, WA; see *e.g.*, U. S. Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094, each of which is specifically incorporated herein by reference in its entirety). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in Intl. Pat. Appl. Publ. No. WO 96/02555 and Intl. Pat. Appl. Publ.

No. WO 99/33488. Immunostimulatory DNA sequences are also described, for example, by Sato *et al.* (1996). Another preferred adjuvant is a saponin, preferably QS21 (Aquila Biopharmaceuticals Inc., Framingham, MA), which may be used alone or in combination with other adjuvants. For example, an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the combination of QS21 and 3D-MPL (see *e.g.*, Intl. Pat. Appl. Publ. No. WO 94/00153), or a less reactogenic composition where the QS21 is quenched with cholesterol (see *e.g.*, Intl. Pat. Appl. Publ. No. WO 96/33739). Other preferred formulations comprise an oil-in-water emulsion and tocopherol. A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion has also been described (see *e.g.*, Intl. Pat. Appl. Publ. No. WO 95/17210).

Other preferred adjuvants include Montanide ISA 720 (Seppic), SAF (Chiron), ISCOMS (CSL), MF-59 (Chiron), the SBAS series of adjuvants (*e.g.*, SBAS-2 or SBAS-4, available from SmithKline Beecham, Rixensart, Belgium), Detox (Corixa Corporation), RC-529 (Corixa Corporation) and aminoalkyl glucosaminide 4-phosphates (AGPs).

Any vaccine provided herein may be prepared using well-known methods that result in a combination of one or more antigens, one or more immunostimulants or adjuvants and one or more suitable carriers, excipients, or pharmaceutically acceptable buffers. The compositions described herein may be administered as part of a sustained release formulation (*i.e.*, a formulation such as a capsule, sponge or gel [composed of polysaccharides, for example] that effects a slow release of compound following administration). Such formulations may generally be prepared using well-known technology (Coombes *et al.*, 1996) and administered by, for example, oral, rectal or subcutaneous implantation, or by implantation at the desired target site. Sustained-release formulations may contain a peptide, polynucleotide or antibody dispersed in a carrier matrix and/or contained within a reservoir surrounded by a rate-controlling membrane.

Carriers for use within such formulations are preferably biocompatible, and may also be biodegradable; preferably the formulation provides a relatively constant level of active component release. Such carriers include microparticles of poly(lactide-co-glycolide), as well as polyacrylate, latex, starch, cellulose and dextran. Other delayed-release carriers

include supramolecular biovectors, which comprise a non-liquid hydrophilic core (*e.g.*, a cross-linked polysaccharide or oligosaccharide) and, optionally, an external layer comprising an amphiphilic compound, such as a phospholipid (U. S. Patent No. 5,151,254; Intl. Pat. Appl. Publ. No. WO 94/20078; Intl. Pat. Appl. Publ. No. WO/94/23701; and Intl. Pat. Appl. Publ. No. WO 96/06638). The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within pharmaceutical compositions and vaccines to facilitate production of an antigen-specific immune response that targets tumor cells. Delivery vehicles include antigen-presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (Timmerman and Levy, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*), their ability to take up, process and present antigens with high efficiency and their ability to activate naive T cell responses. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (Zitvogel *et al.*, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF α to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF α , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce differentiation, maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc γ receptor and mannose receptor. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules (*e.g.*, CD40, CD80, CD86 and 4-1BB).

APCs may generally be transfected with a polynucleotide encoding a hematological malignancy related peptide, such that the peptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a composition or vaccine comprising such transfected cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen-presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in Intl. Pat. Appl. Publ. No. WO 97/24447, or the gene gun approach described by Mahvi *et al.* (1997). Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the hematological malignancy related peptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.*,

vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the peptide may be covalently conjugated to an immunological partner that provides T cell help (*e.g.*, a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the peptide.

5 Combined therapeutics is also contemplated, and the same type of underlying pharmaceutical compositions may be employed for both single and combined medicaments. Vaccines and pharmaceutical compositions may be presented in unit-dose or multi-dose containers, such as sealed ampoules or vials. Such containers are preferably hermetically sealed to preserve sterility of the formulation until use. In general, formulations may be
10 stored as suspensions, solutions or emulsions in oily or aqueous vehicles. Alternatively, a vaccine or pharmaceutical composition may be stored in a freeze-dried condition requiring only the addition of a sterile liquid carrier immediately prior to use.

15 4.5 DIAGNOSTIC AND PROGNOSTIC METHODS FOR HEMATOLOGICAL MALIGNANCY DISEASES

The present invention further provides methods for detecting a malignant disease associated with one or more of the polypeptide or polynucleotide compositions disclosed herein, and for monitoring the effectiveness of an immunization or therapy for such a disease. To determine the presence or absence of a malignant disease associated with one or more of
20 the polypeptide or polynucleotide compositions disclosed herein, a patient may be tested for the level of T cells specific for one or more of such compositions. Within certain methods, a biological sample comprising CD4⁺ and/or CD8⁺ T cells isolated from a patient is incubated with one or more of the polypeptide or polynucleotide compositions disclosed herein, and/or an APC that expresses one or more of such peptides or polypeptides, and the presence or
25 absence of specific activation of the T cells is detected, as described herein. Suitable biological samples include, but are not limited to, isolated T cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with one or more of the disclosed peptide, polypeptide or
30 polynucleotide compositions (*e.g.*, 5-25 µg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of the composition to serve as a control. For CD4⁺

T cells, activation is preferably detected by evaluating proliferation of the T cells. For CD8⁺ T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a malignant disease associated with expression or one or more of the disclosed polypeptide or polynucleotide compositions. Further correlation may be made, using methods well known in the art, between the level of proliferation and/or cytolytic activity and the predicted response to therapy. In particular, patients that display a higher antibody, proliferative and/or lytic response may be expected to show a greater response to therapy.

Within other methods, a biological sample obtained from a patient is tested for the level of antibody specific for one or more of the hematological malignancy-related peptides or polypeptides disclosed herein. The biological sample is incubated with hematological malignancy-related peptide or polypeptide, or a polynucleotide encoding such a peptide or polypeptide, and/or an APC that expresses such a peptide or polypeptide under conditions and for a time sufficient to allow immunocomplexes to form. Immunocomplexes formed between the selected peptide or polypeptide and antibodies in the biological sample that specifically bind to the selected peptide or polypeptide are then detected. A biological sample for use within such methods may be any sample obtained from a patient that would be expected to contain antibodies. Suitable biological samples include blood, sera, ascites, bone marrow, pleural effusion, and cerebrospinal fluid.

The biological sample is incubated with the selected peptide or polypeptide in a reaction mixture under conditions and for a time sufficient to permit immunocomplexes to form between the selected peptide or polypeptide and antibodies that are immunospecific for such a peptide or polypeptide. For example, a biological sample and a selected peptide or polypeptide may be incubated at 4°C for 24-48 hrs.

Following the incubation, the reaction mixture is tested for the presence of immunocomplexes. Detection of immunocomplexes formed between the selected peptide or polypeptide and antibodies present in the biological sample may be accomplished by a variety of known techniques, such as radioimmunoassays (RIA) and enzyme linked immunosorbent assays (ELISA). Suitable assays are well known in the art and are amply

described in the scientific and patent literature (Harlow and Lane, 1988). Assays that may be used include, but are not limited to, the double monoclonal antibody sandwich immunoassay technique (U. S. Patent No. 4,376,110); monoclonal-polyclonal antibody sandwich assays (Wide *et al.*, 1970); the "western blot" method (U. S. Patent No. 4,452,901);
5 immunoprecipitation of labeled ligand (Brown *et al.*, 1980); enzyme-linked immunosorbent assays (Raines and Ross, 1982); immunocytochemical techniques, including the use of fluorochromes (Brooks *et al.*, 1980); and neutralization of activity (Bowen-Pope *et al.*, 1984). Other immunoassays include, but are not limited to, those described in U. S. Patent Nos. 3,817,827; 3,850,752; 3,901,654; 3,935,074; 3,984,533; 3,996,345; 4,034,074; and
10 4,098,876.

For detection purposes, the selected peptide or polypeptide may either be labeled or unlabeled. Unlabeled polypeptide peptide may be used in agglutination assays or in combination with labeled detection reagents that bind to the immunocomplexes (*e.g.*, anti-immunoglobulin, protein G, Protein A or a lectin and secondary antibodies, or antigen-
15 binding fragments thereof, capable of binding to the antibodies that specifically bind to the selected hematological malignancy-related peptide or polypeptide). If the selected peptide or polypeptide is labeled, the reporter group may be any suitable reporter group known in the art, including radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin and dye particles.

20 Within certain assays, unlabeled peptide or polypeptide is immobilized on a solid support. The solid support may be any material known to those of ordinary skill in the art to which the peptide may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene
25 or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U. S. Patent No. 5,359,681. The peptide may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as
30 adsorption, and covalent attachment (which may be a direct linkage between the antigen and

functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the selected peptide or polypeptide, in a suitable buffer, with the solid support for a suitable amount of time. The contact time
5 varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of peptide ranging from about 10 ng to about 10 µg, and preferably about 100 ng to about 1 µg, is sufficient to immobilize an adequate amount of peptide.

Following immobilization, the remaining protein binding sites on the support are
10 typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin, Tween™ 20™ (Sigma Chemical Co., St. Louis, MO), heat-inactivated normal goat serum (NGS), or BLOTTO (buffered solution of nonfat dry milk which also contains a preservative, salts, and an antifoaming agent) may be used. The support is then incubated with a biological sample suspected of containing specific antibody.
15 The sample can be applied neat, or, more often, it can be diluted, usually in a buffered solution which contains a small amount (0.1%-5.0% by weight) of protein, such as BSA, NGS, or BLOTTO. In general, an appropriate contact time (*i.e.*, incubation time) is a period of time that is sufficient to detect the presence of antibody or an antigen binding fragment that is immunospecific for the selected peptide or polypeptide within a sample containing
20 such an antibody or binding fragment thereof. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound antibody or antibody fragment. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an
25 incubation time of about 30 min is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween™ 20. A detection reagent that binds to the immunocomplexes and that comprises at least a first detectable label or "reporter" molecule may then be added. The detection reagent is incubated with the immunocomplex
30 for an amount of time sufficient to detect the bound antibody or antigen binding fragment

thereof. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound label or detection reagent is then removed and bound label or detection reagent is detected using a suitable assay or analytical instrument. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive labels, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent or chemiluminescent moieties and various chromogens, fluorescent labels and such like. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups (*e.g.*, horseradish peroxidase, β -galactosidase, alkaline phosphatase and glucose oxidase) may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products. Regardless of the specific method employed, a level of bound detection reagent that is at least two fold greater than background (*i.e.*, the level observed for a biological sample obtained from a disease-free individual) indicates the presence of a malignant disease associated with expression of the selected peptide or polypeptide.

In general, methods for monitoring the effectiveness of an immunization or therapy involve monitoring changes in the level of antibodies or T cells specific for the selected peptide or polypeptide in a sample, or in an animal such as a human patient. Methods in which antibody levels are monitored may comprise the steps of: (a) incubating a first biological sample, obtained from a patient prior to a therapy or immunization, with a selected peptide or polypeptide, wherein the incubation is performed under conditions and for a time sufficient to allow immunocomplexes to form; (b) detecting immunocomplexes formed between the selected peptide or polypeptide and antibodies or antigen binding fragments in the biological sample that specifically bind to the selected peptide or polypeptide; (c) repeating steps (a) and (b) using a second biological sample taken from the patient at a later time, such as for example, following a given therapy or immunization; and (d) comparing the number of immunocomplexes detected in the first and second biological samples. Alternatively, a polynucleotide encoding the selected peptide or polypeptide, or an APC expressing the selected peptide or polypeptide may be employed in place of the selected

peptide or polypeptide itself. Within such methods, immunocomplexes between the selected peptide or polypeptide encoded by a polynucleotide, or expressed by the APC, and antibodies and/or antigen binding fragments in the biological sample are detected.

Methods in which T cell activation and/or the number of hematological malignancy polypeptide-specific precursors are monitored may comprise the steps of: (a) incubating a first biological sample comprising CD4⁺ and/or CD8⁺ cells (*e.g.*, bone marrow, peripheral blood or a fraction thereof), obtained from a patient prior to a therapy or immunization, with a hematological malignancy peptide or polypeptide, wherein the incubation is performed under conditions and for a time sufficient to allow specific activation, proliferation and/or lysis of T cells; (b) detecting an amount of activation, proliferation and/or lysis of the T cells; (c) repeating steps (a) and (b) using a second biological sample comprising CD4⁺ and/or CD8⁺ T cells, and taken from the same patient following therapy or immunization; and (d) comparing the amount of activation, proliferation and/or lysis of T cells in the first and second biological samples. Alternatively, a polynucleotide encoding a hematological malignancy related peptide, or an APC expressing such a peptide may be employed in place of the hematological malignancy peptide itself.

A biological sample for use within such methods may be any sample obtained from a patient that would be expected to contain antibodies, CD4⁺ T cells and/or CD8⁺ T cells. Suitable biological samples include blood, sera, ascites, bone marrow, pleural effusion and cerebrospinal fluid. A first biological sample may be obtained prior to initiation of therapy or immunization or part way through a therapy or vaccination regime. The second biological sample should be obtained in a similar manner, but at a time following additional therapy or immunization. The second biological sample may be obtained at the completion of, or part way through, therapy or immunization, provided that at least a portion of therapy or immunization takes place between the isolation of the first and second biological samples.

Incubation and detection steps for both samples may generally be performed as described above. A statistically significant increase in the number of immunocomplexes in the second sample relative to the first sample reflects successful therapy or immunization.

4.6 ADMINISTRATION OF PHARMACEUTICAL COMPOSITIONS AND FORMULATIONS

In certain embodiments, the present invention concerns formulation of one or more of the polynucleotide, polypeptide, peptide, antibody, or antigen binding fragment compositions disclosed herein in pharmaceutically acceptable solutions for administration to a cell or an animal, either alone, or in combination with one or more other modalities of anti-cancer therapy, or in combination with one or more diagnostic or therapeutic agents.

It will also be understood that, if desired, the nucleic acid segment, RNA, or DNA compositions disclosed herein may be administered in combination with other agents as well, such as, *e.g.*, proteins or peptides or various pharmaceutically-active agents. As long as the composition comprises at least one of the genetic expression constructs disclosed herein, there is virtually no limit to other components that may also be included, given that the additional agents do not cause a significant adverse effect upon contact with the target cells or host tissues. The RNA- or DNA-derived compositions may thus be delivered along with various other agents as required in the particular instance. Such RNA or DNA compositions may be purified from host cells or other biological sources, or alternatively may be chemically synthesized as described herein. Likewise, such compositions may comprise substituted or derivatized RNA or DNA compositions. Such compositions may include one or more therapeutic gene constructs, either alone, or in combination with one or more modified peptide or nucleic acid substituent derivatives, and/or other anticancer therapeutics.

The formulation of pharmaceutically-acceptable excipients and carrier solutions are well-known to those of skill in the art, as is the development of suitable dosing and treatment regimens for using the particular compositions described herein in a variety of treatment regimens, including *e.g.*, oral, intravenous, intranasal, transdermal, intraprostatic, intratumoral, and/or intramuscular administration and formulation.

4.6.1 INJECTABLE DELIVERY

For example, the pharmaceutical compositions disclosed herein may be administered parenterally, intravenously, intramuscularly, or even intraperitoneally as described in U. S. Patent 5,543,158, U. S. Patent 5,641,515 and U. S. Patent 5,399,363 (each specifically incorporated herein by reference in its entirety). Solutions of the active compounds as free-base

or pharmacologically acceptable salts may be prepared in water suitably mixed with a surfactant, such as hydroxypropylcellulose. Dispersions may also be prepared in glycerol, liquid polyethylene glycols, and mixtures thereof and in oils. Under ordinary conditions of storage and use, these preparations contain a preservative to prevent the growth of microorganisms.

The pharmaceutical forms suitable for injectable use include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions (U. S. Patent 5,466,468, specifically incorporated herein by reference in its entirety). In all cases the form must be sterile and must be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms, such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (*e.g.*, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), suitable mixtures thereof, and/or vegetable oils. Proper fluidity may be maintained, for example, by the use of a coating, such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. The prevention of the action of microorganisms can be brought about by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars or sodium chloride. Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminum monostearate and gelatin.

For parenteral administration in an aqueous solution, for example, the solution should be suitably buffered if necessary and the liquid diluent first rendered isotonic with sufficient saline or glucose. These particular aqueous solutions are especially suitable for intravenous, intramuscular, subcutaneous and intraperitoneal administration. In this connection, sterile aqueous media that can be employed will be known to those of skill in the art in light of the present disclosure. For example, one dosage may be dissolved in 1 ml of isotonic NaCl solution and either added to 1000 ml of hypodermoclysis fluid or injected at the proposed site of infusion, (see for example, Hoover, 1975). Some variation in dosage will necessarily occur depending on the condition of the subject being treated. The person responsible for

administration will, in any event, determine the appropriate dose for the individual subject. Moreover, for human administration, preparations should meet sterility, pyrogenicity, and general safety and purity standards as required by FDA Office of Biologics standards.

5 Sterile injectable solutions may be prepared by incorporating the gene therapy constructs in the required amount in the appropriate solvent with several of the other ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the various sterilized active ingredients into a sterile vehicle which contains the basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable
10 solutions, the preferred methods of preparation are vacuum-drying and freeze-drying techniques which yield a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

The compositions disclosed herein may be formulated in a neutral or salt form. Pharmaceutically-acceptable salts, include the acid addition salts and which are formed with
15 inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups can also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, histidine, procaine and the like. Upon formulation, solutions will be administered in a manner
20 compatible with the dosage formulation and in such amount as is therapeutically effective. The formulations are easily administered in a variety of dosage forms such as injectable solutions, drug release capsules and the like.

As used herein, "carrier" includes any and all solvents, dispersion media, vehicles, coatings, diluents, antibacterial and antifungal agents, isotonic and absorption delaying agents,
25 buffers, carrier solutions, suspensions, colloids, and the like. The use of such media and agents for pharmaceutical active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active ingredient, its use in the therapeutic compositions is contemplated. Supplementary active ingredients can also be incorporated into the compositions.

4.6.2 INTRANASAL DELIVERY

One may use nasal solutions or sprays, aerosols or even inhalants for the treatment of hematological malignancies with one of more of the disclosed peptides and polynucleotides. Nasal solutions are usually aqueous solutions designed for administration to the nasal passages in drops or sprays. Nasal solutions are prepared so that they are similar in many respects to nasal secretions, so that normal ciliary action is maintained. Thus, the aqueous nasal solutions usually are isotonic and slightly buffered to maintain a pH of from about 5.5 to about 6.5. In addition, antimicrobial preservatives, similar to those used in ophthalmic preparations, and appropriate drug stabilizers, if required, may be included in the formulation. Various commercial nasal preparations are known.

Inhalations and inhalants are pharmaceutical preparations designed for delivering a drug or compound into the respiratory tree of a patient. A vapor or mist is administered and reaches the affected area, often to give relief from symptoms of bronchial and nasal congestion. However, this route can also be employed to deliver agents into the systemic circulation. Inhalations may be administered by the nasal or oral respiratory routes. The administration of inhalation solutions is only effective if the droplets are sufficiently fine and uniform in size so that the mist reaches the bronchioles.

Another group of products, also known as inhalations, and sometimes called insufflations, consists of finely powdered or liquid drugs that are carried into the respiratory passages by the use of special delivery systems, such as pharmaceutical aerosols, that hold a solution or suspension of the drug in a liquefied gas propellant. When released through a suitable valve and oral adapter, a metered dose of the inhalation is propelled into the respiratory tract of the patient.

Particle size is of importance in the administration of this type of preparation. It has been reported that the optimum particle size for penetration into the pulmonary cavity is of the order of about 0.5 to about 7 μm . Fine mists are produced by pressurized aerosols and hence their use is considered advantageous.

4.6.3 LIPOSOME-, NANOCAPSULE-, AND MICROPARTICLE-MEDIATED DELIVERY

In certain embodiments, the inventors contemplate the use of liposomes, nanocapsules, microparticles, microspheres, lipid particles, vesicles, and the like, for the introduction of the polynucleotide compositions of the present invention into suitable host cells. In particular, the polynucleotide compositions of the present invention may be formulated for delivery either encapsulated in a lipid particle, a liposome, a vesicle, a nanosphere, or a nanoparticle or the like.

Such formulations may be preferred for the introduction of pharmaceutically acceptable formulations of the nucleic acids disclosed herein. The formation and use of liposomes is generally known to those of skill in the art (see for example, Couvreur *et al.*, 1977; Couvreur, 1988; Lasic, 1998; which describes the use of liposomes and nanocapsules in the targeted antibiotic therapy for intracellular bacterial infections and diseases). Recently, liposomes were developed with improved serum stability and circulation half-lives (Gabizon and Papahadjopoulos, 1988; Allen and Choun, 1987; U. S. Patent 5,741,516, specifically incorporated herein by reference in its entirety). Further, various methods of liposome and liposome like preparations as potential drug carriers have been reviewed (Takakura, 1998; Chandran *et al.*, 1997; Margalit, 1995; U. S. Patent 5,567,434; U. S. Patent 5,552,157; U. S. Patent 5,565,213; U. S. Patent 5,738,868 and U. S. Patent 5,795,587, each specifically incorporated herein by reference in its entirety).

Liposomes have been used successfully with a number of cell types that are normally resistant to transfection by other procedures including T cell suspensions, primary hepatocyte cultures and PC12 cells (Renneisen *et al.*, 1990; Muller *et al.*, 1990). In addition, liposomes are free of the DNA length constraints that are typical of viral-based delivery systems. Liposomes have been used effectively to introduce genes, drugs (Heath and Martin, 1986; Heath *et al.*, 1986; Balazsovits *et al.*, 1989; Fresta and Puglisi, 1996), radiotherapeutic agents (Pikul *et al.*, 1987), enzymes (Imaizumi *et al.*, 1990a; Imaizumi *et al.*, 1990b), viruses (Faller and Baltimore, 1984), transcription factors and allosteric effectors (Nicolau and Gersonde, 1979) into a variety of cultured cell lines and animals. In addition, several successful clinical trials examining the effectiveness of liposome-mediated drug delivery have been completed (Lopez-Berestein *et al.*, 1985a; 1985b; Coune, 1988; Sculier *et al.*, 1988). Furthermore, several studies suggest that the

use of liposomes is not associated with autoimmune responses, toxicity or gonadal localization after systemic delivery (Mori and Fukatsu, 1992).

Liposomes are formed from phospholipids that are dispersed in an aqueous medium and spontaneously form multilamellar concentric bilayer vesicles (also termed multilamellar vesicles (MLVs)). MLVs generally have diameters of from 25 nm to 4 μ m. Sonication of
5 MLVs results in the formation of small unilamellar vesicles (SUVs) with diameters in the range of 200 to 500 Å, containing an aqueous solution in the core.

Liposomes bear resemblance to cellular membranes and are contemplated for use in connection with the present invention as carriers for the peptide compositions. They are widely
10 suitable as both water- and lipid-soluble substances can be entrapped, *i.e.* in the aqueous spaces and within the bilayer itself, respectively. It is possible that the drug-bearing liposomes may even be employed for site-specific delivery of active agents by selectively modifying the liposomal formulation.

In addition to the teachings of Couvreur *et al.* (1977; 1988), the following information
15 may be utilized in generating liposomal formulations. Phospholipids can form a variety of structures other than liposomes when dispersed in water, depending on the molar ratio of lipid to water. At low ratios the liposome is the preferred structure. The physical characteristics of liposomes depend on pH, ionic strength and the presence of divalent cations. Liposomes can show low permeability to ionic and polar substances, but at elevated temperatures undergo a
20 phase transition which markedly alters their permeability. The phase transition involves a change from a closely packed, ordered structure, known as the gel state, to a loosely packed, less-ordered structure, known as the fluid state. This occurs at a characteristic phase-transition temperature and results in an increase in permeability to ions, sugars, and drugs.

Alternatively, the invention provides for pharmaceutically acceptable nanocapsule
25 formulations of the polynucleotide compositions of the present invention. Nanocapsules can generally entrap compounds in a stable and reproducible way (Henry-Michelland *et al.*, 1987; Quintanar-Guerrero *et al.*, 1998; Douglas *et al.*, 1987). To avoid side effects due to intracellular polymeric overloading, such ultrafine particles (sized around 0.1 μ m) should be designed using polymers able to be degraded *in vivo*. Biodegradable polyalkyl-cyanoacrylate
30 nanoparticles that meet these requirements are contemplated for use in the present invention,

and such particles may be easily made, as described (Couvreur *et al.*, 1980; 1988; zur Muhlen *et al.*, 1998; Zambaux *et al.* 1998; Pinto-Alphandry *et al.*, 1995 and U. S. Patent 5,145,684, specifically incorporated herein by reference in its entirety). In particular, methods of polynucleotide delivery to a target cell using either nanoparticles or nanospheres (Schwab *et al.*, 1994; Truong-Le *et al.*, 1998) are also particularly contemplated to be useful in formulating the disclosed compositions for administration to an animal, and to a human in particular.

4.7 THERAPEUTIC AGENTS AND KITS

The invention also provides one or more of the hematological malignancy-related compositions formulated with one or more pharmaceutically acceptable excipients, carriers, diluents, adjuvants, and/or other components for use in the preparation of medicaments, or diagnostic reagents, as well as various kits comprising one or more of such compositions, medicaments, or formulations intended for administration to an animal in need thereof, or for use in one or more diagnostic assays for identifying polynucleotides, polypeptides, and/or antibodies that are specific for one or more hematological malignancy-related compounds as described herein. In addition to the disclosed epitopes, antibodies and antigen binding fragments, antibody- or antigen binding fragment-encoding polynucleotides or additional anticancer agents, polynucleotides, peptides, antigens, or other therapeutic compounds as may be employed in the formulation of particular compositions and formulations disclosed herein, and particularly in the preparation of anticancer agents or anti-hematological malignancies therapies for administration to the affected mammal.

As such, preferred animals for administration of the pharmaceutical compositions disclosed herein include mammals, and particularly humans. Other preferred animals include primates, sheep, goats, bovines, equines, porcines, lupines, canines, and felines, as well as any other mammalian species commonly considered pets, livestock, or commercially relevant animal species. The compositions and formulations may include partially or significantly purified polypeptide, polynucleotide, or antibody or antigen binding fragment compositions, either alone, or in combination with one or more additional active ingredients, anticancer agents, vaccines, adjuvants, or other therapeutics which may be obtained from natural or

recombinant sources, or which may be obtainable naturally or either chemically synthesized, or alternatively produced *in vitro* from recombinant host cells expressing one or more nucleic acid segments that encode one or more such additional active ingredients, carriers, adjuvants, cofactors, or other therapeutic compound.

5

4.8 DIAGNOSTIC REAGENTS AND KITS

The invention further provides diagnostic reagents and kits comprising one or more such reagents for use in a variety of diagnostic assays, including for example, immunoassays such as ELISA and "sandwich"-type immunoassays. Such kits may preferably include at least
10 a first peptide, or a first antibody or antigen binding fragment of the invention, a functional fragment thereof, or a cocktail thereof, and means for signal generation. The kit's components may be pre-attached to a solid support, or may be applied to the surface of a solid support when the kit is used. The signal generating means may come pre-associated with an antibody of the invention or may require combination with one or more components, *e.g.*, buffers, antibody-
15 enzyme conjugates, enzyme substrates, or the like, prior to use. Kits may also include additional reagents, *e.g.*, blocking reagents for reducing nonspecific binding to the solid phase surface, washing reagents, enzyme substrates, and the like. The solid phase surface may be in the form of microtiter plates, microspheres, or other materials suitable for immobilizing proteins, peptides, or polypeptides. Preferably, an enzyme that catalyzes the formation of a
20 chemiluminescent or chromogenic product or the reduction of a chemiluminescent or chromogenic substrate is a component of the signal generating means. Such enzymes are well known in the art.

Such kits are useful in the detection, monitoring and diagnosis of conditions characterized by over-expression or inappropriate expression of hematological malignancy-
25 related peptides, polypeptides, antibodies, and/or polynucleotides, as well as hybridomas, host cells, and vectors comprising one or more such compositions as disclosed herein.

The therapeutic and diagnostic kits of the present invention may also be prepared that comprise at least one of the antibody, peptide, antigen binding fragment, hybridoma, vector, vaccine, polynucleotide, or cellular compositions disclosed herein and instructions for using
30 the composition as a diagnostic reagent or therapeutic agent. Containers for use in such kits

may typically comprise at least one vial, test tube, flask, bottle, syringe or other suitable container, into which one or more of the diagnostic and/or therapeutic composition(s) may be placed, and preferably suitably aliquoted. Where a second therapeutic agent is also provided, the kit may also contain a second distinct container into which this second diagnostic and/or therapeutic composition may be placed. Alternatively, a plurality of compounds may be prepared in a single pharmaceutical composition, and may be packaged in a single container means, such as a vial, flask, syringe, bottle, or other suitable single container. The kits of the present invention will also typically include a means for containing the vial(s) in close confinement for commercial sale, such as, *e.g.*, injection or blow-molded plastic containers into which the desired vial(s) are retained. Where a radiolabel, chromogenic, fluorogenic, or other type of detectable label or detecting means is included within the kit, the labeling agent may be provided either in the same container as the diagnostic or therapeutic composition itself, or may alternatively be placed in a second distinct container means into which this second composition may be placed and suitably aliquoted. Alternatively, the detection reagent and the label may be prepared in a single container means, and in most cases, the kit will also typically include a means for containing the vial(s) in close confinement for commercial sale and/or convenient packaging and delivery.

4.9 POLYNUCLEOTIDE COMPOSITIONS

As used herein, the terms "DNA segment" and "polynucleotide" refer to a DNA molecule that has been isolated free of total genomic DNA of a particular species. Therefore, a DNA segment encoding a polypeptide refers to a DNA segment that contains one or more coding sequences yet is substantially isolated away from, or purified free from, total genomic DNA of the species from which the DNA segment is obtained. Included within the terms "DNA segment" and "polynucleotide" are DNA segments and smaller fragments of such segments, and also recombinant vectors, including, for example, plasmids, cosmids, phagemids, phage, viruses, and the like.

As will be understood by those skilled in the art, the DNA segments of this invention can include genomic sequences, extra-genomic and plasmid-encoded sequences and smaller engineered gene segments that express, or may be adapted to express, proteins, polypeptides,

peptides and the like. Such segments may be naturally isolated, or modified synthetically by the hand of man.

"Isolated," as used herein, means that a polynucleotide is substantially away from other coding sequences, and that the DNA segment does not contain large portions of unrelated coding DNA, such as large chromosomal fragments or other functional genes or polypeptide coding regions. Of course, this refers to the DNA segment as originally isolated, and does not exclude genes or coding regions later added to the segment by the hand of man.

As will be recognized by the skilled artisan, polynucleotides may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-to-one manner, and mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a hematological malignancy-related tumor protein or a portion thereof) or may comprise a variant, or a biological or antigenic functional equivalent of such a sequence. Polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions, as further described below, preferably such that the immunogenicity of the encoded polypeptide is not diminished, relative to a native tumor protein. The effect on the immunogenicity of the encoded polypeptide may generally be assessed as described herein. The term "variants" also encompasses homologous genes of xenogenic origin.

When comparing polynucleotide or polypeptide sequences, two sequences are said to be "identical" if the sequence of nucleotides or amino acids in the two sequences is the same when aligned for maximum correspondence, as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins –
5 Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) *Atlas of Protein Sequence and Structure*, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) *Unified Approach to Alignment and Phylogenesis* pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson,
10 E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad., Sci. USA* 80:726-730.

Alternatively, optimal alignment of sequences for comparison may be conducted by the
15 local identity algorithm of Smith and Waterman (1981) *Add. APL. Math* 2:482, by the identity alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity methods of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85: 2444, by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575
20 Science Dr., Madison, WI), or by inspection.

One preferred example of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.* (1977) *Nucl. Acids Res.* 25:3389-3402 and Altschul *et al.* (1990) *J. Mol. Biol.* 215:403-410, respectively. BLAST and BLAST 2.0 can be used, for example with
25 the parameters described herein, to determine percent sequence identity for the polynucleotides and polypeptides of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. In one illustrative example, cumulative scores can be calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix can be used to
30

calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) *Proc. Natl. Acad. Sci. USA* 89:10915) alignments, (B) of 50, expectation (E) of 10, M=5, N=-4 and a comparison of both strands.

Preferably, the "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Therefore, the present invention encompasses polynucleotide and polypeptide sequences having substantial identity to the sequences disclosed herein, for example those comprising at least 50% sequence identity, preferably at least 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% or higher, sequence identity compared to a polynucleotide or polypeptide sequence of this invention using the methods described herein, (*e.g.*, BLAST analysis using standard parameters, as described below). One skilled in this art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the like.

In additional embodiments, the present invention provides isolated polynucleotides and polypeptides comprising various lengths of contiguous stretches of sequence identical to or

complementary to one or more of the sequences disclosed herein. For example, polynucleotides are provided by this invention that comprise at least about 15, 20, 30, 40, 50, 75, 100, 150, 200, 300, 400, 500 or 1000 or more contiguous nucleotides of one or more of the sequences disclosed herein as well as all intermediate lengths there between. It will be readily
5 understood that "intermediate lengths", in this context, means any length between the quoted values, such as 16, 17, 18, 19, *etc.*; 21, 22, 23, *etc.*; 30, 31, 32, *etc.*; 50, 51, 52, 53, *etc.*; 100, 101, 102, 103, *etc.*; 150, 151, 152, 153, *etc.*; including all integers through 200-500; 500-1,000, and the like.

The polynucleotides of the present invention, or fragments thereof, regardless of the
10 length of the coding sequence itself, may be combined with other DNA sequences, such as promoters, polyadenylation signals, additional restriction enzyme sites, multiple cloning sites, other coding segments, and the like, such that their overall length may vary considerably. It is therefore contemplated that a nucleic acid fragment of almost any length may be employed, with the total length preferably being limited by the ease of preparation and use in the intended
15 recombinant DNA protocol. For example, illustrative DNA segments with total lengths of about 10,000, about 5000, about 3000, about 2,000, about 1,000, about 500, about 200, about 100, about 50 base pairs in length, and the like, (including all intermediate lengths) are contemplated to be useful in many implementations of this invention.

In other embodiments, the present invention is directed to polynucleotides that are
20 capable of hybridizing under moderately stringent conditions to a polynucleotide sequence provided herein, or a fragment thereof, or a complementary sequence thereof. Hybridization techniques are well known in the art of molecular biology. For purposes of illustration, suitable moderately stringent conditions for testing the hybridization of a polynucleotide of this invention with other polynucleotides include prewashing in a solution of 5 X SSC, 0.5% SDS,
25 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5 X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS.

Moreover, it will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to the
30 nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to

differences in codon usage are specifically contemplated by the present invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

4.10 PROBES AND PRIMERS

In other embodiments of the present invention, the polynucleotide sequences provided herein can be advantageously used as probes or primers for nucleic acid hybridization. As such, it is contemplated that nucleic acid segments that comprise a sequence region of at least about 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, or 95 nucleotide long contiguous sequence that has the same sequence as, or is complementary to, at least a 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, or 95 nucleotide long contiguous sequence as disclosed in any one of SEQ ID NO:1 to SEQ ID NO:668 will find particular utility in a variety of hybridization embodiments. Longer contiguous identical or complementary sequences, *e.g.*, those of about 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 525, 550, 575, 600, 650, 700, 750, 800, 850, 900, 950, or even 1000 or so nucleotides (including all intermediate lengths) and all full-length sequences as disclosed in SEQ ID NO:1 to SEQ ID NO:668 will also be of use in certain embodiments as probes, primers, or amplification targets and such like.

The ability of such nucleic acid probes to specifically hybridize to a sequence of interest will enable them to be of use in detecting the presence of complementary sequences in a given sample. However, other uses are also envisioned, such as the use of the sequence information for the preparation of mutant species primers, or primers, for use in preparing other genetic constructions, and for identifying and characterizing full-length polynucleotides and full, or substantially full-length cDNAs, mRNAs, and such like.

Polynucleotide molecules having sequence regions consisting of contiguous nucleotide stretches identical or complementary to one or more polynucleotide sequences as disclosed herein, are particularly contemplated as hybridization probes for use in, *e.g.*, Southern hybridization analyses and Northern blotting. This would allow a gene product, or fragment thereof, to be analyzed, both in diverse cell types and also in various bacterial cells. The total size of fragment, as well as the size of the complementary stretch(es), will ultimately depend on the intended use or application of the particular nucleic acid segment. Smaller fragments will generally find use in hybridization embodiments, wherein the length of the contiguous complementary region may be varied, such as between about 15, 20, 25, 30, 35, 40, 45, 50, 55, 60 or so and up to and including larger contiguous complementary sequences, including those of about 70, 80, 90, 100, 120, 140, 160, 180, or 200 or so nucleotides in length may also be used, according to the given desired goal, and the particular length of the complementary sequences one wishes to detect by hybridization analysis.

The use of a hybridization probe of about between about 20 and about 500 nucleotides in length allows the formation of a duplex molecule that is both stable and selective. Molecules having contiguous complementary sequences over stretches greater than about 20 or so bases in length are generally preferred, though, in order to increase stability and selectivity of the hybrid, and thereby improve the quality and degree of specific hybrid molecules obtained. One will generally prefer to design nucleic acid molecules having gene-complementary stretches of between about 25 and 300 or so contiguous nucleotides, or even longer where desired.

Hybridization probes may be selected from any portion of any of the sequences disclosed herein. All that is required is to review the sequence set forth in any one of SEQ ID NO:1 through SEQ ID NO:668, or to any contiguous portion of such a sequence, from about 15 to 30 nucleotides in length up to and including the full length sequences disclosed in any one of SEQ ID NO:1 through SEQ ID NO:668, that one wishes to utilize as a probe or primer. The choice of probe and primer sequences may be governed by various factors. For example, one may wish to employ primers from towards the termini of the total sequence.

Small polynucleotide segments or fragments may be readily prepared by, for example, directly synthesizing the fragment by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer. Also, fragments may be obtained by application of

nucleic acid reproduction technology, such as the PCR™ technology of U. S. Patent 4,683,202 (incorporated herein by reference), by introducing selected sequences into recombinant vectors for recombinant production, and by other recombinant DNA techniques generally known to those of skill in the art of molecular biology.

5 The nucleotide sequences of the invention may be used for their ability to selectively form duplex molecules with complementary stretches of the entire gene or gene fragments of interest. Depending on the application envisioned, one will typically desire to employ varying conditions of hybridization to achieve varying degrees of selectivity of probe towards target sequence. For applications requiring high selectivity, one will typically desire to employ
10 relatively stringent conditions to form the hybrids, *e.g.*, one will select relatively low salt and/or high temperature conditions, such as provided by a salt concentration of from about 0.02 M to about 0.15 M salt at temperatures of from about 50°C to about 70°C. Such selective conditions tolerate little, if any, mismatch between the probe and the template or target strand, and would be particularly suitable for isolating related sequences.

15 Of course, for some applications, for example, where one desires to prepare mutants employing a mutant primer strand hybridized to an underlying template, less stringent (reduced stringency) hybridization conditions will typically be needed in order to allow formation of the heteroduplex. In these circumstances, one may desire to employ salt conditions such as those of from about 0.15 M to about 0.9 M salt, at temperatures ranging from about 20°C to about
20 55°C. Cross-hybridizing species can thereby be readily identified as positively hybridizing signals with respect to control hybridizations. In any case, it is generally appreciated that conditions can be rendered more stringent by the addition of increasing amounts of formamide, which serves to destabilize the hybrid duplex in the same manner as increased temperature. Thus, hybridization conditions can be readily manipulated, and thus will generally be a method
25 of choice depending on the desired results.

4.11 POLYNUCLEOTIDE IDENTIFICATION AND CHARACTERIZATION

Polynucleotides may be identified, prepared and/or manipulated using any of a variety of well established techniques. For example, a polynucleotide may be identified, as described
30 in more detail below, by screening a microarray of cDNAs for tumor-associated expression

(i.e., expression that is at least two fold greater in a tumor than in normal tissue, as determined using a representative assay provided herein). Such screens may be performed, for example, using a Synteni microarray (Palo Alto, CA) according to the manufacturer's instructions (and essentially as described by Schena *et al.*, *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and
5 Heller *et al.*, *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Alternatively, polynucleotides may be amplified from cDNA prepared from cells expressing the proteins described herein, such as hematological malignancy-related tumor cells. Such polynucleotides may be amplified via polymerase chain reaction (PCR). For this approach, sequence-specific primers may be designed based on the sequences provided herein, and may be purchased or synthesized.

10 An amplified portion of a polynucleotide of the present invention may be used to isolate a full length gene from a suitable library (e.g., a hematological malignancy-related tumor cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random
15 primed libraries may also be preferred for identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridization techniques, a partial sequence may be labeled (e.g., by nick-translation or end-labeling with ³²P) using well known techniques. A bacterial or bacteriophage library is then generally screened by hybridizing filters containing denatured bacterial colonies
20 (or lawns containing phage plaques) with the labeled probe (see Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the
25 vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences can then be assembled into a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments, using well known techniques.

Alternatively, there are numerous amplification techniques for obtaining a full length coding sequence from a partial cDNA sequence. Within such techniques, amplification is generally performed via PCR. Any of a variety of commercially available kits may be used to perform the amplification step. Primers may be designed using, for example, software or algorithms or formulas well known in the art.

One such amplification technique is inverse PCR (*see* Triglia *et al.*, *Nucl. Acids Res.* 16:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Another such technique is known as "rapid amplification of cDNA ends" or RACE. This technique involves the use of an internal primer and an external primer, which hybridizes to a polyA region or vector sequence, to identify sequences that are 5' and 3' of a known sequence. Additional techniques include capture PCR (*Lagerstrom et al.*, *PCR Methods Applic. 1*:111-19, 1991) and walking PCR (*Parker et al.*, *Nucl. Acids. Res.* 19:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (*e.g.*, NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence. Full length DNA sequences may also be obtained by analysis of genomic fragments.

4.12 POLYNUCLEOTIDE EXPRESSION IN HOST CELLS

In other embodiments of the invention, polynucleotide sequences or fragments thereof which encode polypeptides of the invention, or fusion proteins or functional equivalents thereof, may be used in recombinant DNA molecules to direct expression of a polypeptide in
5 appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences that encode substantially the same or a functionally equivalent amino acid sequence may be produced and these sequences may be used to clone and express a given polypeptide.

As will be understood by those of skill in the art, it may be advantageous in some instances to produce polypeptide-encoding nucleotide sequences possessing non-naturally
10 occurring codons. For example, codons preferred by a particular prokaryotic or eukaryotic host can be selected to increase the rate of protein expression or to produce a recombinant RNA transcript having desirable properties, such as a half-life which is longer than that of a transcript generated from the naturally occurring sequence.

Moreover, the polynucleotide sequences of the present invention can be engineered
15 using methods generally known in the art in order to alter polypeptide encoding sequences for a variety of reasons, including but not limited to, alterations which modify the cloning, processing, and/or expression of the gene product. For example, DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. In addition, site-directed mutagenesis may be used
20 to insert new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, or introduce mutations, and so forth.

In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences may be ligated to a heterologous sequence to encode a fusion protein. For example, to screen peptide libraries for inhibitors of polypeptide activity, it may be useful to encode a
25 chimeric protein that can be recognized by a commercially available antibody. A fusion protein may also be engineered to contain a cleavage site located between the polypeptide-encoding sequence and the heterologous protein sequence, so that the polypeptide may be cleaved and purified away from the heterologous moiety.

Sequences encoding a desired polypeptide may be synthesized, in whole or in part,
30 using chemical methods well known in the art (see Caruthers, M. H. *et al.* (1980) *Nucl. Acids*

Res. Symp. Ser. 215-223, Horn, T. *et al.* (1980) *Nucl. Acids Res. Symp. Ser.* 225-232). Alternatively, the protein itself may be produced using chemical methods to synthesize the amino acid sequence of a polypeptide, or a portion thereof. For example, peptide synthesis can be performed using various solid-phase techniques (Roberge, J. Y. *et al.* (1995) *Science* 5 269:202-204) and automated synthesis may be achieved, for example, using the ABI 431A Peptide Synthesizer (Perkin Elmer, Palo Alto, CA).

A newly synthesized peptide may be substantially purified by preparative high performance liquid chromatography (*e.g.*, Creighton, T. (1983) *Proteins, Structures and Molecular Principles*, WH Freeman and Co., New York, N.Y.) or other comparable techniques 10 available in the art. The composition of the synthetic peptides may be confirmed by amino acid analysis or sequencing (*e.g.*, the Edman degradation procedure). Additionally, the amino acid sequence of a polypeptide, or any part thereof, may be altered during direct synthesis and/or combined using chemical methods with sequences from other proteins, or any part thereof, to produce a variant polypeptide.

15 In order to express a desired polypeptide, the nucleotide sequences encoding the polypeptide, or functional equivalents, may be inserted into appropriate expression vector, *i.e.*, a vector which contains the necessary elements for the transcription and translation of the inserted coding sequence. Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding a polypeptide of interest 20 and appropriate transcriptional and translational control elements. These methods include *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination. Such techniques are described in Sambrook, J. *et al.* (1989) *Molecular Cloning, A Laboratory Manual*, Cold Spring Harbor Press, Plainview, N.Y., and Ausubel, F. M. *et al.* (1989) *Current Protocols in Molecular Biology*, John Wiley & Sons, New York, N.Y.

25 A variety of expression vector/host systems may be utilized to contain and express polynucleotide sequences. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with virus expression vectors (*e.g.*, baculovirus); plant cell systems transformed with virus expression

vectors (*e.g.*, cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or with bacterial expression vectors (*e.g.*, Ti or pBR322 plasmids); or animal cell systems.

The "control elements" or "regulatory sequences" present in an expression vector are those non-translated regions of the vector--enhancers, promoters, 5' and 3' untranslated regions--which interact with host cellular proteins to carry out transcription and translation. Such elements may vary in their strength and specificity. Depending on the vector system and host utilized, any number of suitable transcription and translation elements, including constitutive and inducible promoters, may be used. For example, when cloning in bacterial systems, inducible promoters such as the hybrid lacZ promoter of the PBLUESCRIPT phagemid (Stratagene, La Jolla, Calif.) or PSPORT1 plasmid (Gibco BRL, Gaithersburg, MD) and the like may be used. In mammalian cell systems, promoters from mammalian genes or from mammalian viruses are generally preferred. If it is necessary to generate a cell line that contains multiple copies of the sequence encoding a polypeptide, vectors based on SV40 or EBV may be advantageously used with an appropriate selectable marker.

In bacterial systems, a number of expression vectors may be selected depending upon the use intended for the expressed polypeptide. For example, when large quantities are needed, for example for the induction of antibodies, vectors which direct high level expression of fusion proteins that are readily purified may be used. Such vectors include, but are not limited to, the multifunctional *E. coli* cloning and expression vectors such as BLUESCRIPT (Stratagene), in which the sequence encoding the polypeptide of interest may be ligated into the vector in frame with sequences for the amino-terminal Met and the subsequent 7 residues of .beta.-galactosidase so that a hybrid protein is produced; pIN vectors (Van Heeke, G. and S. M. Schuster (1989) *J. Biol. Chem.* 264:5503-5509); and the like. pGEX Vectors (Promega, Madison, Wis.) may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. Proteins made in such systems may be designed to include heparin, thrombin, or factor XA protease cleavage sites so that the cloned polypeptide of interest can be released from the GST moiety at will.

In the yeast, *Saccharomyces cerevisiae*, a number of vectors containing constitutive or inducible promoters such as alpha factor, alcohol oxidase, and PGH may be used. For reviews, see Ausubel *et al.* (supra) and Grant *et al.* (1987) *Methods Enzymol.* 153:516-544.

In cases where plant expression vectors are used, the expression of sequences encoding polypeptides may be driven by any of a number of promoters. For example, viral promoters such as the 35S and 19S promoters of CaMV may be used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) *EMBO J.* 6:307-311. Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used (Coruzzi, G. *et al.* (1984) *EMBO J.* 3:1671-1680; Broglie, R. *et al.* (1984) *Science* 224:838-843; and Winter, J. *et al.* (1991) *Results Probl. Cell Differ.* 17:85-105). These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. Such techniques are described in a number of generally available reviews (see, for example, Hobbs, S. or Murry, L. E. in McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York, N.Y.; pp. 191-196).

An insect system may also be used to express a polypeptide of interest. For example, in one such system, *Autographa californica* nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes in *Spodoptera frugiperda* cells or in *Trichoplusia* larvae. The sequences encoding the polypeptide may be cloned into a non-essential region of the virus, such as the polyhedrin gene, and placed under control of the polyhedrin promoter. Successful insertion of the polypeptide-encoding sequence will render the polyhedrin gene inactive and produce recombinant virus lacking coat protein. The recombinant viruses may then be used to infect, for example, *S. frugiperda* cells or *Trichoplusia* larvae in which the polypeptide of interest may be expressed (Engelhard, E. K. *et al.* (1994) *Proc. Natl. Acad. Sci.* 91 :3224-3227).

In mammalian host cells, a number of viral-based expression systems are generally available. For example, in cases where an adenovirus is used as an expression vector, sequences encoding a polypeptide of interest may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain a viable virus which is capable of expressing the polypeptide in infected host cells (Logan, J. and Shenk, T. (1984)

Proc. Natl. Acad. Sci. 81:3655-3659). In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells.

Specific initiation signals may also be used to achieve more efficient translation of sequences encoding a polypeptide of interest. Such signals include the ATG initiation codon and adjacent sequences. In cases where sequences encoding the polypeptide, its initiation codon, and upstream sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a portion thereof, is inserted, exogenous translational control signals including the ATG initiation codon should be provided. Furthermore, the initiation codon should be in the correct reading frame to ensure translation of the entire insert. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers which are appropriate for the particular cell system which is used, such as those described in the literature (Scharf, D. *et al.* (1994) *Results Probl. Cell Differ.* 20:125-162).

In addition, a host cell strain may be chosen for its ability to modulate the expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" form of the protein may also be used to facilitate correct insertion, folding and/or function. Different host cells such as CHO, HeLa, MDCK, HEK293, and WI38, which have specific cellular machinery and characteristic mechanisms for such post-translational activities, may be chosen to ensure the correct modification and processing of the foreign protein.

For long-term, high-yield production of recombinant proteins, stable expression is generally preferred. For example, cell lines which stably express a polynucleotide of interest may be transformed using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for 1-2 days in an enriched media before they are switched to selective media. The purpose of the selectable marker is to confer resistance to selection, and its presence allows growth and

recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be proliferated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These
5 include, but are not limited to, the herpes simplex virus thymidine kinase (Wigler, M. *et al.* (1977) *Cell* 11:223-32) and adenine phosphoribosyltransferase (Lowy, I. *et al.* (1990) *Cell* 22:817-23) genes which can be employed in tk.sup.- or aprt.sup.- cells, respectively. Also, antimetabolite, antibiotic or herbicide resistance can be used as the basis for selection; for example, dhfr which confers resistance to methotrexate (Wigler, M. *et al.* (1980) *Proc. Natl. Acad. Sci.* 77:3567-70); npt, which confers resistance to the aminoglycosides, neomycin and G-418 (Colbere-Garapin, F. *et al.* (1981) *J. Mol. Biol.* 150:1-14); and als or pat, which confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively (Murry, *supra*). Additional selectable genes have been described, for example, trpB, which allows cells to utilize indole in place of tryptophan, or hisD, which allows cells to utilize histinol in place of
15 histidine (Hartman, S. C. and R. C. Mulligan (1988) *Proc. Natl. Acad. Sci.* 85:8047-51). Recently, the use of visible markers has gained popularity with such markers as anthocyanins, beta-glucuronidase and its substrate GUS, and luciferase and its substrate luciferin, being widely used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system (Rhodes, C. A. *et al.* (1995)
20 *Methods Mol. Biol.* 55:121-131).

Although the presence/absence of marker gene expression suggests that the gene of interest is also present, its presence and expression may need to be confirmed. For example, if the sequence encoding a polypeptide is inserted within a marker gene sequence, recombinant cells containing sequences can be identified by the absence of marker gene function.
25 Alternatively, a marker gene can be placed in tandem with a polypeptide-encoding sequence under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

Alternatively, host cells which contain and express a desired polynucleotide sequence may be identified by a variety of procedures known to those of skill in the art. These procedures
30 include, but are not limited to, DNA-DNA or DNA-RNA hybridizations and protein bioassay

or immunoassay techniques which include membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein.

A variety of protocols for detecting and measuring the expression of polynucleotide-encoded products, using either polyclonal or monoclonal antibodies specific for the product are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA),
5 radioimmunoassay (RIA), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on a given polypeptide may be preferred for some applications, but a competitive binding assay may also be employed. These and other assays are described, among
10 other places, in Hampton, R. *et al.* (1990; *Serological Methods, a Laboratory Manual*, APS Press, St Paul, Minn.) and Maddox, D. E. *et al.* (1983; *J. Exp. Med.* 158:1211-1216).

A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides include
15 oligolabeling, nick translation, end-labeling or PCR amplification using a labeled nucleotide. Alternatively, the sequences, or any portions thereof may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be
20 conducted using a variety of commercially available kits. Suitable reporter molecules or labels, which may be used include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with a polynucleotide sequence of interest may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein
25 produced by a recombinant cell may be secreted or contained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides of the invention may be designed to contain signal sequences which direct secretion of the encoded polypeptide through a prokaryotic or eukaryotic cell membrane. Other recombinant constructions may be used to join sequences
30 encoding a polypeptide of interest to nucleotide sequence encoding a polypeptide domain

which will facilitate purification of soluble proteins. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp., Seattle, Wash.). The inclusion of cleavable linker sequences such as those specific for Factor XA or enterokinase (Invitrogen, San Diego, Calif.) between the purification domain and the encoded polypeptide may be used to facilitate purification. One such expression vector provides for expression of a fusion protein containing a polypeptide of interest and a nucleic acid encoding 6 histidine residues preceding a thioredoxin or an enterokinase cleavage site. The histidine residues facilitate purification on IMIAC (immobilized metal ion affinity chromatography) as described in Porath, J. *et al.* (1992, *Prot. Exp. Purif.* 3:263-281) while the enterokinase cleavage site provides a means for purifying the desired polypeptide from the fusion protein. A discussion of vectors which contain fusion proteins is provided in Kroll, D. J. *et al.* (1993; *DNA Cell Biol.* 12:441-453).

In addition to recombinant production methods, polypeptides of the invention, and fragments thereof, may be produced by direct peptide synthesis using solid-phase techniques (Merrifield J. (1963) *J. Am. Chem. Soc.* 85:2149-2154). Protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be achieved, for example, using Applied Biosystems 431A Peptide Synthesizer (Perkin Elmer). Alternatively, various fragments may be chemically synthesized separately and combined using chemical methods to produce the full length molecule.

4.13 SITE-SPECIFIC MUTAGENESIS

Site-specific mutagenesis is a technique useful in the preparation of individual peptides, or biologically functional equivalent polypeptides, through specific mutagenesis of the underlying polynucleotides that encode them. The technique, well-known to those of skill in the art, further provides a ready ability to prepare and test sequence variants, for example, incorporating one or more of the foregoing considerations, by introducing one or more nucleotide sequence changes into the DNA. Site-specific mutagenesis allows the production of mutants through the use of specific oligonucleotide sequences which encode the DNA sequence

of the desired mutation, as well as a sufficient number of adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complexity to form a stable duplex on both sides of the deletion junction being traversed. Mutations may be employed in a selected polynucleotide sequence to improve, alter, decrease, modify, or otherwise change the properties
5 of the polynucleotide itself, and/or alter the properties, activity, composition, stability, or primary sequence of the encoded polypeptide.

In certain embodiments of the present invention, the inventors contemplate the mutagenesis of the disclosed polynucleotide sequences to alter one or more properties of the encoded polypeptide, such as the antigenicity of a polypeptide vaccine. The techniques of site-
10 specific mutagenesis are well-known in the art, and are widely used to create variants of both polypeptides and polynucleotides. For example, site-specific mutagenesis is often used to alter a specific portion of a DNA molecule. In such embodiments, a primer comprising typically about 14 to about 25 nucleotides or so in length is employed, with about 5 to about 10 residues on both sides of the junction of the sequence being altered.

As will be appreciated by those of skill in the art, site-specific mutagenesis techniques
15 have often employed a phage vector that exists in both a single stranded and double stranded form. Typical vectors useful in site-directed mutagenesis include vectors such as the M13 phage. These phage are readily commercially-available and their use is generally well-known to those skilled in the art. Double-stranded plasmids are also routinely employed in site
20 directed mutagenesis that eliminates the step of transferring the gene of interest from a plasmid to a phage.

In general, site-directed mutagenesis in accordance herewith is performed by first obtaining a single-stranded vector or melting apart of two strands of a double-stranded vector that includes within its sequence a DNA sequence that encodes the desired peptide. An
25 oligonucleotide primer bearing the desired mutated sequence is prepared, generally synthetically. This primer is then annealed with the single-stranded vector, and subjected to DNA polymerizing enzymes such as *E. coli* polymerase I Klenow fragment, in order to complete the synthesis of the mutation-bearing strand. Thus, a heteroduplex is formed wherein one strand encodes the original non-mutated sequence and the second strand bears the desired
30 mutation. This heteroduplex vector is then used to transform appropriate cells, such as *E. coli*

cells, and clones are selected which include recombinant vectors bearing the mutated sequence arrangement.

The preparation of sequence variants of the selected peptide-encoding DNA segments using site-directed mutagenesis provides a means of producing potentially useful species and is not meant to be limiting as there are other ways in which sequence variants of peptides and the DNA sequences encoding them may be obtained. For example, recombinant vectors encoding the desired peptide sequence may be treated with mutagenic agents, such as hydroxylamine, to obtain sequence variants. Specific details regarding these methods and protocols are found in the teachings of Maloy *et al.*, 1994; Segal, 1976; Prokop and Bajpai, 1991; Kuby, 1994; and Maniatis *et al.*, 1982, each incorporated herein by reference, for that purpose.

As used herein, the term "oligonucleotide directed mutagenesis procedure" refers to template-dependent processes and vector-mediated propagation which result in an increase in the concentration of a specific nucleic acid molecule relative to its initial concentration, or in an increase in the concentration of a detectable signal, such as amplification. As used herein, the term "oligonucleotide directed mutagenesis procedure" is intended to refer to a process that involves the template-dependent extension of a primer molecule. The term template dependent process refers to nucleic acid synthesis of an RNA or a DNA molecule wherein the sequence of the newly synthesized strand of nucleic acid is dictated by the well-known rules of complementary base pairing (see, for example, Watson, 1987). Typically, vector mediated methodologies involve the introduction of the nucleic acid fragment into a DNA or RNA vector, the clonal amplification of the vector, and the recovery of the amplified nucleic acid fragment. Examples of such methodologies are provided by U. S. Patent No. 4,237,224, specifically incorporated herein by reference in its entirety.

4.14 POLYNUCLEOTIDE AMPLIFICATION TECHNIQUES

A number of template dependent processes are available to amplify the target sequences of interest present in a sample. One of the best known amplification methods is the polymerase chain reaction (PCR™) which is described in detail in U.S. Patent Nos. 4,683,195, 4,683,202 and 4,800,159, each of which is incorporated herein by reference in its entirety. Briefly, in PCR™, two primer sequences are prepared which are complementary to regions on opposite

complementary strands of the target sequence. An excess of deoxynucleoside triphosphates is added to a reaction mixture along with a DNA polymerase (*e.g.*, *Taq* polymerase). If the target sequence is present in a sample, the primers will bind to the target and the polymerase will cause the primers to be extended along the target sequence by adding on nucleotides. By raising and lowering the temperature of the reaction mixture, the extended primers will dissociate from the target to form reaction products, excess primers will bind to the target and to the reaction product and the process is repeated. Preferably reverse transcription and PCRTM amplification procedure may be performed in order to quantify the amount of mRNA amplified. Polymerase chain reaction methodologies are well known in the art.

Another method for amplification is the ligase chain reaction (referred to as LCR), disclosed in Eur. Pat. Appl. Publ. No. 320,308 (specifically incorporated herein by reference in its entirety). In LCR, two complementary probe pairs are prepared, and in the presence of the target sequence, each pair will bind to opposite complementary strands of the target such that they abut. In the presence of a ligase, the two probe pairs will link to form a single unit. By temperature cycling, as in PCRTM, bound ligated units dissociate from the target and then serve as "target sequences" for ligation of excess probe pairs. U.S. Patent No. 4,883,750, incorporated herein by reference in its entirety, describes an alternative method of amplification similar to LCR for binding probe pairs to a target sequence.

Qbeta Replicase, described in PCT Intl. Pat. Appl. Publ. No. PCT/US87/00880, incorporated herein by reference in its entirety, may also be used as still another amplification method in the present invention. In this method, a replicative sequence of RNA that has a region complementary to that of a target is added to a sample in the presence of an RNA polymerase. The polymerase will copy the replicative sequence that can then be detected.

An isothermal amplification method, in which restriction endonucleases and ligases are used to achieve the amplification of target molecules that contain nucleotide 5'-[α -thio]triphosphates in one strand of a restriction site (Walker *et al.*, 1992, incorporated herein by reference in its entirety), may also be useful in the amplification of nucleic acids in the present invention.

Strand Displacement Amplification (SDA) is another method of carrying out isothermal amplification of nucleic acids which involves multiple rounds of strand displacement and

synthesis, *i.e.* nick translation. A similar method, called Repair Chain Reaction (RCR) is another method of amplification which may be useful in the present invention and is involves annealing several probes throughout a region targeted for amplification, followed by a repair reaction in which only two of the four bases are present. The other two bases can be added as
5 biotinylated derivatives for easy detection. A similar approach is used in SDA.

Sequences can also be detected using a cyclic probe reaction (CPR). In CPR, a probe having a 3' and 5' sequences of non-target DNA and an internal or "middle" sequence of the target protein specific RNA is hybridized to DNA which is present in a sample. Upon hybridization, the reaction is treated with RNaseH, and the products of the probe are identified
10 as distinctive products by generating a signal that is released after digestion. The original template is annealed to another cycling probe and the reaction is repeated. Thus, CPR involves amplifying a signal generated by hybridization of a probe to a target gene specific expressed nucleic acid.

Still other amplification methods described in Great Britain Pat. Appl. No. 2 202 328,
15 and in PCT Intl. Pat. Appl. Publ. No. PCT/US89/01025, each of which is incorporated herein by reference in its entirety, may be used in accordance with the present invention. In the former application, "modified" primers are used in a PCR-like, template and enzyme dependent synthesis. The primers may be modified by labeling with a capture moiety (*e.g.*, biotin) and/or a detector moiety (*e.g.*, enzyme). In the latter application, an excess of labeled probes is added
20 to a sample. In the presence of the target sequence, the probe binds and is cleaved catalytically. After cleavage, the target sequence is released intact to be bound by excess probe. Cleavage of the labeled probe signals the presence of the target sequence.

Other nucleic acid amplification procedures include transcription-based amplification systems (TAS) (Kwoh *et al.*, 1989; PCT Intl. Pat. Appl. Publ. No. WO 88/10315, incorporated
25 herein by reference in its entirety), including nucleic acid sequence based amplification (NASBA) and 3SR. In NASBA, the nucleic acids can be prepared for amplification by standard phenol/chloroform extraction, heat denaturation of a sample, treatment with lysis buffer and minispin columns for isolation of DNA and RNA or guanidinium chloride extraction of RNA. These amplification techniques involve annealing a primer that has sequences specific
30 to the target sequence. Following polymerization, DNA/RNA hybrids are digested with RNase

H while double stranded DNA molecules are heat-denatured again. In either case the single stranded DNA is made fully double stranded by addition of second target-specific primer, followed by polymerization. The double stranded DNA molecules are then multiply transcribed by a polymerase such as T7 or SP6. In an isothermal cyclic reaction, the RNAs are reverse transcribed into DNA, and transcribed once again with a polymerase such as T7 or SP6. The resulting products, whether truncated or complete, indicate target-specific sequences.

Eur. Pat. Appl. Publ. No. 329,822, incorporated herein by reference in its entirety, disclose a nucleic acid amplification process involving cyclically synthesizing single-stranded RNA ("ssRNA"), ssDNA, and double-stranded DNA (dsDNA), which may be used in accordance with the present invention. The ssRNA is a first template for a first primer oligonucleotide, which is elongated by reverse transcriptase (RNA-dependent DNA polymerase). The RNA is then removed from resulting DNA:RNA duplex by the action of ribonuclease H (RNase H, an RNase specific for RNA in a duplex with either DNA or RNA). The resultant ssDNA is a second template for a second primer, which also includes the sequences of an RNA polymerase promoter (exemplified by T7 RNA polymerase) 5' to its homology to its template. This primer is then extended by DNA polymerase (exemplified by the large "Klenow" fragment of *E. coli* DNA polymerase I), resulting as a double-stranded DNA ("dsDNA") molecule, having a sequence identical to that of the original RNA between the primers and having additionally, at one end, a promoter sequence. This promoter sequence can be used by the appropriate RNA polymerase to make many RNA copies of the DNA. These copies can then re-enter the cycle leading to very swift amplification. With proper choice of enzymes, this amplification can be done isothermally without addition of enzymes at each cycle. Because of the cyclical nature of this process, the starting sequence can be chosen to be in the form of either DNA or RNA.

PCT Intl. Pat. Appl. Publ. No. WO 89/06700, incorporated herein by reference in its entirety, disclose a nucleic acid sequence amplification scheme based on the hybridization of a promoter/primer sequence to a target single-stranded DNA ("ssDNA") followed by transcription of many RNA copies of the sequence. This scheme is not cyclic; *i.e.* new templates are not produced from the resultant RNA transcripts. Other amplification methods

H while double stranded DNA molecules are heat-denatured again. In either case the single stranded DNA is made fully double stranded by addition of second target-specific primer, followed by polymerization. The double stranded DNA molecules are then multiply transcribed by a polymerase such as T7 or SP6. In an isothermal cyclic reaction, the RNAs are reverse transcribed into DNA, and transcribed once again with a polymerase such as T7 or SP6. The resulting products, whether truncated or complete, indicate target-specific sequences.

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include "RACE" (Frohman, 1990), and "one-sided PCR" (Ohara, 1989) which are well-known to those of skill in the art.

Methods based on ligation of two (or more) oligonucleotides in the presence of nucleic acid having the sequence of the resulting "di-oligonucleotide", thereby amplifying the di-oligonucleotide (Wu and Dean, 1996, incorporated herein by reference in its entirety), may also be used in the amplification of DNA sequences of the present invention.

4.15 *IN VIVO* POLYNUCLEOTIDE DELIVERY TECHNIQUES

In additional embodiments, genetic constructs comprising one or more of the polynucleotides of the invention are introduced into cells *in vivo*. This may be achieved using any of a variety of well known approaches, several of which are outlined below for the purpose of illustration.

4.15.1 ADENOVIRUS

One of the preferred methods for *in vivo* delivery of one or more nucleic acid sequences involves the use of an adenovirus expression vector. "Adenovirus expression vector" is meant to include those constructs containing adenovirus sequences sufficient to (a) support packaging of the construct and (b) to express a polynucleotide that has been cloned therein in a sense or antisense orientation. Of course, in the context of an antisense construct, expression does not require that the gene product be synthesized.

The expression vector comprises a genetically engineered form of an adenovirus. Knowledge of the genetic organization of adenovirus, a 36 kb, linear, double-stranded DNA virus, allows substitution of large pieces of adenoviral DNA with foreign sequences up to 7 kb (Grunhaus and Horwitz, 1992). In contrast to retrovirus, the adenoviral infection of host cells does not result in chromosomal integration because adenoviral DNA can replicate in an episomal manner without potential genotoxicity. Also, adenoviruses are structurally stable, and no genome rearrangement has been detected after extensive amplification. Adenovirus can infect virtually all epithelial cells regardless of their cell cycle stage. So far, adenoviral infection appears to be linked only to mild disease such as acute respiratory disease in humans.

Adenovirus is particularly suitable for use as a gene transfer vector because of its mid-sized genome, ease of manipulation, high titer, wide target-cell range and high infectivity. Both ends of the viral genome contain 100-200 base pair inverted repeats (ITRs), which are *cis* elements necessary for viral DNA replication and packaging. The early (E) and late (L) regions of the genome contain different transcription units that are divided by the onset of viral DNA replication. The E1 region (E1A and E1B) encodes proteins responsible for the regulation of transcription of the viral genome and a few cellular genes. The expression of the E2 region (E2A and E2B) results in the synthesis of the proteins for viral DNA replication. These proteins are involved in DNA replication, late gene expression and host cell shut-off (Renan, 1990). The products of the late genes, including the majority of the viral capsid proteins, are expressed only after significant processing of a single primary transcript issued by the major late promoter (MLP). The MLP, (located at 16.8 m.u.) is particularly efficient during the late phase of infection, and all the mRNA's issued from this promoter possess a 5'-tripartite leader (TPL) sequence which makes them preferred mRNA's for translation.

In a current system, recombinant adenovirus is generated from homologous recombination between shuttle vector and provirus vector. Due to the possible recombination between two proviral vectors, wild-type adenovirus may be generated from this process. Therefore, it is critical to isolate a single clone of virus from an individual plaque and examine its genomic structure.

Generation and propagation of the current adenovirus vectors, which are replication deficient, depend on a unique helper cell line, designated 293, which was transformed from human embryonic kidney cells by Ad5 DNA fragments and constitutively expresses E1 proteins (Graham *et al.*, 1977). Since the E3 region is dispensable from the adenovirus genome (Jones and Shenk, 1978), the current adenovirus vectors, with the help of 293 cells, carry foreign DNA in either the E1, the D3 or both regions (Graham and Prevec, 1991). In nature, adenovirus can package approximately 105% of the wild-type genome (Ghosh-Choudhury *et al.*, 1987), providing capacity for about 2 extra kB of DNA. Combined with the approximately 5.5 kB of DNA that is replaceable in the E1 and E3 regions, the maximum capacity of the current adenovirus vector is under 7.5 kB, or about 15% of the total length of the vector. More than 80% of the adenovirus viral genome remains in the vector backbone and is the source of

vector-borne cytotoxicity. Also, the replication deficiency of the E1-deleted virus is incomplete. For example, leakage of viral gene expression has been observed with the currently available vectors at high multiplicities of infection (MOI) (Mulligan, 1993).

5 Helper cell lines may be derived from human cells such as human embryonic kidney cells, muscle cells, hematopoietic cells or other human embryonic mesenchymal or epithelial cells. Alternatively, the helper cells may be derived from the cells of other mammalian species that are permissive for human adenovirus. Such cells include, *e.g.*, Vero cells or other monkey embryonic mesenchymal or epithelial cells. As stated above, the currently preferred helper cell line is 293.

10 Recently, Racher *et al.* (1995) disclosed improved methods for culturing 293 cells and propagating adenovirus. In one format, natural cell aggregates are grown by inoculating individual cells into 1 liter siliconized spinner flasks (Techne, Cambridge, UK) containing 100-200 ml of medium. Following stirring at 40 rpm, the cell viability is estimated with trypan blue. In another format, Fibra-Cel microcarriers (Bibby Sterlin, Stone, UK) (5 g/l) is employed
15 as follows. A cell inoculum, resuspended in 5 ml of medium, is added to the carrier (50 ml) in a 250 ml Erlenmeyer flask and left stationary, with occasional agitation, for 1 to 4 h. The medium is then replaced with 50 ml of fresh medium and shaking initiated. For virus production, cells are allowed to grow to about 80% confluence, after which time the medium is replaced (to 25% of the final volume) and adenovirus added at an MOI of 0.05. Cultures are
20 left stationary overnight, following which the volume is increased to 100% and shaking commenced for another 72 h.

Other than the requirement that the adenovirus vector be replication defective, or at least conditionally defective, the nature of the adenovirus vector is not believed to be crucial to the successful practice of the invention. The adenovirus may be of any of the 42 different known
25 serotypes or subgroups A-F. Adenovirus type 5 of subgroup C is the preferred starting material in order to obtain a conditional replication-defective adenovirus vector for use in the present invention, since Adenovirus type 5 is a human adenovirus about which a great deal of biochemical and genetic information is known, and it has historically been used for most constructions employing adenovirus as a vector.

As stated above, the typical vector according to the present invention is replication defective and will not have an adenovirus E1 region. Thus, it will be most convenient to introduce the polynucleotide encoding the gene of interest at the position from which the E1-coding sequences have been removed. However, the position of insertion of the construct within the adenovirus sequences is not critical to the invention. The polynucleotide encoding the gene of interest may also be inserted in lieu of the deleted E3 region in E3 replacement vectors as described by Karlsson *et al.* (1986) or in the E4 region where a helper cell line or helper virus complements the E4 defect.

Adenovirus is easy to grow and manipulate and exhibits broad host range *in vitro* and *in vivo*. This group of viruses can be obtained in high titers, *e.g.*, 10^9 - 10^{11} plaque-forming units per ml, and they are highly infective. The life cycle of adenovirus does not require integration into the host cell genome. The foreign genes delivered by adenovirus vectors are episomal and, therefore, have low genotoxicity to host cells. No side effects have been reported in studies of vaccination with wild-type adenovirus (Couch *et al.*, 1963; Top *et al.*, 1971), demonstrating their safety and therapeutic potential as *in vivo* gene transfer vectors.

Adenovirus vectors have been used in eukaryotic gene expression (Levrero *et al.*, 1991; Gomez-Foix *et al.*, 1992) and vaccine development (Grunhaus and Horwitz, 1992; Graham and Prevec, 1992). Recently, animal studies suggested that recombinant adenovirus could be used for gene therapy (Stratford-Perricaudet and Perricaudet, 1991; Stratford-Perricaudet *et al.*, 1990; Rich *et al.*, 1993). Studies in administering recombinant adenovirus to different tissues include trachea instillation (Rosenfeld *et al.*, 1991; Rosenfeld *et al.*, 1992), muscle injection (Ragot *et al.*, 1993), peripheral intravenous injections (Herz and Gerard, 1993) and stereotactic inoculation into the brain (Le Gal La Salle *et al.*, 1993).

4.15.2 RETROVIRUSES

The retroviruses are a group of single-stranded RNA viruses characterized by an ability to convert their RNA to double-stranded DNA in infected cells by a process of reverse-transcription (Coffin, 1990). The resulting DNA then stably integrates into cellular chromosomes as a provirus and directs synthesis of viral proteins. The integration results in the retention of the viral gene sequences in the recipient cell and its descendants. The retroviral

genome contains three genes, gag, pol, and env that code for capsid proteins, polymerase enzyme, and envelope components, respectively. A sequence found upstream from the gag gene contains a signal for packaging of the genome into virions. Two long terminal repeat (LTR) sequences are present at the 5' and 3' ends of the viral genome. These contain strong promoter and enhancer sequences and are also required for integration in the host cell genome (Coffin, 1990).

In order to construct a retroviral vector, a nucleic acid encoding one or more oligonucleotide or polynucleotide sequences of interest is inserted into the viral genome in the place of certain viral sequences to produce a virus that is replication-defective. In order to produce virions, a packaging cell line containing the gag, pol, and env genes but without the LTR and packaging components is constructed (Mann *et al.*, 1983). When a recombinant plasmid containing a cDNA, together with the retroviral LTR and packaging sequences is introduced into this cell line (by calcium phosphate precipitation for example), the packaging sequence allows the RNA transcript of the recombinant plasmid to be packaged into viral particles, which are then secreted into the culture media (Nicolas and Rubenstein, 1988; Temin, 1986; Mann *et al.*, 1983). The media containing the recombinant retroviruses is then collected, optionally concentrated, and used for gene transfer. Retroviral vectors are able to infect a broad variety of cell types. However, integration and stable expression require the division of host cells (Paskind *et al.*, 1975).

A novel approach designed to allow specific targeting of retrovirus vectors was recently developed based on the chemical modification of a retrovirus by the chemical addition of lactose residues to the viral envelope. This modification could permit the specific infection of hepatocytes *via* sialoglycoprotein receptors.

A different approach to targeting of recombinant retroviruses was designed in which biotinylated antibodies against a retroviral envelope protein and against a specific cell receptor were used. The antibodies were coupled *via* the biotin components by using streptavidin (Roux *et al.*, 1989). Using antibodies against major histocompatibility complex class I and class II antigens, they demonstrated the infection of a variety of human cells that bore those surface antigens with an ecotropic virus *in vitro* (Roux *et al.*, 1989).

4.15.3 ADENO-ASSOCIATED VIRUSES

AAV (Ridgeway, 1988; Hermonat and Muzyczka, 1984) is a parovirus, discovered as a contamination of adenoviral stocks. It is a ubiquitous virus (antibodies are present in 85% of the US human population) that has not been linked to any disease. It is also classified as a dependovirus, because its replications is dependent on the presence of a helper virus, such as adenovirus. Five serotypes have been isolated, of which AAV-2 is the best characterized. AAV has a single-stranded linear DNA that is encapsidated into capsid proteins VP1, VP2 and VP3 to form an icosahedral virion of 20 to 24 nm in diameter (Muzyczka and McLaughlin, 1988).

The AAV DNA is approximately 4.7 kilobases long. It contains two open reading frames and is flanked by two ITRs (FIG. 2). There are two major genes in the AAV genome: *rep* and *cap*. The *rep* gene codes for proteins responsible for viral replications, whereas *cap* codes for capsid protein VP1-3. Each ITR forms a T-shaped hairpin structure. These terminal repeats are the only essential *cis* components of the AAV for chromosomal integration. Therefore, the AAV can be used as a vector with all viral coding sequences removed and replaced by the cassette of genes for delivery. Three viral promoters have been identified and named p5, p19, and p40, according to their map position. Transcription from p5 and p19 results in production of rep proteins, and transcription from p40 produces the capsid proteins (Hermonat and Muzyczka, 1984).

There are several factors that prompted researchers to study the possibility of using rAAV as an expression vector. One is that the requirements for delivering a gene to integrate into the host chromosome are surprisingly few. It is necessary to have the 145-bp ITRs, which are only 6% of the AAV genome. This leaves room in the vector to assemble a 4.5-kb DNA insertion. While this carrying capacity may prevent the AAV from delivering large genes, it is amply suited for delivering the antisense constructs of the present invention.

AAV is also a good choice of delivery vehicles due to its safety. There is a relatively complicated rescue mechanism: not only wild type adenovirus but also AAV genes are required to mobilize rAAV. Likewise, AAV is not pathogenic and not associated with any disease. The removal of viral coding sequences minimizes immune reactions to viral gene expression, and therefore, rAAV does not evoke an inflammatory response.

4.15.4 OTHER VIRAL VECTORS AS EXPRESSION CONSTRUCTS

Other viral vectors may be employed as expression constructs in the present invention for the delivery of oligonucleotide or polynucleotide sequences to a host cell. Vectors derived from viruses such as vaccinia virus (Ridgeway, 1988; Coupar *et al.*, 1988), lentiviruses, polio viruses and herpes viruses may be employed. They offer several attractive features for various mammalian cells (Friedmann, 1989; Ridgeway, 1988; Coupar *et al.*, 1988; Horwich *et al.*, 1990).

With the recent recognition of defective hepatitis B viruses, new insight was gained into the structure-function relationship of different viral sequences. *In vitro* studies showed that the virus could retain the ability for helper-dependent packaging and reverse transcription despite the deletion of up to 80% of its genome (Horwich *et al.*, 1990). This suggested that large portions of the genome could be replaced with foreign genetic material. The hepatotropism and persistence (integration) were particularly attractive properties for liver-directed gene transfer. Chang *et al.* (1991) introduced the chloramphenicol acetyltransferase (CAT) gene into duck hepatitis B virus genome in the place of the polymerase, surface, and pre-surface coding sequences. It was cotransfected with wild-type virus into an avian hepatoma cell line. Culture media containing high titers of the recombinant virus were used to infect primary duckling hepatocytes. Stable CAT gene expression was detected for at least 24 days after transfection (Chang *et al.*, 1991).

4.15.5 NON-VIRAL VECTORS

In order to effect expression of the oligonucleotide or polynucleotide sequences of the present invention, the expression construct must be delivered into a cell. This delivery may be accomplished *in vitro*, as in laboratory procedures for transforming cells lines, or *in vivo* or *ex vivo*, as in the treatment of certain disease states. As described above, one preferred mechanism for delivery is *via* viral infection where the expression construct is encapsulated in an infectious viral particle.

Once the expression construct has been delivered into the cell the nucleic acid encoding the desired oligonucleotide or polynucleotide sequences may be positioned and expressed at

different sites. In certain embodiments, the nucleic acid encoding the construct may be stably integrated into the genome of the cell. This integration may be in the specific location and orientation *via* homologous recombination (gene replacement) or it may be integrated in a random, non-specific location (gene augmentation). In yet further embodiments, the nucleic acid may be stably maintained in the cell as a separate, episomal segment of DNA. Such nucleic acid segments or "episomes" encode sequences sufficient to permit maintenance and replication independent of or in synchronization with the host cell cycle. How the expression construct is delivered to a cell and where in the cell the nucleic acid remains is dependent on the type of expression construct employed.

10 In certain embodiments of the invention, the expression construct comprising one or more oligonucleotide or polynucleotide sequences may simply consist of naked recombinant DNA or plasmids. Transfer of the construct may be performed by any of the methods mentioned above which physically or chemically permeabilize the cell membrane. This is particularly applicable for transfer *in vitro* but it may be applied to *in vivo* use as well.

15 Dubensky *et al.* (1984) successfully injected polyomavirus DNA in the form of calcium phosphate precipitates into liver and spleen of adult and newborn mice demonstrating active viral replication and acute infection. Benvenisty and Reshef (1986) also demonstrated that direct intraperitoneal injection of calcium phosphate-precipitated plasmids results in expression of the transfected genes. It is envisioned that DNA encoding a gene of interest may also be

20 transferred in a similar manner *in vivo* and express the gene product.

Another embodiment of the invention for transferring a naked DNA expression construct into cells may involve particle bombardment. This method depends on the ability to accelerate DNA-coated microprojectiles to a high velocity allowing them to pierce cell membranes and enter cells without killing them (Klein *et al.*, 1987). Several devices for

25 accelerating small particles have been developed. One such device relies on a high voltage discharge to generate an electrical current, which in turn provides the motive force (Yang *et al.*, 1990). The microprojectiles used have consisted of biologically inert substances such as tungsten or gold beads.

Selected organs including the liver, skin, and muscle tissue of rats and mice have been

30 bombarded *in vivo* (Yang *et al.*, 1990; Zelenin *et al.*, 1991). This may require surgical exposure

of the tissue or cells, to eliminate any intervening tissue between the gun and the target organ, *i.e. ex vivo* treatment. Again, DNA encoding a particular gene may be delivered *via* this method and still be incorporated by the present invention.

5 4.16 ANTISENSE OLIGONUCLEOTIDES

The end result of the flow of genetic information is the synthesis of protein. DNA is transcribed by polymerases into messenger RNA and translated on the ribosome to yield a folded, functional protein. Thus there are several steps along the route where protein synthesis can be inhibited. The native DNA segment coding for a polypeptide described herein, as all
10 such mammalian DNA strands, has two strands: a sense strand and an antisense strand held together by hydrogen bonding. The messenger RNA coding for polypeptide has the same nucleotide sequence as the sense DNA strand except that the DNA thymidine is replaced by uridine. Thus, synthetic antisense nucleotide sequences will bind to a mRNA and inhibit expression of the protein encoded by that mRNA.

15 The targeting of antisense oligonucleotides to mRNA is thus one mechanism to shut down protein synthesis, and, consequently, represents a powerful and targeted therapeutic approach. For example, the synthesis of polygalacturonase and the muscarine type 2 acetylcholine receptor are inhibited by antisense oligonucleotides directed to their respective mRNA sequences (U. S. Patent 5,739,119 and U. S. Patent 5,759,829, each specifically
20 incorporated herein by reference in its entirety). Further, examples of antisense inhibition have been demonstrated with the nuclear protein cyclin, the multiple drug resistance gene (MDG1), ICAM-1, E-selectin, STK-1, striatal GABA_A receptor and human EGF (Jaskulski *et al.*, 1988; Vasanthakumar and Ahmed, 1989; Peris *et al.*, 1998; U. S. Patent 5,801,154; U. S. Patent 5,789,573; U. S. Patent 5,718,709 and U. S. Patent 5,610,288, each specifically incorporated
25 herein by reference in its entirety). Antisense constructs have also been described that inhibit and can be used to treat a variety of abnormal cellular proliferations, *e.g.* cancer (U. S. Patent 5,747,470; U. S. Patent 5,591,317 and U. S. Patent 5,783,683, each specifically incorporated herein by reference in its entirety).

Therefore, in exemplary embodiments, the invention provides oligonucleotide
30 sequences that comprise all, or a portion of, any sequence that is capable of specifically binding

to polynucleotide sequence described herein, or a complement thereof. In one embodiment, the antisense oligonucleotides comprise DNA or derivatives thereof. In another embodiment, the oligonucleotides comprise RNA or derivatives thereof. In a third embodiment, the oligonucleotides are modified DNAs comprising a phosphorothioated modified backbone. In a
5 fourth embodiment, the oligonucleotide sequences comprise peptide nucleic acids or derivatives thereof. In each case, preferred compositions comprise a sequence region that is complementary, and more preferably substantially-complementary, and even more preferably, completely complementary to one or more portions of polynucleotides disclosed herein.

Selection of antisense compositions specific for a given gene sequence is based upon
10 analysis of the chosen target sequence (*i.e.* in these illustrative examples the rat and human sequences) and determination of secondary structure, T_m , binding energy, relative stability, and antisense compositions were selected based upon their relative inability to form dimers, hairpins, or other secondary structures that would reduce or prohibit specific binding to the target mRNA in a host cell.

15 Highly preferred target regions of the mRNA, are those which are at or near the AUG translation initiation codon, and those sequences which were substantially complementary to 5' regions of the mRNA. These secondary structure analyses and target site selection considerations were performed using v.4 of the OLIGO primer analysis software (Rychlik, 1997) and the BLASTN 2.0.5 algorithm software (Altschul *et al.*, 1997).

20 The use of an antisense delivery method employing a short peptide vector, termed MPG (27 residues), is also contemplated. The MPG peptide contains a hydrophobic domain derived from the fusion sequence of HIV gp41 and a hydrophilic domain from the nuclear localization sequence of SV40 T-antigen (Morris *et al.*, 1997). It has been demonstrated that several molecules of the MPG peptide coat the antisense oligonucleotides and can be delivered into
25 cultured mammalian cells in less than 1 hour with relatively high efficiency (90%). Further, the interaction with MPG strongly increases both the stability of the oligonucleotide to nuclease and the ability to cross the plasma membrane (Morris *et al.*, 1997).

4.17 RIBOZYMES

Although proteins traditionally have been used for catalysis of nucleic acids, another class of macromolecules has emerged as useful in this endeavor. Ribozymes are RNA-protein complexes that cleave nucleic acids in a site-specific fashion. Ribozymes have specific catalytic domains that possess endonuclease activity (Kim and Cech, 1987; Gerlach *et al.*, 1987; Forster and Symons, 1987). For example, a large number of ribozymes accelerate phosphoester transfer reactions with a high degree of specificity, often cleaving only one of several phosphoesters in an oligonucleotide substrate (Cech *et al.*, 1981; Michel and Westhof, 1990; Reinhold-Hurek and Shub, 1992). This specificity has been attributed to the requirement that the substrate bind via specific base-pairing interactions to the internal guide sequence ("IGS") of the ribozyme prior to chemical reaction.

Ribozyme catalysis has primarily been observed as part of sequence-specific cleavage/ligation reactions involving nucleic acids (Joyce, 1989; Cech *et al.*, 1981). For example, U. S. Patent No. 5,354,855 (specifically incorporated herein by reference) reports that certain ribozymes can act as endonucleases with a sequence specificity greater than that of known ribonucleases and approaching that of the DNA restriction enzymes. Thus, sequence-specific ribozyme-mediated inhibition of gene expression may be particularly suited to therapeutic applications (Scanlon *et al.*, 1991; Sarver *et al.*, 1990). Recently, it was reported that ribozymes elicited genetic changes in some cells lines to which they were applied; the altered genes included the oncogenes *H-ras*, *c-fos* and genes of HIV. Most of this work involved the modification of a target mRNA, based on a specific mutant codon that is cleaved by a specific ribozyme.

Six basic varieties of naturally-occurring enzymatic RNAs are known presently. Each can catalyze the hydrolysis of RNA phosphodiester bonds *in trans* (and thus can cleave other RNA molecules) under physiological conditions. In general, enzymatic nucleic acids act by first binding to a target RNA. Such binding occurs through the target binding portion of an enzymatic nucleic acid which is held in close proximity to an enzymatic portion of the molecule that acts to cleave the target RNA. Thus, the enzymatic nucleic acid first recognizes and then binds a target RNA through complementary base-pairing, and once bound to the correct site, acts enzymatically to cut the target RNA. Strategic cleavage of such a target RNA

will destroy its ability to direct synthesis of an encoded protein. After an enzymatic nucleic acid has bound and cleaved its RNA target, it is released from that RNA to search for another target and can repeatedly bind and cleave new targets.

The enzymatic nature of a ribozyme is advantageous over many technologies, such as
5 antisense technology (where a nucleic acid molecule simply binds to a nucleic acid target to block its translation) since the concentration of ribozyme necessary to affect a therapeutic treatment is lower than that of an antisense oligonucleotide. This advantage reflects the ability of the ribozyme to act enzymatically. Thus, a single ribozyme molecule is able to cleave many molecules of target RNA. In addition, the ribozyme is a highly specific inhibitor, with the
10 specificity of inhibition depending not only on the base pairing mechanism of binding to the target RNA, but also on the mechanism of target RNA cleavage. Single mismatches, or base-substitutions, near the site of cleavage can completely eliminate catalytic activity of a ribozyme. Similar mismatches in antisense molecules do not prevent their action (Woolf *et al.*, 1992). Thus, the specificity of action of a ribozyme is greater than that of an antisense oligonucleotide
15 binding the same RNA site.

The enzymatic nucleic acid molecule may be formed in a hammerhead, hairpin, a hepatitis δ virus, group I intron or RNaseP RNA (in association with an RNA guide sequence) or Neurospora VS RNA motif. Examples of hammerhead motifs are described by Rossi *et al.* (1992). Examples of hairpin motifs are described by Hampel *et al.* (Eur. Pat. Appl. Publ. No.
20 EP 0360257), Hampel and Tritz (1989), Hampel *et al.* (1990) and U. S. Patent 5,631,359 (specifically incorporated herein by reference). An example of the hepatitis δ virus motif is described by Perrotta and Been (1992); an example of the RNaseP motif is described by Guerrier-Takada *et al.* (1983); Neurospora VS RNA ribozyme motif is described by Collins (Saville and Collins, 1990; Saville and Collins, 1991; Collins and Olive, 1993); and an example
25 of the Group I intron is described in (U. S. Patent 4,987,071, specifically incorporated herein by reference). All that is important in an enzymatic nucleic acid molecule of this invention is that it has a specific substrate binding site which is complementary to one or more of the target gene RNA regions, and that it have nucleotide sequences within or surrounding that substrate binding site which impart an RNA cleaving activity to the molecule. Thus the ribozyme
30 constructs need not be limited to specific motifs mentioned herein.

In certain embodiments, it may be important to produce enzymatic cleaving agents which exhibit a high degree of specificity for the RNA of a desired target, such as one of the sequences disclosed herein. The enzymatic nucleic acid molecule is preferably targeted to a highly conserved sequence region of a target mRNA. Such enzymatic nucleic acid molecules
5 can be delivered exogenously to specific cells as required. Alternatively, the ribozymes can be expressed from DNA or RNA vectors that are delivered to specific cells.

Small enzymatic nucleic acid motifs (*e.g.*, of the hammerhead or the hairpin structure) may also be used for exogenous delivery. The simple structure of these molecules increases the ability of the enzymatic nucleic acid to invade targeted regions of the mRNA structure.
10 Alternatively, catalytic RNA molecules can be expressed within cells from eukaryotic promoters (*e.g.*, Scanlon *et al.*, 1991; Kashani-Sabet *et al.*, 1992; Dropulic *et al.*, 1992; Weerasinghe *et al.*, 1991; Ojwang *et al.*, 1992; Chen *et al.*, 1992; Sarver *et al.*, 1990). Those skilled in the art realize that any ribozyme can be expressed in eukaryotic cells from the appropriate DNA vector. The activity of such ribozymes can be augmented by their release
15 from the primary transcript by a second ribozyme (Int. Pat. Appl. Publ. No. WO 93/23569, and Int. Pat. Appl. Publ. No. WO 94/02595, both hereby incorporated by reference; Ohkawa *et al.*, 1992; Taira *et al.*, 1991; and Ventura *et al.*, 1993).

Ribozymes may be added directly, or can be complexed with cationic lipids, lipid complexes, packaged within liposomes, or otherwise delivered to target cells. The RNA or
20 RNA complexes can be locally administered to relevant tissues *ex vivo*, or *in vivo* through injection, aerosol inhalation, infusion pump or stent, with or without their incorporation in biopolymers.

Ribozymes may be designed as described in Int. Pat. Appl. Publ. No. WO 93/23569 and Int. Pat. Appl. Publ. No. WO 94/02595, each specifically incorporated herein by reference) and
25 synthesized to be tested *in vitro* and *in vivo*, as described. Such ribozymes can also be optimized for delivery. While specific examples are provided, those in the art will recognize that equivalent RNA targets in other species can be utilized when necessary.

Hammerhead or hairpin ribozymes may be individually analyzed by computer folding (Jaeger *et al.*, 1989) to assess whether the ribozyme sequences fold into the appropriate
30 secondary structure. Those ribozymes with unfavorable intramolecular interactions between

the binding arms and the catalytic core are eliminated from consideration. Varying binding arm lengths can be chosen to optimize activity. Generally, at least 5 or so bases on each arm are able to bind to, or otherwise interact with, the target RNA.

Ribozymes of the hammerhead or hairpin motif may be designed to anneal to various
5 sites in the mRNA message, and can be chemically synthesized. The method of synthesis used follows the procedure for normal RNA synthesis as described in Usman *et al.* (1987) and in Scaringe *et al.* (1990) and makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. Average stepwise coupling yields are typically >98%. Hairpin ribozymes may be synthesized in two parts and
10 annealed to reconstruct an active ribozyme (Chowrira and Burke, 1992). Ribozymes may be modified extensively to enhance stability by modification with nuclease resistant groups, for example, 2'-amino, 2'-C-allyl, 2'-fluoro, 2'-O-methyl, 2'-H (for a review see *e.g.*, Usman and Cedergren, 1992). Ribozymes may be purified by gel electrophoresis using general methods or by high pressure liquid chromatography and resuspended in water.

Ribozyme activity can be optimized by altering the length of the ribozyme binding
15 arms, or chemically synthesizing ribozymes with modifications that prevent their degradation by serum ribonucleases (see *e.g.*, Int. Pat. Appl. Publ. No. WO 92/07065; Perrault *et al.*, 1990; Pieken *et al.*, 1991; Usman and Cedergren, 1992; Int. Pat. Appl. Publ. No. WO 93/15187; Int. Pat. Appl. Publ. No. WO 91/03162; Eur. Pat. Appl. Publ. No. 92110298.4; U. S. Patent
20 5,334,711; and Int. Pat. Appl. Publ. No. WO 94/13688, which describe various chemical modifications that can be made to the sugar moieties of enzymatic RNA molecules), modifications which enhance their efficacy in cells, and removal of stem II bases to shorten RNA synthesis times and reduce chemical requirements.

Sullivan *et al.* (Int. Pat. Appl. Publ. No. WO 94/02595) describes the general methods
25 for delivery of enzymatic RNA molecules. Ribozymes may be administered to cells by a variety of methods known to those familiar to the art, including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by incorporation into other vehicles, such as hydrogels, cyclodextrins, biodegradable nanocapsules, and bioadhesive microspheres. For some indications, ribozymes may be directly delivered *ex vivo* to cells or tissues with or without
30 the aforementioned vehicles. Alternatively, the RNA/vehicle combination may be locally

delivered by direct inhalation, by direct injection or by use of a catheter, infusion pump or stent. Other routes of delivery include, but are not limited to, intravascular, intramuscular, subcutaneous or joint injection, aerosol inhalation, oral (tablet or pill form), topical, systemic, ocular, intraperitoneal and/or intrathecal delivery. More detailed descriptions of ribozyme
5 delivery and administration are provided in Int. Pat. Appl. Publ. No. WO 94/02595 and Int. Pat. Appl. Publ. No. WO 93/23569, each specifically incorporated herein by reference.

Another means of accumulating high concentrations of a ribozyme(s) within cells is to incorporate the ribozyme-encoding sequences into a DNA expression vector. Transcription of the ribozyme sequences are driven from a promoter for eukaryotic RNA polymerase I (pol I),
10 RNA polymerase II (pol II), or RNA polymerase III (pol III). Transcripts from pol II or pol III promoters will be expressed at high levels in all cells; the levels of a given pol II promoter in a given cell type will depend on the nature of the gene regulatory sequences (enhancers, silencers, etc.) present nearby. Prokaryotic RNA polymerase promoters may also be used, providing that the prokaryotic RNA polymerase enzyme is expressed in the appropriate cells (Elroy-Stein and
15 Moss, 1990; Gao and Huang, 1993; Lieber *et al.*, 1993; Zhou *et al.*, 1990). Ribozymes expressed from such promoters can function in mammalian cells (*e.g.* Kashani-Saber *et al.*, 1992; Ojwang *et al.*, 1992; Chen *et al.*, 1992; Yu *et al.*, 1993; L'Huillier *et al.*, 1992; Lisiewicz *et al.*, 1993). Such transcription units can be incorporated into a variety of vectors for introduction into mammalian cells, including but not restricted to, plasmid DNA vectors, viral
20 DNA vectors (such as adenovirus or adeno-associated vectors), or viral RNA vectors (such as retroviral, semliki forest virus, sindbis virus vectors).

Ribozymes may be used as diagnostic tools to examine genetic drift and mutations within diseased cells. They can also be used to assess levels of the target RNA molecule. The close relationship between ribozyme activity and the structure of the target RNA allows the
25 detection of mutations in any region of the molecule which alters the base-pairing and three-dimensional structure of the target RNA. By using multiple ribozymes, one may map nucleotide changes which are important to RNA structure and function *in vitro*, as well as in cells and tissues. Cleavage of target RNAs with ribozymes may be used to inhibit gene expression and define the role (essentially) of specified gene products in the progression of
30 disease. In this manner, other genetic targets may be defined as important mediators of the

disease. These studies will lead to better treatment of the disease progression by affording the possibility of combinational therapies (*e.g.*, multiple ribozymes targeted to different genes, ribozymes coupled with known small molecule inhibitors, or intermittent treatment with combinations of ribozymes and/or other chemical or biological molecules). Other *in vitro* uses of ribozymes are well known in the art, and include detection of the presence of mRNA associated with an IL-5 related condition. Such RNA is detected by determining the presence of a cleavage product after treatment with a ribozyme using standard methodology.

4.18 PEPTIDE NUCLEIC ACIDS

In certain embodiments, the inventors contemplate the use of peptide nucleic acids (PNAs) in the practice of the methods of the invention. PNA is a DNA mimic in which the nucleobases are attached to a pseudopeptide backbone (Good and Nielsen, 1997). PNA is able to be utilized in a number methods that traditionally have used RNA or DNA. Often PNA sequences perform better in techniques than the corresponding RNA or DNA sequences and have utilities that are not inherent to RNA or DNA. A review of PNA including methods of making, characteristics of, and methods of using, is provided by Corey (1997) and is incorporated herein by reference. As such, in certain embodiments, one may prepare PNA sequences that are complementary to one or more portions of the ACE mRNA sequence, and such PNA compositions may be used to regulate, alter, decrease, or reduce the translation of ACE-specific mRNA, and thereby alter the level of ACE activity in a host cell to which such PNA compositions have been administered.

PNAs have 2-aminoethyl-glycine linkages replacing the normal phosphodiester backbone of DNA (Nielsen *et al.*, 1991; Hanvey *et al.*, 1992; Hyrup and Nielsen, 1996; Neilsen, 1996). This chemistry has three important consequences: firstly, in contrast to DNA or phosphorothioate oligonucleotides, PNAs are neutral molecules; secondly, PNAs are achiral, which avoids the need to develop a stereoselective synthesis; and thirdly, PNA synthesis uses standard Boc (Dueholm *et al.*, 1994) or Fmoc (Thomson *et al.*, 1995) protocols for solid-phase peptide synthesis, although other methods, including a modified Merrifield method, have been used (Christensen *et al.*, 1995).

PNA monomers or ready-made oligomers are commercially available from PerSeptive Biosystems (Framingham, MA). PNA syntheses by either Boc or Fmoc protocols are straightforward using manual or automated protocols (Norton *et al.*, 1995). The manual protocol lends itself to the production of chemically modified PNAs or the simultaneous
5 synthesis of families of closely related PNAs.

As with peptide synthesis, the success of a particular PNA synthesis will depend on the properties of the chosen sequence. For example, while in theory PNAs can incorporate any combination of nucleotide bases, the presence of adjacent purines can lead to deletions of one or more residues in the product. In expectation of this difficulty, it is suggested that, in
10 producing PNAs with adjacent purines, one should repeat the coupling of residues likely to be added inefficiently. This should be followed by the purification of PNAs by reverse-phase high-pressure liquid chromatography (Norton *et al.*, 1995) providing yields and purity of product similar to those observed during the synthesis of peptides.

Modifications of PNAs for a given application may be accomplished by coupling amino
15 acids during solid-phase synthesis or by attaching compounds that contain a carboxylic acid group to the exposed N-terminal amine. Alternatively, PNAs can be modified after synthesis by coupling to an introduced lysine or cysteine. The ease with which PNAs can be modified facilitates optimization for better solubility or for specific functional requirements. Once synthesized, the identity of PNAs and their derivatives can be confirmed by mass spectrometry.
20 Several studies have made and utilized modifications of PNAs (Norton *et al.*, 1995; Haaime *et al.*, 1996; Stetsenko *et al.*, 1996; Petersen *et al.*, 1995; Ulmann *et al.*, 1996; Koch *et al.*, 1995; Orum *et al.*, 1995; Footer *et al.*, 1996; Griffith *et al.*, 1995; Kremsky *et al.*, 1996; Pardridge *et al.*, 1995; Boffa *et al.*, 1995; Landsorp *et al.*, 1996; Gambacorti-Passerini *et al.*, 1996; Armitage *et al.*, 1997; Seeger *et al.*, 1997; Ruskowski *et al.*, 1997). U.S. Patent No. 5,700,922
25 discusses PNA-DNA-PNA chimeric molecules and their uses in diagnostics, modulating protein in organisms, and treatment of conditions susceptible to therapeutics.

In contrast to DNA and RNA, which contain negatively charged linkages, the PNA backbone is neutral. In spite of this dramatic alteration, PNAs recognize complementary DNA and RNA by Watson-Crick pairing (Egholm *et al.*, 1993), validating the initial modeling by

Nielsen *et al.* (1991). PNAs lack 3' to 5' polarity and can bind in either parallel or antiparallel fashion, with the antiparallel mode being preferred (Egholm *et al.*, 1993).

Hybridization of DNA oligonucleotides to DNA and RNA is destabilized by electrostatic repulsion between the negatively charged phosphate backbones of the complementary strands. By contrast, the absence of charge repulsion in PNA-DNA or PNA-RNA duplexes increases the melting temperature (T_m) and reduces the dependence of T_m on the concentration of mono- or divalent cations (Nielsen *et al.*, 1991). The enhanced rate and affinity of hybridization are significant because they are responsible for the surprising ability of PNAs to perform strand invasion of complementary sequences within relaxed double-stranded DNA. In addition, the efficient hybridization at inverted repeats suggests that PNAs can recognize secondary structure effectively within double-stranded DNA. Enhanced recognition also occurs with PNAs immobilized on surfaces, and Wang *et al.* have shown that support-bound PNAs can be used to detect hybridization events (Wang *et al.*, 1996).

One might expect that tight binding of PNAs to complementary sequences would also increase binding to similar (but not identical) sequences, reducing the sequence specificity of PNA recognition. As with DNA hybridization, however, selective recognition can be achieved by balancing oligomer length and incubation temperature. Moreover, selective hybridization of PNAs is encouraged by PNA-DNA hybridization being less tolerant of base mismatches than DNA-DNA hybridization. For example, a single mismatch within a 16 bp PNA-DNA duplex can reduce the T_m by up to 15°C (Egholm *et al.*, 1993). This high level of discrimination has allowed the development of several PNA-based strategies for the analysis of point mutations (Wang *et al.*, 1996; Carlsson *et al.*, 1996; Thiede *et al.*, 1996; Webb and Hurskainen, 1996; Perry-O'Keefe *et al.*, 1996).

High-affinity binding provides clear advantages for molecular recognition and the development of new applications for PNAs. For example, 11-13 nucleotide PNAs inhibit the activity of telomerase, a ribonucleo-protein that extends telomere ends using an essential RNA template, while the analogous DNA oligomers do not (Norton *et al.*, 1996).

Neutral PNAs are more hydrophobic than analogous DNA oligomers, and this can lead to difficulty solubilizing them at neutral pH, especially if the PNAs have a high purine content

or if they have the potential to form secondary structures. Their solubility can be enhanced by attaching one or more positive charges to the PNA termini (Nielsen *et al.*, 1991).

Findings by Allfrey and colleagues suggest that strand invasion will occur spontaneously at sequences within chromosomal DNA (Boffa *et al.*, 1995; Boffa *et al.*, 1996).

5 These studies targeted PNAs to triplet repeats of the nucleotides CAG and used this recognition to purify transcriptionally active DNA (Boffa *et al.*, 1995) and to inhibit transcription (Boffa *et al.*, 1996). This result suggests that if PNAs can be delivered within cells then they will have the potential to be general sequence-specific regulators of gene expression. Studies and reviews concerning the use of PNAs as antisense and anti-gene agents include Nielsen *et al.* (1993b),
10 Hanvey *et al.* (1992), and Good and Nielsen (1997). Koppelhus *et al.* (1997) have used PNAs to inhibit HIV-1 inverse transcription, showing that PNAs may be used for antiviral therapies.

Methods of characterizing the antisense binding properties of PNAs are discussed in Rose (1993) and Jensen *et al.* (1997). Rose uses capillary gel electrophoresis to determine binding of PNAs to their complementary oligonucleotide, measuring the relative binding
15 kinetics and stoichiometry. Similar types of measurements were made by Jensen *et al.* using BIAcore™ technology.

Other applications of PNAs include use in DNA strand invasion (Nielsen *et al.*, 1991), antisense inhibition (Hanvey *et al.*, 1992), mutational analysis (Orum *et al.*, 1993), enhancers of transcription (Mollegaard *et al.*, 1994), nucleic acid purification (Orum *et al.*, 1995), isolation
20 of transcriptionally active genes (Boffa *et al.*, 1995), blocking of transcription factor binding (Vickers *et al.*, 1995), genome cleavage (Veselkov *et al.*, 1996), biosensors (Wang *et al.*, 1996), *in situ* hybridization (Thisted *et al.*, 1996), and in a alternative to Southern blotting (Perry-O'Keefe, 1996).

25 4.19 POLYPEPTIDE, PEPTIDES AND PEPTIDE VARIANTS

The present invention, in other aspects, provides polypeptide compositions. Generally, a polypeptide of the invention will be an isolated polypeptide (or an epitope, variant, or active fragment thereof) derived from a mammalian species. Preferably, the polypeptide is encoded by a polynucleotide sequence disclosed herein or a sequence which hybridizes under
30 moderately stringent conditions to a polynucleotide sequence disclosed herein. Alternatively,

the polypeptide may be defined as a polypeptide which comprises a contiguous amino acid sequence from an amino acid sequence disclosed herein, or which polypeptide comprises an entire amino acid sequence disclosed herein.

In the present invention, a polypeptide composition is also understood to comprise one or more polypeptides that are immunologically reactive with antibodies generated against a polypeptide of the invention, particularly a polypeptide having the amino acid sequence encoded by the polynucleotides disclosed in SEQ ID NO: 1-146, or to active fragments, or to variants or biological functional equivalents thereof.

Likewise, a polypeptide composition of the present invention is understood to comprise one or more polypeptides that are capable of eliciting antibodies that are immunologically reactive with one or more polypeptides encoded by one or more contiguous nucleic acid sequences contained in SEQ ID NO: 1-146, or to active fragments, or to variants thereof, or to one or more nucleic acid sequences which hybridize to one or more of these sequences under conditions of moderate to high stringency. Particularly illustrative polypeptides include the amino acid sequences encoded by polynucleotides disclosed in SEQ ID NO: 1-146.

As used herein, an active fragment of a polypeptide includes a whole or a portion of a polypeptide which is modified by conventional techniques, *e.g.*, mutagenesis, or by addition, deletion, or substitution, but which active fragment exhibits substantially the same structure function, antigenicity, etc., as a polypeptide as described herein.

In certain illustrative embodiments, the polypeptides of the invention will comprise at least an immunogenic portion of a hematological malignancy-related tumor protein or a variant thereof, as described herein. As noted above, a "hematological malignancy-related tumor protein" is a protein that is expressed by hematological malignancy-related tumor cells. Proteins that are hematological malignancy-related tumor proteins also react detectably within an immunoassay (such as an ELISA) with antisera from a patient with hematological malignancy. Polypeptides as described herein may be of any length. Additional sequences derived from the native protein and/or heterologous sequences may be present, and such sequences may (but need not) possess further immunogenic or antigenic properties.

An "immunogenic portion," as used herein is a portion of a protein that is recognized (*i.e.*, specifically bound) by a B-cell and/or T-cell surface antigen receptor. Such immunogenic

portions generally comprise at least 5 amino acid residues, more preferably at least 10, and still more preferably at least 20 amino acid residues of a hematological malignancy-related tumor protein or a variant thereof. Certain preferred immunogenic portions include peptides in which an N-terminal leader sequence and/or transmembrane domain have been deleted. Other preferred immunogenic portions may contain a small N- and/or C-terminal deletion (e.g., 1-30 amino acids, preferably 5-15 amino acids), relative to the mature protein.

Immunogenic portions may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they specifically bind to an antigen (i.e., they react with the protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well known techniques. An immunogenic portion of a native hematological malignancy-related tumor protein is a portion that reacts with such antisera and/or T-cells at a level that is not substantially less than the reactivity of the full length polypeptide (e.g., in an ELISA and/or T-cell reactivity assay). Such immunogenic portions may react within such assays at a level that is similar to or greater than the reactivity of the full length polypeptide. Such screens may generally be performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. For example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ¹²⁵I-labeled Protein A.

As noted above, a composition may comprise a variant of a native hematological malignancy-related tumor protein. A polypeptide "variant," as used herein, is a polypeptide that differs from a native hematological malignancy-related tumor protein in one or more substitutions, deletions, additions and/or insertions, such that the immunogenicity of the polypeptide is not substantially diminished. In other words, the ability of a variant to react with antigen-specific antisera may be enhanced or unchanged, relative to the native protein, or may

be diminished by less than 50%, and preferably less than 20%, relative to the native protein. Such variants may generally be identified by modifying one of the above polypeptide sequences and evaluating the reactivity of the modified polypeptide with antigen-specific antibodies or antisera as described herein. Preferred variants include those in which one or
5 more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other preferred variants include variants in which a small portion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein.

Polypeptide variants encompassed by the present invention include those exhibiting at
10 least about 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or more identity (determined as described above) to the polypeptides disclosed herein.

Preferably, a variant contains conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and
15 hydrophathic nature of the polypeptide to be substantially unchanged. Amino acid substitutions may generally be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar
20 hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. In a preferred
25 embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydrophathic nature of the polypeptide.

As noted above, polypeptides may comprise a signal (or leader) sequence at the N-
30 terminal end of the protein, which co-translationally or post-translationally directs transfer of

the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

5 Polypeptides may be prepared using any of a variety of well known techniques. Recombinant polypeptides encoded by DNA sequences as described above may be readily prepared from the DNA sequences using any of a variety of expression vectors known to those of ordinary skill in the art. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that
10 encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast, and higher eukaryotic cells, such as mammalian cells and plant cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line such as COS or CHO. Supernatants from suitable host/vector systems which secrete recombinant protein or polypeptide into culture media may be first concentrated using a commercially available filter. Following concentration, the
15 concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant polypeptide.

Portions and other variants having less than about 100 amino acids, and generally less than about 50 amino acids, may also be generated by synthetic means, using techniques well
20 known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin
25 Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Within certain specific embodiments, a polypeptide may be a fusion protein that comprises multiple polypeptides as described herein, or that comprises at least one polypeptide as described herein and an unrelated sequence, such as a known tumor protein. A fusion
30 partner may, for example, assist in providing T helper epitopes (an immunological fusion

partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the protein or to enable
5 the protein to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the protein.

Fusion proteins may generally be prepared using standard techniques, including chemical conjugation. Preferably, a fusion protein is expressed as a recombinant protein, allowing the production of increased levels, relative to a non-fused protein, in an expression
10 system. Briefly, DNA sequences encoding the polypeptide components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion protein that retains the
15 biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen
20 based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may
25 also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea *et al.*, *Gene* 40:39-46, 1985; Murphy *et al.*, *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-

terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Fusion proteins are also provided. Such proteins comprise a polypeptide as described herein together with an unrelated immunogenic protein. Preferably the immunogenic protein is capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (*see, for example, Stoute et al. New Engl. J. Med.*, 336:86-91, 1997).

Within preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenza B* (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as amidase LYTA (encoded by the *LytA* gene; *Gene* 43:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins

containing the C-LYTA fragment at the amino terminus has been described (*see Biotechnology 10:795-798, 1992*). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion protein. A repeat portion is found in the C-terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

5 In general, polypeptides (including fusion proteins) and polynucleotides as described herein are isolated. An "isolated" polypeptide or polynucleotide is one that is removed from its original environment. For example, a naturally-occurring protein is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are at least about 90% pure, more preferably at least about 95% pure and most
10 preferably at least about 99% pure. A polynucleotide is considered to be isolated if, for example, it is cloned into a vector that is not a part of the natural environment.

4.20 BINDING AGENTS

The present invention further employs agents, such as antibodies and antigen-binding
15 fragments thereof, that specifically bind to a hematological malignancy-related antigen. As used herein, an antibody, or antigen-binding fragment thereof, is said to "specifically bind" to a hematological malignancy-related antigen if it reacts at a detectable level (within, for example, an ELISA) with , and does not react detectably with unrelated proteins under similar conditions. As used herein, "binding" refers to a noncovalent association between two separate molecules
20 such that a complex is formed. The ability to bind may be evaluated by, for example, determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind," in the context of the present invention, when the binding constant for complex formation exceeds about 10^3 L/mol.
25 The binding constant maybe determined using methods well known in the art.

Binding agents may be further capable of differentiating between patients with and without a hematological malignancy. Such binding agents generate a signal indicating the presence of a hematological malignancy in at least about 20% of patients with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of
30 individuals without the disease. To determine whether a binding agent satisfies this

requirement, biological samples (e.g., blood, sera, urine and/or tumor biopsies) from patients with and without a hematological malignancy (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. It will be apparent that a statistically significant number of samples with and without the disease should be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (i.e., reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells

obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Within certain embodiments, the use of antigen-binding fragments of antibodies may be preferred. Such fragments include Fab fragments, which may be prepared using standard techniques. Briefly, immunoglobulins may be purified from rabbit serum by affinity chromatography on Protein A bead columns (Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988) and digested by papain to yield Fab and Fc fragments. The Fab and Fc fragments may be separated by affinity chromatography on protein A bead columns.

Monoclonal antibodies, and fragments thereof, of the present invention may be coupled to one or more therapeutic agents, such as radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ^{90}Y , ^{123}I , ^{125}I , ^{131}I , ^{186}Re , ^{188}Re , ^{211}At , and ^{212}Bi . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and

pokeweed antiviral protein. For certain *in vivo* and *ex vivo* therapies, an antibody or fragment thereof is preferably coupled to a cytotoxic agent, such as a radioactive or chemotherapeutic moiety.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U. S. Patent No. 4,671,958.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U. S. Patent No. 4,489,710), by irradiation of a photolabile bond (*e.g.*, U. S. Patent No. 4,625,014), by hydrolysis of derivatized amino acid side chains (*e.g.*, U. S. Patent No. 4,638,045), by serum complement-mediated hydrolysis (*e.g.*, U. S. Patent No. 4,671,958), and acid-catalyzed hydrolysis (*e.g.*, U. S. Patent No. 4,569,789).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U. S. Patent No. 4,507,234), peptides and polysaccharides such as aminodextran (*e.g.*, U. S. Patent No. 4,699,784). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U. S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U. S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U. S. Patent No. 4,673,562 discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

4.21 VACCINES

In certain preferred embodiments of the present invention, vaccines are provided. The vaccines will generally comprise one or more pharmaceutical compositions, such as those discussed above, in combination with an immunostimulant. An immunostimulant may be any substance that enhances or potentiates an immune response (antibody and/or cell-mediated) to an exogenous antigen. Examples of immunostimulants include adjuvants, biodegradable

microspheres (e.g., polylactic galactide) and liposomes (into which the compound is incorporated; see e.g., Fullerton, U.S. Patent No. 4,235,877). Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, which may be biologically active or inactive. For example, one or more immunogenic portions of other tumor antigens may be present, either incorporated into a fusion polypeptide or as a separate compound, within the composition or vaccine.

Illustrative vaccines may contain DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems* 15:143-198, 1998, and references cited therein. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch *et al.*, *Proc. Natl. Acad. Sci. USA* 86:317-321, 1989; Flexner *et al.*, *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner *et al.*, *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld *et al.*, *Science* 252:431-434, 1991; Kolls *et al.*, *Proc. Natl. Acad. Sci. USA* 91:215-219, 1994; Kass-Eisler *et al.*, *Proc. Natl. Acad. Sci. USA* 90:11498-11502, 1993; Guzman *et al.*, *Circulation* 88:2838-2848, 1993; and Guzman *et al.*, *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in

Ulmer *et al.*, *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells. It will be apparent that a vaccine may comprise both a polynucleotide and a polypeptide component. Such vaccines may provide for
5 an enhanced immune response.

It will be apparent that a vaccine may contain pharmaceutically acceptable salts of the polynucleotides and polypeptides provided herein. Such salts may be prepared from pharmaceutically acceptable non-toxic bases, including organic bases (*e.g.*, salts of primary, secondary and tertiary amines and basic amino acids) and inorganic bases (*e.g.*, sodium,
10 potassium, lithium, ammonium, calcium and magnesium salts).

While any suitable carrier known to those of ordinary skill in the art may be employed in the vaccine compositions of this invention, the type of carrier will vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous,
15 intracranial, intraperitoneal, subcutaneous or intramuscular administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable
20 microspheres (*e.g.*, polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268; 5,075,109; 5,928,647; 5,811,128; 5,820,883; 5,853,763; 5,814,344 and 5,942,252. One may also employ a carrier comprising the particulate-protein complexes described in U.S. Patent No. 5,928,647, which are capable of
25 inducing a class I-restricted cytotoxic T lymphocyte responses in a host.

Such compositions may also comprise buffers (*e.g.*, neutral buffered saline or phosphate buffered saline), carbohydrates (*e.g.*, glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, bacteriostats, chelating agents such as EDTA or glutathione, adjuvants (*e.g.*, aluminum hydroxide), solutes that render
30 the formulation isotonic, hypotonic or weakly hypertonic with the blood of a recipient,

suspending agents, thickening agents and/or preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate. Compounds may also be encapsulated within liposomes using well known technology.

Any of a variety of immunostimulants may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

Within the vaccines provided herein, the adjuvant composition is preferably designed to induce an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (e.g., IFN- γ , TNF α , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (e.g., IL-4, IL-5, IL-6 and IL-10) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Preferred adjuvants for use in eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt. MPL adjuvants are available from Corixa Corporation (Seattle, WA; see US Patent Nos. 4,436,727; 4,877,611;

4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555, WO 99/33488 and U.S. Patent Nos. 6,008,200 and 5,856,462. Immunostimulatory DNA sequences are also described, for example,
5 by Sato *et al.*, *Science* 273:352, 1996. Another preferred adjuvant is a saponin, preferably QS21 (Aquila Biopharmaceuticals Inc., Framingham, MA), which may be used alone or in combination with other adjuvants. For example, an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the combination of QS21 and 3D-MPL as described in WO 94/00153, or a less reactogenic composition where the QS21 is
10 quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprise an oil-in-water emulsion and tocopherol. A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion is described in WO 95/17210.

Other preferred adjuvants include Montanide ISA 720 (Seppic, France), SAF (Chiron,
15 California, United States), ISCOMS (CSL), MF-59 (Chiron), the SBAS series of adjuvants (e.g., SBAS-2 or SBAS-4, available from SmithKline Beecham, Rixensart, Belgium), Detox (Corixa, Hamilton, MT), RC-529 (Corixa, Hamilton, MT) and other aminoalkyl glucosaminide 4-phosphates (AGPs), such as those described in pending U.S. Patent Application Serial Nos. 08/853,826 and 09/074,720, the disclosures of which are incorporated herein by reference in
20 their entireties.

Any vaccine provided herein may be prepared using well known methods that result in a combination of antigen, immune response enhancer and a suitable carrier or excipient. The compositions described herein may be administered as part of a sustained release formulation (i.e., a formulation such as a capsule, sponge or gel (composed of polysaccharides, for example)
25 that effects a slow release of compound following administration). Such formulations may generally be prepared using well known technology (*see, e.g., Coombes et al., Vaccine* 14:1429-1438, 1996) and administered by, for example, oral, rectal or subcutaneous implantation, or by implantation at the desired target site. Sustained-release formulations may contain a polypeptide, polynucleotide or antibody dispersed in a carrier matrix and/or contained
30 within a reservoir surrounded by a rate controlling membrane.

Carriers for use within such formulations are biocompatible, and may also be biodegradable; preferably the formulation provides a relatively constant level of active component release. Such carriers include microparticles of poly(lactide-co-glycolide), polyacrylate, latex, starch, cellulose, dextran and the like. Other delayed-release carriers
5 include supramolecular biovectors, which comprise a non-liquid hydrophilic core (*e.g.*, a cross-linked polysaccharide or oligosaccharide) and, optionally, an external layer comprising an amphiphilic compound, such as a phospholipid (*see e.g.*, U.S. Patent No. 5,151,254 and PCT applications WO 94/20078, WO/94/23701 and WO 96/06638). The amount of active compound contained within a sustained release formulation depends upon the site of
10 implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within pharmaceutical compositions and vaccines to facilitate production of an antigen-specific immune response that targets tumor cells. Delivery vehicles include antigen presenting cells (APCs), such as
15 dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological
20 fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to be effective as
25 a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (*see* Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (*stellate in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*), their ability to take up, process and present antigens with high efficiency and their ability to activate naïve T cell responses. Dendritic cells may, of course, be
30 engineered to express specific cell-surface receptors or ligands that are not commonly found on

dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (*see Zitvogel et al., Nature Med. 4:594-600, 1998*).

5 Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF α to cultures of monocytes harvested from peripheral blood. Alternatively, CD34
10 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF α , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce differentiation, maturation and proliferation of dendritic cells.

 Dendritic cells are conveniently categorized as "immature" and "mature" cells, which
15 allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc γ receptor and mannose receptor. The mature phenotype is typically characterized by a lower expression of
20 these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules (*e.g.*, CD40, CD80, CD86 and 4-1BB).

 APCs may generally be transfected with a polynucleotide encoding a hematological malignancy-related tumor protein (or portion or other variant thereof) such that the
25 hematological malignancy-related tumor polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a composition or vaccine comprising such transfected cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In*
30 *vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using

any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi *et al.*, *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the hematological malignancy-related tumor polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.*, vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that provides T cell help (*e.g.*, a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

Vaccines and pharmaceutical compositions may be presented in unit-dose or multi-dose containers, such as sealed ampoules or vials. Such containers are preferably hermetically sealed to preserve sterility of the formulation until use. In general, formulations may be stored as suspensions, solutions or emulsions in oily or aqueous vehicles. Alternatively, a vaccine or pharmaceutical composition may be stored in a freeze-dried condition requiring only the addition of a sterile liquid carrier immediately prior to use.

4.22 CANCER THERAPY

In further aspects of the present invention, the compositions described herein may be used for immunotherapy of cancer, such as hematological malignancy. Within such methods, pharmaceutical compositions and vaccines are typically administered to a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions and vaccines may be used to prevent the development of a cancer or to treat a patient afflicted with a cancer. A cancer may be diagnosed using criteria generally accepted in the art, including the presence of a malignant tumor. Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration of radiotherapy or conventional chemotherapeutic drugs. Administration may be by any suitable method, including administration by intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal, intradermal, anal, vaginal, topical and oral routes.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react against tumors with the administration of immune response-modifying agents (such as polypeptides and polynucleotides as provided herein).

5 Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T cells as discussed above, T lymphocytes (such as CD8⁺ cytotoxic T lymphocytes and CD4⁺ T-
10 helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The polypeptides provided
15 herein may also be used to generate antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Effector cells may generally be obtained in sufficient quantities for adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen
20 recognition *in vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above, immunoreactive polypeptides as provided herein may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic,
25 macrophage, monocyte, fibroblast and/or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example, antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system. Cultured effector cells for use in therapy must be able to grow and
30 distribute widely, and to survive long term *in vivo*. Studies have shown that cultured effector

cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (*see, for example, Cheever et al., Immunological Reviews 157:177, 1997*).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into
5 antigen presenting cells taken from a patient and clonally propagated *ex vivo* for transplant back into the same patient. Transfected cells may be reintroduced into the patient using any means known in the art, preferably in sterile form by intravenous, intracavitary, intraperitoneal or intratumor administration.

Routes and frequency of administration of the therapeutic compositions described
10 herein, as well as dosage, will vary from individual to individual, and may be readily established using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are administered, at intervals
15 of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50% above the basal (*i.e.*, untreated) level. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent
20 generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of
25 each polypeptide present in a dose ranges from about 25 μ g to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a
30 response can be monitored by establishing an improved clinical outcome (*e.g.*, more frequent

remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a hematological malignancy-related tumor protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

4.23 CANCER DETECTION AND DIAGNOSIS

In general, a cancer may be detected in a patient based on the presence of one or more hematological malignancy-related tumor proteins and/or polynucleotides encoding such proteins in a biological sample (for example, blood, sera, sputum urine and/or tumor biopsies) obtained from the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as hematological malignancy. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein generally permit detection of the level of antigen that binds to the agent in the biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer. In general, a hematological malignancy-related tumor sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

There are a variety of assay formats known to those of ordinary skill in the art for using a binding agent to detect polypeptide markers in a sample. *See, e.g., Harlow and Lane, Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b) detecting in the sample a level of polypeptide that binds to the binding agent; and (c) comparing the level of polypeptide with a predetermined cut-off value.

In a preferred embodiment, the assay involves the use of binding agent immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection reagent that contains a reporter group and specifically binds to the binding agent/polypeptide complex. Such detection reagents may

comprise, for example, a binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G, protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding agent. Suitable polypeptides for use within such assays include full length hematological malignancy-related tumor proteins and portions thereof to which the binding agent binds, as described above.

The solid support may be any material known to those of ordinary skill in the art to which the tumor protein may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 μ g, and preferably about 100 ng to about 1 μ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the

binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.*, Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

5 In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a
10 second antibody capable of binding to a different site on the polypeptide) containing a reporter group is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

 More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking
15 agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is a period of time that is sufficient to detect the
20 presence of polypeptide within a sample obtained from an individual with hematological malignancy. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time.
25 At room temperature, an incubation time of about 30 minutes is generally sufficient.

 Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound detection reagent is then removed and bound detection reagent is
5 detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an
10 enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of a cancer, such as hematological malignancy, the signal detected from the reporter group that remains bound to the solid support is generally
15 compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred embodiment, the
20 cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett *et al.*, *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on
25 the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than
30 the cut-off value determined by this method is considered positive for a cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the tumor proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use hematological malignancy-related tumor polypeptides to detect antibodies that bind to such polypeptides in a biological sample. The detection of such hematological malignancy-related tumor protein specific antibodies may correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with a hematological malignancy-related tumor protein in a biological sample. Within certain methods, a biological sample comprising CD4⁺ and/or CD8⁺ T cells isolated

from a patient is incubated with a hematological malignancy-related tumor polypeptide, a polynucleotide encoding such a polypeptide and/or an APC that expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T
5 cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with polypeptide (*e.g.*, 5 - 25 µg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of hematological malignancy-related tumor polypeptide to serve as a control. For CD4⁺ T cells,
10 activation is preferably detected by evaluating proliferation of the T cells. For CD8⁺ T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

As noted above, a cancer may also, or alternatively, be detected based on the level of
15 mRNA encoding a hematological malignancy-related tumor protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of a hematological malignancy-related tumor cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.*, hybridizes to) a polynucleotide encoding the hematological malignancy-related tumor
20 protein. The amplified cDNA is then separated and detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding a hematological malignancy-related tumor protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the tumor protein in a biological sample.

25 To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding a hematological malignancy-related tumor protein that is at least 10 nucleotides, and preferably at least 20 nucleotides, in length. Preferably, oligonucleotide primers and/or probes
30 hybridize to a polynucleotide encoding a polypeptide described herein under moderately

stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers comprise at least 10 contiguous nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a sequence recited in SEQ ID NO:1-146. Techniques for both PCR based assays and hybridization assays are well known in the art (*see*, for example, Mullis *et al.*, *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989).

One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample, such as biopsy tissue, and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered positive.

In another embodiment, the compositions described herein may be used as markers for the progression of cancer. In this embodiment, assays as described above for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) or polynucleotide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a cancer is progressing in those patients in whom the level of polypeptide or polynucleotide detected increases over time. In contrast, the cancer is not progressing when the level of reactive polypeptide or polynucleotide either remains constant or decreases with time.

Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

As noted above, to improve sensitivity, multiple hematological malignancy-related tumor protein markers may be assayed within a given sample. It will be apparent that binding agents specific for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of tumor protein markers may be based on routine experiments to determine combinations that results in optimal sensitivity. In addition, or alternatively, assays for tumor proteins provided herein may be combined with assays for other known tumor antigens.

4.24 PREPARATION OF DNA SEQUENCES

Certain nucleic acid sequences of cDNA molecules encoding portions of hematological malignancy-related antigens were isolated by PCRTM-based subtraction. This technique serves to normalize differentially expressed cDNAs, facilitating the recovery of rare transcripts, and also has the advantage of permitting enrichment of cDNAs with small amounts of polyA RNA material and without multiple rounds of hybridization. To obtain antigens overexpressed in non-Hodgkin's lymphomas, two subtractions were performed with a tester library prepared from a pool of three T cell non-Hodgkin's lymphoma mRNAs. The two libraries were independently subtracted with different pools of driver cDNAs. Driver #1 contained cDNA prepared from specific normal tissues (lymph node, bone marrow, T cells, heart and brain), and this subtraction generated the library TCS-D1 (T cell non-Hodgkin's lymphoma subtracted library with driver #1). Driver #2 contained non-specific normal tissues (colon, large intestine, lung, pancreas, spinal cord, skeletal muscle, liver, kidney, skin and brain), and this subtraction generated the library TCS-D2 (T cell non-Hodgkin's lymphoma subtraction library with driver #2). Two other subtractions were performed with a tester library prepared from a pool of three B cell non-Hodgkin's lymphoma mRNAs. The two libraries were independently subtracted with different pools of driver cDNAs. Driver #1 contained cDNA prepared from specific normal tissues (lymph node, bone marrow, B cells, heart and brain), and this subtraction generated the library BCNHL/D1 (B cell non-Hodgkin's lymphoma subtracted library with driver #1). Driver #2 contained non-specific normal tissues (brain, lung, pancreas, spinal cord, skeletal muscle, colon, spleen, large intestine and PBMC), and this subtraction generated the library BCNHL/D2 (B cell non-Hodgkin's lymphoma subtraction library with driver #2).

PCRTM-amplified pools were generated from the subtracted libraries and clones were sequenced.

Hematological malignancy-related antigen sequences may be further characterized using any of a variety of well known techniques. For example, PCRTM amplified clones may be arrayed onto glass slides for microarray analysis. To determine tissue distribution, the arrayed clones may be used as targets to be hybridized with different first strand cDNA probes, including lymphoma probes, leukemia probes and probes from different normal tissues. Leukemia and lymphoma probes may be generated from cryopreserved samples obtained at the time of diagnosis from NHL, Hodgkin's disease, AML, CML, CLL, ALL, MDS and myeloma patients with poor outcome (patients who failed to achieve complete remission following conventional chemotherapy or relapsed) or good outcome (patients who achieved long term remission). To analyze gene expression during hematopoietic differentiation, probes may be generated from >95% pure fractions of CD34+, CD2+, CD14+, CD15+ and CD19+ cells derived from healthy individuals.

Polynucleotide variants may generally be prepared by any method known in the art, including chemical synthesis by, for example, solid phase phosphoramidite chemical synthesis. Modifications in a polynucleotide sequence may also be introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (*see* Adelman *et al.*, *DNA* 2:183, 1983). Alternatively, RNA molecules may be generated by *in vitro* or *in vivo* transcription of DNA sequences, provided that the DNA is incorporated into a vector with a suitable RNA polymerase promoter (such as T7 or SP6). Certain portions may be used to prepare an encoded polypeptide, as described herein. In addition, or alternatively, a portion may be administered to a patient such that the encoded polypeptide is generated *in vivo* (*e.g.*, by transfecting antigen-presenting cells, such as dendritic cells, with a cDNA construct encoding a hematological malignancy-related antigen, and administering the transfected cells to the patient).

A portion of a sequence complementary to a coding sequence (*i.e.*, an antisense polynucleotide) may also be used as a probe or to modulate hematological malignancy-related antigen expression. cDNA constructs that can be transcribed into antisense RNA may also be introduced into cells or tissues to facilitate the production of antisense RNA. An antisense

polynucleotide may be used, as described herein, to inhibit expression of a hematological malignancy-related antigen. Antisense technology can be used to control gene expression through triple-helix formation, which compromises the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors or regulatory molecules (see

5 Gee *et al.*, In Huber and Carr, *Molecular and Immunologic Approaches*, Futura Publishing Co. (Mt. Kisco, NY; 1994)). Alternatively, an antisense molecule may be designed to hybridize with a control region of a gene (*e.g.*, promoter, enhancer or transcription initiation site), and block transcription of the gene; or to block translation by inhibiting binding of a transcript to ribosomes.

10 A portion of a coding sequence or of a complementary sequence may also be designed as a probe or primer to detect gene expression. Probes may be labeled with a variety of reporter groups, such as radionuclides and enzymes, and are preferably at least 10 nucleotides in length, more preferably at least 20 nucleotides in length and still more preferably at least 30 nucleotides in length. Primers, as noted above, are preferably 22-30 nucleotides in length.

15 Any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such as inosine, queosine and wybutosine, as well as acetyl-, methyl-, thio- and other modified forms of adenine, cytidine, 20 guanine, thymine and uridine.

Hematological malignancy-related antigen polynucleotides may be joined to a variety of other nucleotide sequences using established recombinant DNA techniques. For example, a polynucleotide may be cloned into any of a variety of cloning vectors, including plasmids, phagemids, lambda phage derivatives and cosmids. Vectors of particular interest include

25 expression vectors, replication vectors, probe generation vectors and sequencing vectors. In general, a vector will contain an origin of replication functional in at least one organism, convenient restriction endonuclease sites and one or more selectable markers. Other elements will depend upon the desired use, and will be apparent to those of ordinary skill in the art.

Within certain embodiments, polynucleotides may be formulated so as to permit entry

30 into a cell of a mammal, and expression therein. Such formulations are particularly useful for

therapeutic purposes, as described below. Those of ordinary skill in the art will appreciate that there are many ways to achieve expression of a polynucleotide in a target cell, and any suitable method may be employed. For example, a polynucleotide may be incorporated into a viral vector such as, but not limited to, adenovirus, adeno-associated virus, retrovirus, or vaccinia or other pox virus (*e.g.*, avian pox virus). Techniques for incorporating DNA into such vectors are well known to those of ordinary skill in the art. A retroviral vector may additionally transfer or incorporate a gene for a selectable marker (to aid in the identification or selection of transduced cells) and/or a targeting moiety, such as a gene that encodes a ligand for a receptor on a specific target cell, to render the vector target specific. Targeting may also be accomplished using an antibody, by methods known to those of ordinary skill in the art.

Other formulations for therapeutic purposes include colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. A preferred colloidal system for use as a delivery vehicle *in vitro* and *in vivo* is a liposome (*i.e.*, an artificial membrane vesicle). The preparation and use of such systems is well known in the art.

4.25 THERAPEUTIC METHODS

In further aspects of the present invention, the compositions described herein may be used for immunotherapy of hematological malignancies including adult and pediatric AML, CML, ALL, CLL, myelodysplastic syndromes (MDS), myeloproliferative syndromes (MPS), secondary leukemia, multiple myeloma, Hodgkin's lymphoma and Non-Hodgkin's lymphomas. In addition, compositions described herein may be used for therapy of diseases associated with an autoimmune response against hematopoietic precursor cells, such as severe aplastic anemia.

Immunotherapy may be performed using any of a variety of techniques, in which compounds or cells provided herein function to remove hematological malignancy-related antigen-expressing cells from a patient. Such removal may take place as a result of enhancing or inducing an immune response in a patient specific for hematological malignancy-related antigen or a cell expressing hematological malignancy-related antigen. Alternatively, hematological malignancy-related antigen-expressing cells may be removed *ex vivo* (*e.g.*, by

treatment of autologous bone marrow, peripheral blood or a fraction of bone marrow or peripheral blood). Fractions of bone marrow or peripheral blood may be obtained using any standard technique in the art.

Within such methods, pharmaceutical compositions and vaccines are typically administered to a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may or may not be afflicted with a hematological malignancy. Accordingly, the above pharmaceutical compositions and vaccines may be used to prevent the development of a malignancy or to treat a patient afflicted with a malignancy. A hematological malignancy may be diagnosed using criteria generally accepted in the art. Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration of radiotherapy or conventional chemotherapeutic drugs, or bone marrow transplantation (autologous, allogeneic or syngeneic).

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react against tumors with the administration of immune response-modifying agents (such as polypeptides and polynucleotides as provided herein).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T cells as discussed above, T lymphocytes (such as CD8⁺ cytotoxic T lymphocytes and CD4⁺ T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The polypeptides provided herein may also be used to generate antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Effector cells may generally be obtained in sufficient quantities for adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding

single antigen-specific effector cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above, immunoreactive polypeptides as provided herein may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example, antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system. Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies have shown that cultured effector cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (*see, for example, Cheever et al., Immunological Reviews 157:177, 1997*).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into antigen presenting cells taken from a patient and clonally propagated *ex vivo* for transplant back into the same patient. Transfected cells may be reintroduced into the patient using any means known in the art, preferably in sterile form by intravenous, intracavitary, intraperitoneal or intratumor administration.

The compositions provided herein may be used alone or in combination with conventional therapeutic regimens such as surgery, irradiation, chemotherapy and/or bone marrow transplantation (autologous, syngeneic, allogeneic or unrelated). As discussed in greater detail below, binding agents and T cells as provided herein may be used for purging of autologous stem cells. Such purging may be beneficial prior to, for example, bone marrow transplantation or transfusion of blood or components thereof. Binding agents, T cells, antigen presenting cells (APC) and compositions provided herein may further be used for expanding and stimulating (or priming) autologous, allogeneic, syngeneic or unrelated hematological malignancy-related antigen-specific T-cells *in vitro* and/or *in vivo*. Such hematological malignancy-related antigen-specific T cells may be used, for example, within donor lymphocyte infusions.

Routes and frequency of administration of the therapeutic compositions described herein, as well as dosage, will vary from individual to individual, and may be readily established using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50% above the basal (*i.e.*, untreated) level. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about 100 µg to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a hematological malignancy-related antigen generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

Within further aspects, methods for inhibiting the development of a malignant disease associated with hematological malignancy-related antigen expression involve the

administration of autologous T cells that have been activated in response to a hematological malignancy-related antigen polypeptide or hematological malignancy-related antigen-expressing APC, as described above. Such T cells may be CD4⁺ and/or CD8⁺, and may be proliferated as described above. The T cells may be administered to the individual in an amount effective to inhibit the development of a malignant disease. Typically, about 1×10^9 to 1×10^{11} T cells/M² are administered intravenously, intracavitary or in the bed of a resected tumor. It will be evident to those skilled in the art that the number of cells and the frequency of administration will be dependent upon the response of the patient.

Within certain embodiments, T cells may be stimulated prior to an autologous bone marrow transplantation. Such stimulation may take place *in vivo* or *in vitro*. For *in vitro* stimulation, bone marrow and/or peripheral blood (or a fraction of bone marrow or peripheral blood) obtained from a patient may be contacted with a hematological malignancy-related antigen polypeptide, a polynucleotide encoding a hematological malignancy-related antigen polypeptide and/or an APC that expresses a hematological malignancy-related antigen polypeptide under conditions and for a time sufficient to permit the stimulation of T cells as described above. Bone marrow, peripheral blood stem cells and/or hematological malignancy-related antigen-specific T cells may then be administered to a patient using standard techniques.

Within related embodiments, T cells of a related or unrelated donor may be stimulated prior to a syngeneic or allogeneic (related or unrelated) bone marrow transplantation. Such stimulation may take place *in vivo* or *in vitro*. For *in vitro* stimulation, bone marrow and/or peripheral blood (or a fraction of bone marrow or peripheral blood) obtained from a related or unrelated donor may be contacted with a hematological malignancy-related antigen polypeptide, hematological malignancy-related antigen polynucleotide and/or APC that expresses a hematological malignancy-related antigen polypeptide under conditions and for a time sufficient to permit the stimulation of T cells as described above. Bone marrow, peripheral blood stem cells and/or hematological malignancy-related antigen-specific T cells may then be administered to a patient using standard techniques.

Within other embodiments, hematological malignancy-related antigen-specific T cells, antibodies or antigen-binding fragments thereof as described herein may be used to remove cells expressing hematological malignancy-related antigen from a biological sample, such as

autologous bone marrow, peripheral blood or a fraction of bone marrow or peripheral blood (e.g., CD34⁺ enriched peripheral blood (PB) prior to administration to a patient). Such methods may be performed by contacting the biological sample with such T cells, antibodies or antibody fragments under conditions and for a time sufficient to permit the reduction of hematological malignancy-related antigen expressing cells to less than 10%, preferably less than 5% and more preferably less than 1%, of the total number of myeloid or lymphatic cells in the bone marrow or peripheral blood. Such contact may be achieved, for example, using a column to which antibodies are attached using standard techniques. Antigen-expressing cells are retained on the column. The extent to which such cells have been removed may be readily determined by standard methods such as, for example, qualitative and quantitative PCR analysis, morphology, immunohistochemistry and FACS analysis. Bone marrow or PB (or a fraction thereof) may then be administered to a patient using standard techniques.

4.26 DIAGNOSTIC METHODS

In general, a hematological malignancy may be detected in a patient based on the presence of hematological malignancy-related antigen and/or polynucleotide in a biological sample (such as blood, sera, urine and/or tumor biopsies) obtained from the patient. In other words, hematological malignancy-related antigens may be used as a marker to indicate the presence or absence of such a malignancy. The binding agents provided herein generally permit detection of the level of antigen that binds to the agent in the biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding hematological malignancy-related antigen, which is also indicative of the presence or absence of a hematological malignancy. In general, hematological malignancy-related antigen should be present at a level that is at least three fold higher in a sample obtained from a patient afflicted with a hematological malignancy than in the sample obtained from an individual not so afflicted.

There are a variety of assay formats known to those of ordinary skill in the art for using a binding agent to detect polypeptide markers in a sample. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a hematological malignancy in a patient may be determined by (a)

contacting a biological sample obtained from a patient with a binding agent; (b) detecting in the sample a level of polypeptide that binds to the binding agent; and (c) comparing the level of polypeptide with a predetermined cut-off value.

In a preferred embodiment, the assay involves the use of binding agent immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection reagent that contains a reporter group and specifically binds to the binding agent/polypeptide complex. Such detection reagents may comprise, for example, a binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G, protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding agent. Suitable polypeptides for use within such assays include full length hematological malignancy-related antigens and portions thereof to which the binding agent binds, as described above.

The solid support may be any material known to those of ordinary skill in the art to which the hematological malignancy-related antigen polypeptide may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact

time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 μ g, and preferably about 100 ng to about 1 μ g, is sufficient to immobilize an adequate amount of binding agent.

5 Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and
10 an active hydrogen on the binding partner (*see, e.g.*, Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the
15 sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to a different site on the polypeptide) containing a reporter group is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

20 More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20TM (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a
25 suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with a hematological malignancy. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide.
30 Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium

may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which
5 contains a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a
10 period of time. Unbound detection reagent is then removed and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to
15 detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of a hematological malignancy, the signal
20 detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a hematological malignancy is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without the malignancy. In general, a sample generating a signal that is three standard deviations above the
25 predetermined cut-off value is considered positive for the malignancy. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett *et al.*, *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates
30 (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result.

The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a malignancy.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the presence of a hematological malignancy. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the hematological malignancy-related antigen sequences or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to

those of ordinary skill in the art that the above protocols may be readily modified to use hematological malignancy-related antigen polypeptides to detect antibodies that bind to such polypeptides in a biological sample. The detection of hematological malignancy-related antigen-specific antibodies may correlate with the presence of a hematological.

5 A malignancy may also, or alternatively, be detected based on the presence of T cells that specifically react with hematological malignancy-related antigen in a biological sample. Within certain methods, a biological sample comprising CD4⁺ and/or CD8⁺ T cells isolated from a patient is incubated with a hematological malignancy-related antigen polypeptide, a polynucleotide encoding such a polypeptide and/or an APC that expresses such a polypeptide,
10 and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with Mtb-81 or Mtb-67.2 polypeptide (*e.g.*, 5 - 25 µg/ml). It may be desirable to
15 incubate another aliquot of a T cell sample in the absence of hematological malignancy-related antigen polypeptide to serve as a control. For CD4⁺ T cells, activation is preferably detected by evaluating proliferation of the T cells. For CD8⁺ T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the
20 presence of a hematological malignancy in the patient.

 As noted above, a hematological malignancy may also, or alternatively, be detected based on the level of mRNA encoding hematological malignancy-related antigen in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of hematological malignancy-related
25 antigen cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.*, hybridizes to) a polynucleotide encoding the hematological malignancy-related antigen protein. The amplified cDNA is then separated and detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding hematological malignancy-related

antigen may be used in a hybridization assay to detect the presence of polynucleotide encoding hematological malignancy-related antigen in a biological sample.

To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least
5 about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding hematological malignancy-related antigen that is at least 10 nucleotides, and preferably at least 20 nucleotides, in length. Preferably, oligonucleotide primers and/or probes hybridize to a polynucleotide encoding a polypeptide described herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be
10 usefully employed in the diagnostic methods described herein preferably are at least 10-40 nucleotides in length. Techniques for both PCR based assays and hybridization assays are well known in the art (*see, for example, Mullis et al., Cold Spring Harbor Symp. Quant. Biol., 51:263, 1987; Erlich ed., PCR Technology, Stockton Press, NY, 1989*).

One preferred assay employs RT-PCR, in which PCR is applied in conjunction with
15 reverse transcription. Typically, RNA is extracted from a biological sample such as a biopsy tissue and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a hematological malignancy.
20 The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the sample from a normal individual is typically considered positive.

In preferred embodiments, such assays may be performed using samples enriched for
25 cells expressing the hematological malignancy-related antigen(s) of interest. Such enrichment may be achieved, for example, using a binding agent as provided herein to remove the cells from the remainder of the biological sample. The removed cells may then be assayed as described above for biological samples.

In further embodiments, hematological malignancy-related antigens may be used as
30 markers for monitoring disease progression or the response to therapy of a hematological

malignancy. In this embodiment, assays as described above for the diagnosis of a hematological malignancy may be performed over time, and the change in the level of reactive polypeptide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a malignancy is progressing in those patients in whom the level of polypeptide detected by the binding agent increases over time. In contrast, the malignancy is not progressing when the level of reactive polypeptide either remains constant or decreases with time.

Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

As noted above, to improve sensitivity, multiple markers may be assayed within a given sample. It will be apparent that binding agents specific for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of markers may be based on routine experiments to determine combinations that results in optimal sensitivity.

Further diagnostic applications include the detection of extramedullary disease (e.g., cerebral infiltration of blasts in leukemias). Within such methods, a binding agent may be coupled to a tracer substance, and the diagnosis is performed *in vivo* using well known techniques. Coupled binding agent may be administered as described above, and extramedullary disease may be detected based on assaying the presence of tracer substance. Alternatively, a tracer substance may be associated with a T cell specific for hematological malignancy-related antigen, permitting detection of extramedullary disease based on assays to detect the location of the tracer substance.

4.27 EXEMPLARY DEFINITIONS

In accordance with the present invention, nucleic acid sequences include, but are not limited to, DNAs (including and not limited to genomic or extragenomic DNAs), genes, peptide nucleic acids (PNAs) RNAs (including, but not limited to, rRNAs, mRNAs and

tRNAs), nucleosides, and suitable nucleic acid segments either obtained from native sources, chemically synthesized, modified, or otherwise prepared in whole or in part by the hand of man.

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any methods and compositions similar or equivalent to those described herein can be used in the practice or testing of the present invention, the preferred methods and compositions are described herein. For purposes of the present invention, the following terms are defined below:

10 **A, an:** In accordance with long standing patent law convention, the words "a" and "an" when used in this application, including the claims, denotes "one or more".

Expression: The combination of intracellular processes, including transcription and translation undergone by a polynucleotide such as a structural gene to synthesize the encoded peptide or polypeptide.

15 **Promoter:** a term used to generally describe the region or regions of a nucleic acid sequence that regulates transcription.

Regulatory Element: a term used to generally describe the region or regions of a nucleic acid sequence that regulates transcription.

Structural gene: A gene or sequence region that is expressed to produce an encoded peptide or polypeptide.

20 **Transformation:** A process of introducing an exogenous polynucleotide sequence (e.g., a vector, a recombinant DNA or RNA molecule) into a host cell or protoplast in which that exogenous nucleic acid segment is incorporated into at least a first chromosome or is capable of autonomous replication within the transformed host cell. Transfection, 25 electroporation, and naked nucleic acid uptake all represent examples of techniques used to transform a host cell with one or more polynucleotides.

Transformed cell: A host cell whose nucleic acid complement has been altered by the introduction of one or more exogenous polynucleotides into that cell.

Transgenic cell: Any cell derived or regenerated from a transformed cell or derived from a transgenic cell, or from the progeny or offspring of any generation of such a transformed host cell.

Transgenic animal: An animal or a progeny or an offspring of any generation thereof
5 that is derived from a transformed animal cell, wherein the animal's DNA contains an introduced exogenous nucleic acid molecule not originally present in a native, wild type, non-transgenic animal of the same species. The terms "transgenic animal" and "transformed animal" have sometimes been used in the art as synonymous terms to define an animal, the genetic contents of which has been modified to contain one or more exogenous nucleic acid
10 segments.

Vector: A nucleic acid molecule, typically comprised of DNA, capable of replication in a host cell and/or to which another nucleic acid segment can be operatively linked so as to bring about replication of the attached segment. A plasmid, cosmid, or a virus is an exemplary vector.

15 The terms "substantially corresponds to", "substantially homologous", or "substantial identity" as used herein denotes a characteristic of a nucleic acid or an amino acid sequence, wherein a selected nucleic acid or amino acid sequence has at least about 70 or about 75 percent sequence identity as compared to a selected reference nucleic acid or amino acid sequence. More typically, the selected sequence and the reference sequence will have at least
20 about 76, 77, 78, 79, 80, 81, 82, 83, 84 or even 85 percent sequence identity, and more preferably at least about 86, 87, 88, 89, 90, 91, 92, 93, 94, or 95 percent sequence identity. More preferably still, highly homologous sequences often share greater than at least about 96, 97, 98, or 99 percent sequence identity between the selected sequence and the reference sequence to which it was compared. The percentage of sequence identity may be calculated
25 over the entire length of the sequences to be compared, or may be calculated by excluding small deletions or additions which total less than about 25 percent or so of the chosen reference sequence. The reference sequence may be a subset of a larger sequence, such as a portion of a gene or flanking sequence, or a repetitive portion of a chromosome. However, in the case of sequence homology of two or more polynucleotide sequences, the reference
30 sequence will typically comprise at least about 18-25 nucleotides, more typically at least

about 26 to 35 nucleotides, and even more typically at least about 40, 50, 60, 70, 80, 90, or even 100 or so nucleotides. Desirably, which highly homologous fragments are desired, the extent of percent identity between the two sequences will be at least about 80%, preferably at least about 85%, and more preferably about 90% or 95% or higher, as readily determined by one or more of the sequence comparison algorithms well-known to those of skill in the art, such as e.g., the FASTA program analysis described by Pearson and Lipman (1988).

The term "naturally occurring" as used herein as applied to an object refers to the fact that an object can be found in nature. For example, a polypeptide or polynucleotide sequence that is present in an organism (including viruses) that can be isolated from a source in nature and which has not been intentionally modified by the hand of man in a laboratory is naturally-occurring. As used herein, laboratory strains of rodents that may have been selectively bred according to classical genetics are considered naturally occurring animals.

As used herein, a "heterologous" is defined in relation to a predetermined referenced gene sequence. For example, with respect to a structural gene sequence, a heterologous promoter is defined as a promoter which does not naturally occur adjacent to the referenced structural gene, but which is positioned by laboratory manipulation. Likewise, a heterologous gene or nucleic acid segment is defined as a gene or segment that does not naturally occur adjacent to the referenced promoter and/or enhancer elements.

"Transcriptional regulatory element" refers to a polynucleotide sequence that activates transcription alone or in combination with one or more other nucleic acid sequences. A transcriptional regulatory element can, for example, comprise one or more promoters, one or more response elements, one or more negative regulatory elements, and/or one or more enhancers.

As used herein, a "transcription factor recognition site" and a "transcription factor binding site" refer to a polynucleotide sequence(s) or sequence motif(s) which are identified as being sites for the sequence-specific interaction of one or more transcription factors, frequently taking the form of direct protein-DNA binding. Typically, transcription factor binding sites can be identified by DNA footprinting, gel mobility shift assays, and the like, and/or can be predicted on the basis of known consensus sequence motifs, or by other methods known to those of skill in the art.

As used herein, the term "operably linked" refers to a linkage of two or more polynucleotides or two or more nucleic acid sequences in a functional relationship. A nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For instance, a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the coding sequence. Operably linked means that the DNA sequences being linked are typically contiguous and, where necessary to join two protein coding regions, contiguous and in reading frame. However, since enhancers generally function when separated from the promoter by several kilobases and intronic sequences may be of variable lengths, some polynucleotide elements may be operably linked but not contiguous.

"Transcriptional unit" refers to a polynucleotide sequence that comprises at least a first structural gene operably linked to at least a first *cis*-acting promoter sequence and optionally linked operably to one or more other *cis*-acting nucleic acid sequences necessary for efficient transcription of the structural gene sequences, and at least a first distal regulatory element as may be required for the appropriate tissue-specific and developmental transcription of the structural gene sequence operably positioned under the control of the promoter and/or enhancer elements, as well as any additional *cis* sequences that are necessary for efficient transcription and translation (*e.g.*, polyadenylation site(s), mRNA stability controlling sequence(s), *etc.*

As noted above, the present invention is generally directed to compositions and methods for using the compositions, for example in the therapy and diagnosis of cancer, such as hematological malignancy. Certain illustrative compositions described herein include hematological malignancy-related tumor polypeptides, polynucleotides encoding such polypeptides, binding agents such as antibodies, antigen presenting cells (APCs) and/or immune system cells (*e.g.*, T cells). A "hematological malignancy-related tumor protein," as the term is used herein, refers generally to a protein that is expressed in hematological malignancy-related tumor cells at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in a normal tissue, as determined using a representative assay provided herein. Certain hematological malignancy-related tumor proteins

are tumor proteins that react detectably (within an immunoassay, such as an ELISA or Western blot) with antisera of a patient afflicted with hematological malignancy.

4.28 BIOLOGICAL FUNCTIONAL EQUIVALENTS

5 Modification and changes may be made in the structure of the polynucleotides and peptides of the present invention and still obtain a functional molecule that encodes a peptide with desirable characteristics, or still obtain a genetic construct with the desirable expression specificity and/or properties. As it is often desirable to introduce one or more mutations into a specific polynucleotide sequence, various means of introducing mutations into a polynucleotide
10 or peptide sequence known to those of skill in the art may be employed for the preparation of heterologous sequences that may be introduced into the selected cell or animal species. In certain circumstances, the resulting encoded peptide sequence is altered by this mutation, or in other cases, the sequence of the peptide is unchanged by one or more mutations in the encoding polynucleotide. In other circumstances, one or more changes are introduced into the promoter
15 and/or enhancer regions of the polynucleotide constructs to alter the activity, or specificity of the expression elements and thus alter the expression of the heterologous therapeutic nucleic acid segment operably positioned under the control of the elements.

 When it is desirable to alter the amino acid sequence of one or more of the heterologous peptides encoded by the expression construct to create an equivalent, or even an improved,
20 second-generation molecules, the amino acid changes may be achieved by changing one or more of the codons of the encoding DNA sequence, according to Table 1.

 For example, certain amino acids may be substituted for other amino acids in a protein structure without appreciable loss of interactive binding capacity with structures such as, for example, antigen-binding regions of antibodies or binding sites on substrate molecules. Since it
25 is the interactive capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid sequence substitutions can be made in a protein sequence, and, of course, its underlying DNA coding sequence, and nevertheless obtain a protein with like properties. It is thus contemplated by the inventors that various changes may be made in the peptide sequences of the disclosed compositions, or corresponding DNA sequences which
30 encode said peptides without appreciable loss of their biological utility or activity.

TABLE 1

Amino Acids			Codons						
Alanine	Ala	A	GCA	GCC	GCG	GCU			
Cysteine	Cys	C	UGC	UGU					
Aspartic acid	Asp	D	GAC	GAU					
Glutamic acid	Glu	E	GAA	GAG					
Phenylalanine	Phe	F	UUC	UUU					
Glycine	Gly	G	GGA	GGC	GGG	GGU			
Histidine	His	H	CAC	CAU					
Isoleucine	Ile	I	AUA	AUC	AUU				
Lysine	Lys	K	AAA	AAG					
Leucine	Leu	L	UUA	UUG	CUA	CUC	CUG	CUU	
Methionine	Met	M	AUG						
Asparagine	Asn	N	AAC	AAU					
Proline	Pro	P	CCA	CCC	CCG	CCU			
Glutamine	Gln	Q	CAA	CAG					
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGU	
Serine	Ser	S	AGC	AGU	UCA	UCC	UCG	UCU	
Threonine	Thr	T	ACA	ACC	ACG	ACU			
Valine	Val	V	GUA	GUC	GUG	GUU			
Tryptophan	Trp	W	UGG						
Tyrosine	Tyr	Y	UAC	UAU					

In making such changes, the hydropathic index of amino acids may be considered. The importance of the hydropathic amino acid index in conferring interactive biologic function on a protein is generally understood in the art (Kyte and Doolittle, 1982, incorporate herein by reference). It is accepted that the relative hydropathic character of the amino acid contributes to the secondary structure of the resultant protein, which in turn defines the interaction of the protein with other molecules, for example, enzymes, substrates, receptors, DNA, antibodies, antigens, and the like. Each amino acid has been assigned a hydropathic index on the basis of

their hydrophobicity and charge characteristics (Kyte and Doolittle, 1982), these are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (-0.4); threonine (-0.7); serine (-0.8); tryptophan (-0.9); tyrosine (-1.3); proline (-1.6); histidine (-3.2); glutamate (-3.5); glutamine (-3.5); aspartate (-3.5);
5 asparagine (-3.5); lysine (-3.9); and arginine (-4.5).

It is known in the art that certain amino acids may be substituted by other amino acids having a similar hydropathic index or score and still result in a protein with similar biological activity, *i.e.* still obtain a biological functionally equivalent protein. In making such changes, the substitution of amino acids whose hydropathic indices are within ± 2 is preferred, those that
10 are within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred. It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. U. S. Patent 4,554,101, incorporated herein by reference, states that the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with a biological property of the protein.

15 As detailed in U. S. Patent 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0); lysine (+3.0); aspartate ($+3.0 \pm 1$); glutamate ($+3.0 \pm 1$); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (-0.4); proline (-0.5 ± 1); alanine (-0.5); histidine (-0.5); cysteine (-1.0); methionine (-1.3); valine (-1.5); leucine (-1.8); isoleucine (-1.8); tyrosine (-2.3); phenylalanine (-2.5); tryptophan (-3.4).

20 It is understood that an amino acid can be substituted for another having a similar hydrophilicity value and still obtain a biologically equivalent, and in particular, an immunologically equivalent protein. In such changes, the substitution of amino acids whose hydrophilicity values are within ± 2 is preferred, those that are within ± 1 are particularly preferred, and those within ± 0.5 are even more particularly preferred.

25 As outlined above, amino acid substitutions are generally therefore based on the relative similarity of the amino acid side-chain substituents, for example, their hydrophobicity, hydrophilicity, charge, size, and the like. Exemplary substitutions which take several of the foregoing characteristics into consideration are well known to those of skill in the art and include: arginine and lysine; glutamate and aspartate; serine and threonine; glutamine and
30 asparagine; and valine, leucine and isoleucine.

5. EXAMPLES

The following examples are included to demonstrate preferred embodiments of the invention. However, those of skill in the art should, in light of the present disclosure, appreciate that many changes can be made in the specific embodiments which are disclosed and still obtain a like or similar result without departing from the spirit and scope of the invention described in the appended claims.

5.1 EXAMPLE 1 -- IDENTIFICATION OF HEMATOLOGICAL MALIGNANCY-RELATED ANTIGEN POLYNUCLEOTIDES

This Example illustrates the identification of hematological malignancy-related antigen polynucleotides from non-Hodgkin's lymphomas.

Hematological malignancy-related antigen polynucleotides were isolated by PCR-based subtraction. PolyA mRNA was prepared from T cell non-Hodgkin's lymphomas, B cell non-Hodgkin's lymphomas and normal tissues. Six cDNA libraries were constructed, PCR-subtracted and analyzed. Two libraries were constructed using pools of three T cell non-Hodgkin's lymphoma mRNAs (referred to herein as TCS libraries). Two others were constructed using pools of three B cell non-Hodgkin's lymphoma mRNAs (referred to herein as BCNHL libraries). Two other libraries were constructed using a pool of 2 Hodgkin's lymphoma mRNAs (referred to herein as HLS libraries. cDNA synthesis, hybridization and PCR amplification were performed according to Clontech's user manual (PCR-Select cDNA Subtraction), with the following changes: 1) cDNA was restricted with a mixture of enzymes, including *MscI*, *PvuII*, *SstI* and *DraI*, instead of the single enzyme *RsaI*; and 2) the ratio of driver to tester cDNA was increased in the hybridization steps (to 76:1) to give a more stringent subtraction.

The two TCS libraries were independently subtracted with different pools of driver cDNAs. Driver #1 contained cDNA prepared from specific normal tissues (lymph node, bone marrow, T cells, heart and brain), and this subtraction generated the library TCS-D1 (T cell non-Hodgkin's lymphoma subtracted library with driver #1). Driver #2 contained non-specific normal tissues (colon, large intestine, lung, pancreas, spinal cord, skeletal muscle, liver, kidney,

skin and brain), and this subtraction generated the library TCS-D2 (T cell non-Hodgkin's lymphoma subtraction library with driver #2).

Similarly, the two BCNHL libraries were independently subtracted with different pools of driver cDNAs. Driver #1 contained cDNA prepared from specific normal tissues (lymph node, bone marrow, B cells, heart and brain), and this subtraction generated the library BCNHL/D1 (B cell non-Hodgkin's lymphoma subtracted library with driver #1). Driver #2 contained non-specific normal tissues (brain, lung, pancreas, spinal cord, skeletal muscle, colon, spleen, large intestine and PBMC), and this subtraction generated the library BCNHL/D2 (B cell non-Hodgkin's lymphoma subtraction library with driver #2).

The two HLS libraries were independently subtracted with different pools of driver cDNAs. Driver #1 contained cDNA prepared from specific normal tissues (lymph node, bone marrow, B cells and lung) and this subtraction generated HLS-D1 (Hodgkin's lymphoma subtraction library with driver #1). Driver #2 contained non-specific normal tissues (colon, large intestine, lung, pancreas, spinal cord, skeletal muscle, liver, kidney, skin and brain) and this generated the library HLS-D2 (Hodgkin's lymphoma subtraction library with driver #2).

To analyze the efficiency of the subtraction, actin (a housekeeping gene) was PCR amplified from dilutions of subtracted as well as unsubtracted PCR samples. Furthermore, the complexity and redundancy of each library was characterized by sequencing 96 clones from each of the PCR subtraction libraries (TCS-D1, TCS-D2, BCNHL/D1, BCNHL/D2, HLS-D1 and HLS-D2). These analyses indicated that the libraries are enriched for genes overexpressed in leukemia tissues and specifically T cell and B cell non-Hodgkin's lymphoma and M. Hodgkin's lymphoma samples.

Following PCR amplification, the cDNAs were cloned into the pCR2.1-TOPO plasmid vector (Invitrogen).

Sequences obtained from these analyses were searched against known sequences in the publicly available databases using the BLAST 2.0 release. The default BLAST parameters used were as follows: GAP PARAMETERS: Open Gap = 0, Extended Gap = 0; OUTPUT PARAMETERS: Expect = 10.0, Threshold = 0, Number of Alignments = 250; For BLASTN, the search parameters were as follows: Mismatch = -3, Reward = 1, Word size = 0. The alignments were presented pair-wise, with a window percent identity = 22. All available

protein and nucleotide databases were searched, including, PIR, SwissPROT, GenBank, Mouse EST, Human EST, Other EST, Human repeat and high throughput sequences, and published patents and patent application database.

From these, a number of unique sequences were identified that represented novel polynucleotide sequences that had not previously been described in the GenBank and other sequence databases. A number of other sequences were identified that appeared to contain significant homology with one or more sequences previously identified in the databases, although they were described only as genomic or cDNA clones, and had no known function. The remaining sequences corresponded to known genes. The clones obtained from this analysis are summarized in Tables 2-5.

TABLE 2

T CELL NON-HODGKIN'S LYMPHOMA SUBTRACTED PCR™ LIBRARY – SPECIFIC TISSUE DRIVER

Clone No.	Comments
TCD1_F1	Previously Unknown
TCD1_C2	Previously Unknown
TCD1_D6	Previously Unknown
TCD1_F8	Previously Unknown
TCD1_G8	Previously Unknown
TCD1_H12	Previously Unknown
TCD1_B12	Previously Unknown
TCD1_F12	Previously Unknown
TCD1_H5	Previously Unknown
TCD1_A6	Previously Unknown
TCD1_B1	Previously Unknown
TCD1_E1	Previously Unknown
TCD1_D2	Previously Unknown
TCD1_H2	Previously Unknown
TCD1_C4	Previously Unknown
TCD1_F5	Previously Unknown

Clone No.	Comments
TCD1_C6	Previously Unknown
TCD1_A7	Previously Unknown
TCD1_B7	Previously Unknown
TCD1_F7	Previously Unknown
TCD1_A8	Previously Unknown
TCD1_D8	Previously Unknown
TCD1_E8	Previously Unknown
TCD1_H9	Previously Unknown
TCD1_C10	Previously Unknown
TCD1_G11	Previously Unknown
TCD1_A12	Previously Unknown
TCD1_D12	Previously Unknown
TCD1_G6	<i>H. sapiens</i> mRNA; cDNA DKFZp566A201
TCD1_C11	<i>H. sapiens</i> mRNA; cDNA DKFZp566A201
TCD1_F2	<i>H. sapiens</i> chromosome 11 from 11p15.5 region
TCD1_G12	<i>H. sapiens</i> chromosome 11 from 11p15.5 region
TCD1_D4	<i>H. sapiens</i> mRNA for T cell leukemia/lymphoma 1
TCD1_B6	<i>H. sapiens</i> mRNA for T cell leukemia/lymphoma 1
TCD1_A2	Human chromosome 14 DNA sequence
TCD1_B2	<i>H. sapiens</i> clone 25226 mRNA sequence
TCD1_E3	Human DNA sequence from clone 686C3 on chr. 20
TCD1_C5	<i>H. sapiens</i> upregulated by 1,25-dihydroxyvitamin D-3 (VDUP1)
TCD1_D5	<i>H. sapiens</i> DNA sequence from PAC 63G5 on chr. 22q12.3-13.1
TCD1_H6	<i>H. sapiens</i> chr. 17, clone hRPK.318_A_15
TCD1_G7	Genomic sequence from human 9q34
TCD1_D9	Human mRNA for KIAA0386 gene
TCD1_E9	<i>H. sapiens</i> DNA sequence from PAC 434O14 on chr. 1q32.3.-41
TCD1_E11	<i>H. sapiens</i> chr. 22q12 BAC clone bk256d12 in MDR region
TCD1_E12	<i>H. sapiens</i> mRNA for KIAA1055 protein
TCD1_G3	<i>H. sapiens</i> tumor necrosis factor receptor superfamily member 8 (TNFRSF8)
TCD1_B8	<i>H. sapiens</i> tumor necrosis factor receptor superfamily member 8 (TNFRSF8)

Clone No.	Comments
TCD1_A1	<i>H. sapiens</i> mRNA for GS3955 (putative serine/threonine kinase)
TCD1_C1	<i>H. sapiens</i> mRNA for IRC1 protein
TCD1_D1	<i>H. sapiens</i> nucleolar phosphoprotein p130
TCD1_G1	<i>H. sapiens</i> splicing factor (45kD) (SPF45)
TCD1_E2	<i>H. sapiens</i> cAMP phosphodiesterase PDE7 (PDE7A1)
TCD1_A3	<i>H. sapiens</i> CDC13 (cell division cycle 16, <i>S. cerevisiae</i> , homolog)
TCD1_B3	<i>H. sapiens</i> cyclin Cd
TCD1_A4	<i>H. sapiens</i> retinoblastoma-like 2 (P130) (RBL2)
TCD1_B5	Human lymphocyte associated receptor of death 8 mRNA, altern. splice
TCD1_G5	<i>H. sapiens</i> clathrin, heavy polypeptide-like 2 (CLTCL2)
TCD1_F6	Human tumor necrosis factor type 1 receptor assoc. protein (TRAP1)
TCD1_C7	<i>H. sapiens</i> phospholipase C, beta 2 (PLCB2)
TCD1_D7	<i>H. sapiens</i> NADH:ubiquinone dehydrogenase 51 kDa subunit (NDUFV1)
TCD1_E7	<i>H. sapiens</i> T-cell gamma receptor locus
TCD1_H8	Rbr-2=retinoblastoma susceptibility gene
TCD1_B9	<i>H. sapiens</i> mRNA for eukaryotic initiation factor 4All
TCD1_C9	<i>H. sapiens</i> asparaginyl-tRNA synthetase (NARS)
TCD1_F10	<i>H. sapiens</i> coatomer protein complex, subunit alpha (COPA) mRNA
TCD1_G10	<i>H. sapiens</i> enterocyte differentiation associated factor EDAF-1 mRNA
TCD1_A11	<i>H. sapiens</i> ATP synthase, subunit b-like (ATP-BL)
TCD1_D11	<i>H. sapiens</i> butyrophilin, subfamily 3, member A3 (BTN3A3) mRNA
TCD1_H11	<i>H. sapiens</i> T cell receptor alpha delta locus
TCD1_H7	<i>H. sapiens</i> ribosomal protein L31, exons

TABLE 3

**T CELL NON-HODGKIN'S LYMPHOMA SUBTRACTED PCR™ LIBRARY – NONSPECIFIC
TISSUE DRIVER**

Clone No.	Comments
TCD2_D7	Previously Unknown
TCD2_E7	Previously Unknown
TCD2_H8	Previously Unknown

Clone No.	Comments
TCD2_E5	Previously Unknown
TCD2_B11	Previously Unknown
TCD2_D1	Previously Unknown
TCD2_B3	Previously Unknown
TCD2_D3	Previously Unknown
TCD2_D4	Previously Unknown
TCD2_C5	Previously Unknown
TCD2_G5	Previously Unknown
TCD2_H5	Previously Unknown
TCD2_A6	Previously Unknown
TCD2_G6	Previously Unknown
TCD2_B7	Previously Unknown
TCD2_F8	Previously Unknown
TCD2_G8	Previously Unknown
TCD2_E9	Previously Unknown
TCD2_D10	Previously Unknown
TCD2_H10	Previously Unknown
TCD2_D2	<i>H. sapiens</i> mRNA for KIAA0855 protein
TCD2_D9	<i>H. sapiens</i> mRNA for KIAA0855 protein
TCD2_H1	<i>H. sapiens</i> mRNA for KIAA0810 protein
TCD2_A2	Human DNA sequence from clone bG279B7 on chr. 1q25.1-31.1
TCD2_B2	<i>H. sapiens</i> mRNA for KIAA1049 protein
TCD2_H3	<i>H. sapiens</i> mRNA for KIAA0955 protein
TCD2_A4	<i>H. sapiens</i> chr. 17, clone hRPC.1171_I_10
TCD2_B4	<i>H. sapiens</i> mRNA for KIAA1068 protein
TCD2_B6	<i>H. sapiens</i> chr. 4 clone B266E3 map 4q25
TCD2_E8	<i>H. sapiens</i> chr. 11 from 11p15.5 region
TCD2_F9	<i>H. sapiens</i> mRNA for KIAA0926 protein
TCD2_E10	Human DNA seq from clone 328E19 on chr. 1q12-21.2
TCD2_D11	<i>H. sapiens</i> clone DJ0876A24
TCD2_E1	Human mRNA for T cell receptor alpha chain (TCR-alpha)

Clone No.	Comments
TCD2_G3	Human T-cell receptor active alpha-chain mRNA
TCD2_F7	<i>H. sapiens</i> mRNA for T-cell antigen receptor alpha-chain
TCD2_A8	<i>H. sapiens</i> mRNA for T-cell antigen receptor alpha-chain
TCD2_F10	Human T-cell receptor rearranged alpha-chain V-region
TCD2_G10	Human T-cell receptor active alpha-chain mRNA
TCD2_C11	Human mRNA for T-cell receptor alpha chain
TCD2_E11	Human mRNA for T-cell receptor alpha chain (TCR-alpha)
TCD2_G1	Human T-cell receptor beta
TCD2_F4	Human T-cell receptor beta
TCD2_B8	<i>H. sapiens</i> (clone HVB15) germline T-cell receptor beta chain variable seq.
TCD2_F3	<i>H. sapiens</i> interleukin 16
TCD2_C9	<i>H. sapiens</i> interleukin 16
TCD2_A11	<i>H. sapiens</i> small inducible cytokine subfamily A (Cys-Cys), member 21 (SCYA21)
TCD2_E12	<i>H. sapiens</i> small inducible cytokine subfamily A (Cys-Cys), member 21 (SCYA21)
TCD2_E4	Human mRNA for CD8 beta-chain glycoprotein beta chain
TCD2_C8	Human mRNA for CD8 T lymphocyte surface glycoprotein beta chain
TCD2_F1	<i>H. sapiens</i> T cell receptor alpha delta locus
TCD2_C2	<i>H. sapiens</i> WD repeat domain 1 (WDR1) mRNA
TCD2_E2	<i>H. sapiens</i> gene for TMEM1 and PWP2
TCD2_F2	<i>H. sapiens</i> chemokine receptor-4 (CXCR4) mRNA
TCD2_G2	<i>H. sapiens</i> glycogenin-2 like mRNA sequence
TCD2_H2	<i>H. sapiens</i> core-binding factor, runt domain, alpha subunit 3 (CBFA3) mRNA
TCD2_C4	<i>H. sapiens</i> EWS gene, intron 8
TCD2_G4	Human GT334 protein (GT334) gene mRNA
TCD2_H4	<i>H. sapiens</i> mRNA for squamous cell carcinoma antigen SART-3
TCD2_A5	<i>H. sapiens</i> mRNA for leucocyte adhesion receptor, L-selectin
TCD2_D5	<i>H. sapiens</i> nuclear factor related to kappa B binding protein (NFRKB) mRNA
TCD2_F5	<i>H. sapiens</i> T-cell receptor alpha delta locus

Clone No.	Comments
TCD2_E6	Human DNA for T-cell receptor constant region alpha-chain exon4
TCD2_F6	<i>H. sapiens</i> CD48 antigen
TCD2_G7	<i>H. sapiens</i> CXCR4 gene
TCD2_A9	Human APRT gene for adenine phosphoribosyltransferase
TCD2_B9	Human nuclear pore complex-associated protein TPR (tpr) mRNA
TCD2_H9	<i>H. sapiens</i> mRNA for YSK1
TCD2_B10	<i>H. sapiens</i> inositol polyphosphate-5-phosphatase, 145 kD
TCD2_C10	<i>H. sapiens</i> FUS/TLS protein gene, altern. spliced products
TCD2_F11	<i>H. sapiens</i> RH gene, promoter region
TCD2_G11	<i>H. sapiens</i> IL2-inducible T-cell kinase (ITK) mRNA
TCD2_H11	<i>H. sapiens</i> transcription factor 7 (T-cell specific, HMG-box) (TCF7)
TCD2_A12	Human O-linked GlcNAc transferase mRNA
TCD2_B12	Human tyrosine kinase TXK (txk) gene
TCD2_D12	Human T-cell antigen receptor gene T3 delta
TCD2_G12	<i>H. sapiens</i> proteasome subunit, alpha type, 3 (PSMA3) mRNA
TCD2_H12	<i>H. sapiens</i> integrin, alpha L (antigen CD11A (p180), lymphocyte function-assoc.)
TCD2_C12	<i>H. sapiens</i> ribosomal protein S20 (RPS20) mRNA
TCD2_H7	Unknown (sequence withdrawn by NCBI)
TCD2_C3	Human repeat

TABLE 4

B CELL NON-HODGKIN'S LYMPHOMA SUBTRACTED PCR™ LIBRARY – DRIVER #1

Clone No.	Comments
BCNHL/D1_B11	Previously Unknown
BCNHL/D1_F7	Previously Unknown
BCNHL/D1_H4	Previously Unknown
BCNHL/D1_H10	Previously Unknown
BCNHL/D1_H12	Previously Unknown
BCNHL/D1_A3	Previously Unknown
BCNHL/D1_A9	Previously Unknown

Clone No.	Comments
BCNHL/D1_A12	Previously Unknown
BCNHL/D1_B1	Previously Unknown
BCNHL/D1_B5	Previously Unknown
BCNHL/D1_B12	Previously Unknown
BCNHL/D1_C1	Previously Unknown
BCNHL/D1_C7	Previously Unknown
BCNHL/D1_D7	Previously Unknown
BCNHL/D1_D8	Previously Unknown
BCNHL/D1_D11	Previously Unknown
BCNHL/D1_E4	Previously Unknown
BCNHL/D1_E7	Previously Unknown
BCNHL/D1_E11	Previously Unknown
BCNHL/D1_G4	Previously Unknown
BCNHL/D1_G5	Previously Unknown
BCNHL/D1_G8	Previously Unknown
BCNHL/D1_H5	Previously Unknown
BCNHL/D1_A4	cDNA clone DKFZp564C1563, from fetal brain
BCNHL/D1_A6	cDNA clone DKFZp586E1120, from uterus
BCNHL/D1_A8	cDNA clone KIAA0663, from adult brain
BCNHL/D1_B9	Chromosome 19, cosmid R29882
BCNHL/D1_B10	cDNA clone KIAA1082, from brain
BCNHL/D1_D3	cDNA clone KIAA0084, from myeloblast cell line KG-1
BCNHL/D1_D4	cDNA clone 23851, from infant brain
BCNHL/D1_D12	cDNA clone DKFZp434B103, from adult testis
BCNHL/D1_E3	cDNA clone KIAA0008, from myeloblast cell line KG-1
BCNHL/D1_E12	cDNA clone DKFZp586J0917, from uterus
BCNHL/D1_F6	Chromosome 1, clone 97P20, Previously Unknown CDS
BCNHL/D1_G3	cDNA clone KIAA0981, from adult brain
BCNHL/D1_H2	cDNA clone DKFZp434L1435, from adult testis
BCNHL/D1_H6	cDNA clone DKFZp564B0262, from fetal brain
BCNHL/D1_H11	cDNA clone KIAA0372, from brain

Clone No.	Comments
BCNHL/D1_A7	CD20 (B1) B lymphocyte cell surface antigen
BCNHL/D1_G6	CD20 (B1) B lymphocyte cell surface antigen
BCNHL/D1_H9	CD20 (B1) B lymphocyte cell surface antigen
BCNHL/D1_D6	Ig lambda light chain
BCNHL/D1_E5	Ig lambda light chain
BCNHL/D1_D1	Lymphoid-restricted membrane protein (LRMP)
BCNHL/D1_G12	Lymphoid-restricted membrane protein (LRMP)
BCNHL/D1_A1	Nucleoporin
BCNHL/D1_A5	Kinesin-related protein
BCNHL/D1_B6	Methyl-CpG binding protein 1 (MBD4)
BCNHL/D1_B7	Heterogeneous nuclear ribonucleoprotein H1 (H)
BCNHL/D1_B8	Ubiquitin-specific protease homolog (UPH)
BCNHL/D1_C2	GTPase activating protein (GAP), 100% 86/423 bp
BCNHL/D1_C3	TCP1 ring complex, polypeptide 5 (TRIC5), cytoplasmic chaperonin
BCNHL/D1_C5	Nuclear distribution protein C homolog (NUDC)
BCNHL/D1_C6	BAX (apoptosis regulator)
BCNHL/D1_C12	Centromeric autoantigen (27 kD) (P27)
BCNHL/D1_D10	Ig kappa light chain
BCNHL/D1_F1	Serine/Threonine-protein kinase PRP4 homolog
BCNHL/D1_F4	Myocyte-specific enhancer factor 2 (XMEF2)
BCNHL/D1_F9	mRNA for 130 kD protein (p130), Rb family member
BCNHL/D1_F10	CD53 cell surface glycoprotein
BCNHL/D1_F11	Synovial sarcoma, translocated to X chromosome (SYT..SSXT)
BCNHL/D1_F12	Cyclin B
BCNHL/D1_G7	Regulator of G protein signaling (RGS13)
BCNHL/D1_G9	DEAD/H box polypeptide 16 (DDX16), mRNA helicase
BCNHL/D1_G10	Pre-mRNA splicing factor (PRP16), a putative helicase
BCNHL/D1_G11	hn ribonucleoprotein D-like gene (JKTBP1/2)
BCNHL/D1_H1	SH2 containing inositol-5-phosphatase (SHIP)
BCNHL/D1_H3	Dystrophin-related protein, utrophin (UTRN)
BCNHL/D1_H7	Inter-alpha-trypsin inhibitor H4 (ITI4)

Clone No.	Comments
BCNHL/D1_H8	Ig heavy chain

TABLE 5

B CELL NON-HODGKIN'S LYMPHOMA SUBTRACTED PCR™ LIBRARY –DRIVER #2

Clone No.	Comments
BCNHL/D2_A4	Previously Unknown
BCNHL/D2_C12	Previously Unknown
BCNHL/D2_D11	Previously Unknown
BCNHL/D2_E6	Previously Unknown
BCNHL/D2_E9	Previously Unknown
BCNHL/D2_E12	Previously Unknown
BCNHL/D2_F4	Previously Unknown
BCNHL/D2_G11	Previously Unknown
BCNHL/D2_H4	Previously Unknown
BCNHL/D2_H11	Previously Unknown
BCNHL/D2_A2	Previously Unknown
BCNHL/D2_A7	Previously Unknown
BCNHL/D2_B2	Previously Unknown
BCNHL/D2_C5	Previously Unknown
BCNHL/D2_C6	Previously Unknown
BCNHL/D2_C11	Previously Unknown
BCNHL/D2_D1	Previously Unknown
BCNHL/D2_D3	Previously Unknown
BCNHL/D2_D12	Previously Unknown
BCNHL/D2_E4	Previously Unknown
BCNHL/D2_E11	Previously Unknown
BCNHL/D2_F3	Previously Unknown
BCNHL/D2_F5	Previously Unknown
BCNHL/D2_F10	Previously Unknown
BCNHL/D2_G7	Previously Unknown
BCNHL/D2_H12	Previously Unknown

Clone No.	Comments
BCNHL/D2_B8	cDNA clone DKFZp586E0518 from uterus (telomerase, hTLP2)
BCNHL/D2_C8	cDNA clone DKFZp586E0518 from uterus (telomerase, hTLP2)
BCNHL/D2_A5	cDNA clone KIAA0101 from myeloblast cell line KG-1
BCNHL/D2_B6	Chromosome 22 (also chromosome 21 and 4)
BCNHL/D2_C2	cDNA clone DKFZp566L034, from fetal kidney
BCNHL/D2_C3	Chromosome 16, clone RPCI-11
BCNHL/D2_C10	cDNA clone KIAA0121 from myeloblast cell line KG-1
BCNHL/D2_F11	cDNA clone KIAA0185 (KG-1); apoptosis-linked gene 4 (Alg-4)
BCNHL/D2_G8	cDNA clone DKFZp434C171, from adult testis
BCNHL/D2_G9	cDNA clone KIAA0209, from myeloblast cell line KG-1
BCNHL/D2_H8	cDNA clone KIAA0855, from adult brain
BCNHL/D2_H10	Chromosome 19, cosmid R28051
BCNHL/D2_B1	Ig lambda light chain
BCNHL/D2_C1	Ig lambda light chain
BCNHL/D2_C4	Ig lambda light chain
BCNHL/D2_D8	Ig lambda light chain
BCNHL/D2_E7	Ig lambda light chain
BCNHL/D2_E8	Ig lambda light chain
BCNHL/D2_F8	Ig lambda light chain
BCNHL/D2_G4	Ig lambda light chain
BCNHL/D2_H3	Ig lambda light chain
BCNHL/D2_A8	Ig kappa light chain (82% identity)
BCNHL/D2_H7	Ig kappa light chain
BCNHL/D2_A10	CD20 (B1) B lymphocyte cell-surface antigen
BCNHL/D2_E5	CD20 (B1) B lymphocyte cell-surface antigen
BCNHL/D2_A6	CD37 antigen (CD37)
BCNHL/D2_A12	5'-end (221/408) is 100% part of histone deacetylase (HD1) CDS
BCNHL/D2_B5	p56lck (lck), protein tyrosine kinase (membrane)
BCNHL/D2_B7	Lymphoid-restricted membrane protein
BCNHL/D2_B9	Interferon consensus sequence binding protein 1 (ICSBP1)
BCNHL/D2_C7	Dp-1 transcription factor (TFDP1)

Clone No.	Comments
BCNHL/D2_D10	Transcription termination factor, RNA polymerase II (TTF2)
BCNHL/D2_E2	BCL2-related protein A1 (BCL2A1)
BCNHL/D2_E10	RNA helicase p68 (HUMP68)
BCNHL/D2_F7	Phosphate carrier, mitochondrial (PHC), nt#1-138; SWAP-70 (Ig switching), nt#135-311
BCNHL/D2_F9	TNF-induced protein (GG2-1); dendritic cell differentiation factor
BCNHL/D2_G3	Hepatocyte nuclear factor-3/forke head homolog 11B (HFH-11B)
BCNHL/D2_G5	MHC class II HLA-DQA1
BCNHL/D2_G6	90 kD heat shock protein
BCNHL/D2_G12	5'-end (120/347) is 100% part of Gamma 2-adaptin (G2AD) CDS
BCNHL/H5_H5	Ras homolog gene family, member H (ARHH)

TABLE 6
HODGKIN'S LYMPHOMA SUBTRACTED PCR™ LIBRARY

Clone No.	Comments
HLS_E3	Previously Unknown
HLS_C4	Previously Unknown
HLS_G8	Previously Unknown
HLS_D11	Previously Unknown
HLS_C1	Previously Unknown
HLS_E1	Previously Unknown
HLS_B2	Previously Unknown
HLS_A3	Previously Unknown
HLS_G3	Previously Unknown
HLS_H4	Previously Unknown
HLS_H5	Previously Unknown
HLS_D6	Previously Unknown
HLS_H7	Previously Unknown
HLS_B8	Previously Unknown
HLS_C8	Previously Unknown
HLS_D8	Previously Unknown

Clone No.	Comments
HLS_F9	Previously Unknown
HLS_F11	Previously Unknown
HLS_E5	Previously Unknown
HLS_B7	Previously Unknown
HLS_H9	Previously Unknown
HLS_H10	Previously Unknown
HLS_H1	Human mRNA for KIAA0143 gene
HLS_E2	<i>H. sapiens</i> DNA seq from PAC 163M9 on chr 1p35.1-p36.21.
HLS_H3	Human DNA seq fr clone CTA-407F11 on chr. 22q12
HLS_G5	Human HMG-17 gene for non-histone chr. protein HMG-17
HLS_B6	Human Chr. 11q12.2 PAC clone pDJ606g6
HLS_H6	<i>H. sapiens</i> mRNA; cDNA DKFZp564A132
HLS_D7	Human DNA sequence from clone RP1-506 on chr 22q12
HLS_E7	<i>H. sapiens</i> chr. 17, clone hRPC.1028_K_7
HLS_F8	<i>H. sapiens</i> 12p13.3-2.7-4.6 BAC RP11-372B4
HLS_H8	Human Chr. 16 BAC clone CIT987SK-A-355G7
HLS_A9	<i>H. sapiens</i> PAC clone DJ0320J15 from Xq23
HLS_B9	Human interferon-inducible mRNA (cDNA 6-26)
HLS_C12	Human DNA seq fr clone RP1-90L6 on chr. 22q11.21-11.23
HLS_D12	Human Chr. 16 BAC clone CIT987SK-A-735G6
HLS_E12	<i>H. sapiens</i> hypothetical protein SBBI42 mRNA
HLS_F12	<i>H. sapiens</i> DNA sequence from PAC 747L4 on chr. 1 q23-24
HLS_G12	<i>H. sapiens</i> mRNA; cDNA DKFZp586H0519
HLS_H12	<i>H. sapiens</i> clone 25114 mRNA sequence
HLS_G1	<i>H. sapiens</i> mRNA for KIAA0776 protein
HLS_A7	<i>H. sapiens</i> mRNA for KIAA0776 protein
HLS_A1	<i>H. sapiens</i> protective protein for beta-galactosidase
HLS_B1	Human proliferating cell nuclear antigen (PCNA) gene
HLS_A2	Human mRNA for myoblast cell surface antigen 24.1D5
HLS_F2	Human mRNA for interferon regulatory factor-2 (IRF-2)
HLS_C3	<i>H. sapiens</i> ADP/ATP carrier protein (ANT-2) gene

Clone No.	Comments
HLS_F3	Human GDP-dissociation inhibitor protein (Ly-GDI) mRNA
HLS_A4	<i>H. sapiens</i> microfibrillar-associated protein 1 (MFAP1) mRNA
HLS_B4	<i>H. sapiens</i> caspase 3, apoptosis-related cysteine protease (CASP3)
HLS_D4	Human thymosin beta-4 mRNA, complete cds
HLS_E4	Human lymphocyte specific INF regul. factor/INF reg. factor 4 (LSIRF/TRF4)
HLS_F4	<i>H. sapiens</i> integrin, beta 1 (fibronectin receptor, antigen CD29) (ITGB1)
HLS_G4	<i>H. sapiens</i> proteasome (prosome, macropain) subunit, alpha type, 3 (PSMA3)
HLS_A5	<i>H. sapiens</i> mRNA for Prer protein
HLS_B5	<i>H. sapiens</i> purinergic receptor P2X, ligand-gated ion channel, 5 (P2RX5)
HLS_D5	<i>H. sapiens</i> IRLB gene (3'-region)
HLS_A6	<i>H. sapiens</i> initiation factor 4B cDNA
HLS_C6	Human poly(A)-binding protein (PABP) gene, exon 15
HLS_G6	Rat proto-oncogene (Ets-1) mRNA, complete cds
HLS_G7	Human 78 kdalton glucose-regulated protein (GRP78) gene
HLS_A8	Human t-complex polypeptide 1 gene
HLS_E8	Human TRAF-interacting protein I-TRAF mRNA
HLS_C9	<i>H. sapiens</i> collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV)
HLS_D9	<i>H. sapiens</i> E46 protein mRNA, complete cds
HLS_E9	<i>H. sapiens</i> chromodomain helicase DNA binding protein 4 (CHD4)
HLS_G9	<i>H. sapiens</i> DNA for monoamine oxidase type A (14) (partial)
HLS_A10	<i>H. sapiens</i> ATP binding protein assoc. with cell differentiation (APACD)
HLS_D10	Human non-histone chr. protein HMG-14 gene, complete cds
HLS_F10	Human protein phosphatase-1 gamma 1 mRNA
HLS_C11	Human hnRNP B1 protein mRNA
HLS_E11	<i>H. sapiens</i> epithelial protein lost in neoplasm alpha (EPLIN)
HLS_G11	Human ferritin heavy chain mRNA
HLS_H11	<i>H. sapiens</i> foocen-s mRNA
HLS_B12	Human myocyte-specific enhancer factor 2A (MEF2A) gene
HLS_D1	<i>H. sapiens</i> osf-2 mRNA for osteoblast specific factor 2 (OSF-2p1)

Clone No.	Comments
HLS_H2	<i>H. sapiens</i> osf-2 mRNA for osteoblast specific factor 2 (OSF-2p1)
HLS_D3	<i>H. sapiens</i> osf-2 mRNA for osteoblast specific factor 2 (OSF-2p1)
HLS_B10	<i>H. sapiens</i> osf-2 mRNA for osteoblast specific factor 2 (OSF-2p1)
HLS_C10	<i>H. sapiens</i> osf-2 mRNA for osteoblast specific factor 2 (OSF-2p1)
HLS_G10	<i>H. sapiens</i> osf-2 mRNA for osteoblast specific factor 2 (OSF-2p1)
HLS_F1	Hu Ig superfamily cytotoxic T-lymphocyte-assoc. protein (CTLA-4) gene
HLS_C2	Hu Ig superfamily cytotoxic T-lymphocyte-assoc. protein (CTLA-4) gene
HLS_G2	<i>H. sapiens</i> beta-2-microglobulin (B2M) mRNA
HLS_F6	<i>H. sapiens</i> beta-2-microglobulin (B2M) mRNA
HLS_C5	Hu common acute lymphoblastic leukemia antigen (CALLA)
HLS_C7	Hu common acute lymphoblastic leukemia antigen (CALLA)
HLS_E10	<i>H. sapiens</i> B-cell-homing chemokine (ligand for Burkitt's lymph. Receptor-1) (BLC)
HLS_A11	<i>H. sapiens</i> B-cell-homing chemokine (ligand for Burkitt's lymph. Receptor-1) (BLC)
HLS_D2	<i>H. sapiens</i> genes for ribosomal protein L13a
HLS_F5	<i>H. sapiens</i> ribosomal protein S7 (RPS7)
HLS_F7	<i>H. sapiens</i> ribosomal protein S17 (RPS17) mRNA
HLS_A12	<i>H. sapiens</i> ribosomal protein S17 (RPS17) mRNA

5.2 EXAMPLE 2 -- ANALYSIS OF SUBTRACTED cDNA SEQUENCES BY MICROARRAY ANALYSIS

Subtracted cDNA sequences were analyzed by microarray analysis to evaluate their
5 expression in hematological malignancies and normal tissues. Using this approach, cDNA
sequences were PCR amplified and their mRNA expression profiles in hematological
malignancies and normal tissues are examined using cDNA microarray technology
essentially as described (Shena *et al.*, 1995).

In brief, the clones identified from the subtracted cDNA libraries analyses were
10 immobilized and arrayed onto glass slides as multiple replicas on microarray slides and the
slides were hybridized with two different sets of probes. , with each location corresponding
to a unique cDNA clone (as many as 5500 clones can be arrayed on a single slide, or chip).

Each chip is hybridized with a pair of cDNA probes that are fluorescence-labeled with Cy3 and Cy5, respectively. The set of probes derived from the hematological malignancies was labeled with cy3 while the other set of probes derived from a pool of normal tissues was labeled with cy5. Typically, 1 µg of polyA⁺ RNA was used to generate each cDNA probe.

5 After hybridization, the chips were scanned and the fluorescence intensity recorded for both Cy3 and Cy5 channels. The difference in intensities (*i.e.*, cy3/cy5 ratios) following hybridization with both probe sets provided the information on the relative expression level of each cDNA sequences immobilized on the slide in tumor versus normal tissues. There are multiple built-in quality control steps. First, the probe quality is monitored using a panel

10 of ubiquitously expressed genes. Secondly, the control plate also can include yeast DNA fragments of which complementary RNA may be spiked into the probe synthesis for measuring the quality of the probe and the sensitivity of the analysis. This methodology provides a sensitivity of 1 in 100,000 copies of mRNA, and the reproducibility of the technology may be ensured by including duplicated control cDNA elements at different

15 locations.

Analysis of hematological malignancy subtracted clones by microarray analyses on a variety of microarray chips identified the sequences set forth in SEQ ID NO:1 through SEQ ID NO:668 as being at least two-fold overexpressed in hematological malignancies versus normal tissues.

20

5.3 EXAMPLE 3 – POLYNUCLEOTIDE AND POLYPEPTIDE COMPOSITIONS: BRIEF DESCRIPTION OF THE cDNA CLONES AND OPEN READING FRAMES IDENTIFIED BY SUBTRACTIVE HYBRIDIZATION AND MICROARRAY ANALYSIS

25 Table 7 lists the sequences of the polynucleotides obtained during the analyses of the present invention. Shown are the 669 polynucleotide sequences, along with their clone name identifiers, as well as the serial number and filing date of the priority provisional patent application in which the clone was first identified.

30

TABLE 7
POLYNUCLEOTIDE SEQUENCES OF THE PRESENT INVENTION

SEQ ID NO:	Clone Identifier	Priority Application Number	Filing Date
SEQ ID NO:1	'41567.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:2	'41557.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:3	'41577.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:4	'41571.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:5	'41594.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:6	'41605.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:7	'41627.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:8	'41620.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:9	'41628.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:10	'41635.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:11	'41649.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:12	'41648.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:13	'41653.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:14	'41664.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:15	'41667.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:16	'41687.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:17	'41708.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:18	'41721.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:19	'41746.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:20	'41751.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:21	'41762.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:22	'41764.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:23	'41793.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:24	'41794.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:25	'41807.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:26	'41802.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:27	'41804.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:28	'41810.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:29	'41847.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:30	'41865.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:31	'41859.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:32	'41878.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:33	'41869.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:34	'41888.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:35	'41907.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:36	'41908.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:37	'41912.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:38	'41916.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:39	'41925.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:40	'41929.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:41	'41930.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:42	'41933.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:43	'41944.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:44	'41986.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:45	'42017.1_gaiger.ABI'	60/190,479	03/17/00

SEQ ID NO:	Clone Identifier	Priority Application Number	Filing Date
SEQ ID NO:46	'42033.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:47	'42040.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:48	'42041.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:49	'42053.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:50	'42101.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:51	'42131.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:52	R0232:A08	60/206,201	05/22/00
SEQ ID NO:53	R0232:C10	60/206,201	05/22/00
SEQ ID NO:54	R0232:H11	60/206,201	05/22/00
SEQ ID NO:55	R0232:H03	60/206,201	05/22/00
SEQ ID NO:56	R0233:A12	60/206,201	05/22/00
SEQ ID NO:57	R0233:A06	60/206,201	05/22/00
SEQ ID NO:58	R0233:A08	60/206,201	05/22/00
SEQ ID NO:59	R0233:B10	60/206,201	05/22/00
SEQ ID NO:60	R0233:B04	60/206,201	05/22/00
SEQ ID NO:61	R0233:C04	60/206,201	05/22/00
SEQ ID NO:62	R0233:D01	60/206,201	05/22/00
SEQ ID NO:63	R0233:D02	60/206,201	05/22/00
SEQ ID NO:64	R0233:F10	60/206,201	05/22/00
SEQ ID NO:65	R0233:F05	60/206,201	05/22/00
SEQ ID NO:66	R0233:F07	60/206,201	05/22/00
SEQ ID NO:67	'42324.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:68	'42349.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:69	'42379.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:70	'42394.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:71	'42387.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:72	'42396.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:73	'42424.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:74	'42438.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:75	'42447.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:76	'42524.1;gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:77	'42555.1;gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:78	'42560.1;gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:79	'42594.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:80	'42595.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:81	'42602.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:82	'42665.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:83	'42703.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:84	'42709.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:85	'42756.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:86	'42802.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:87	R0234:A06	60/206,201	05/22/00
SEQ ID NO:88	R0234:A07	60/206,201	05/22/00
SEQ ID NO:89	R0234:B03	60/206,201	05/22/00
SEQ ID NO:90	R0234:B06	60/206,201	05/22/00

SEQ ID NO:	Clone Identifier	Priority Application Number	Filing Date
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SEQ ID NO:92	R0234:C02	60/206,201	05/22/00
SEQ ID NO:93	R0234:C06	60/206,201	05/22/00
SEQ ID NO:94	R0234:D06	60/206,201	05/22/00
SEQ ID NO:95	R0234:D08	60/206,201	05/22/00
SEQ ID NO:96	R0234:E01	60/206,201	05/22/00
SEQ ID NO:97	R0234:E12	60/206,201	05/22/00
SEQ ID NO:98	R0234:E02	60/206,201	05/22/00
SEQ ID NO:99	R0234:E04	60/206,201	05/22/00
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SEQ ID NO:107	R0234:G02	60/206,201	05/22/00
SEQ ID NO:108	R0234:G03	60/206,201	05/22/00
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SEQ ID NO:126	R0235:E02	60/206,201	05/22/00
SEQ ID NO:127	R0235:F01	60/206,201	05/22/00
SEQ ID NO:128	R0235:F02	60/206,201	05/22/00
SEQ ID NO:129	R0235:F06	60/206,201	05/22/00
SEQ ID NO:130	R0235:F07	60/206,201	05/22/00
SEQ ID NO:131	R0235:F09	60/206,201	05/22/00
SEQ ID NO:132	R0235:G07	60/206,201	05/22/00
SEQ ID NO:133	R0235:H06	60/206,201	05/22/00
SEQ ID NO:134	R0235:H08	60/206,201	05/22/00
SEQ ID NO:135	R0236:A06	60/206,201	05/22/00

SEQ ID NO:	Clone Identifier	Priority Application Number	Filing Date
SEQ ID NO:136	R0236:A09	60/206,201	05/22/00
SEQ ID NO:137	R0236:B06	60/206,201	05/22/00
SEQ ID NO:138	R0236:C01	60/206,201	05/22/00
SEQ ID NO:139	R0236:E05	60/206,201	05/22/00
SEQ ID NO:140	R0236:F12	60/206,201	05/22/00
SEQ ID NO:141	R0236:F05	60/206,201	05/22/00
SEQ ID NO:142	R0236:F06	60/206,201	05/22/00
SEQ ID NO:143	R0236:G08	60/206,201	05/22/00
SEQ ID NO:144	R0249:A11	60/222,903	08/03/00
SEQ ID NO:145	R0249:B02	60/222,903	08/03/00
SEQ ID NO:146	R0249:B04	60/222,903	08/03/00
SEQ ID NO:147	R0249:B06	60/222,903	08/03/00
SEQ ID NO:148	R0249:D11	60/222,903	08/03/00
SEQ ID NO:149	R0249:E11	60/222,903	08/03/00
SEQ ID NO:150	R0249:E06	60/222,903	08/03/00
SEQ ID NO:151	R0249:H09	60/222,903	08/03/00
SEQ ID NO:152	R0250:C09	60/222,903	08/03/00
SEQ ID NO:153	R0250:D10	60/222,903	08/03/00
SEQ ID NO:154	R0250:D03	60/222,903	08/03/00
SEQ ID NO:155	R0250:E09	60/222,903	08/03/00
SEQ ID NO:156	R0250:F09	60/222,903	08/03/00
SEQ ID NO:157	R0250:G01	60/222,903	08/03/00
SEQ ID NO:158	R0251:A12	60/222,903	08/03/00
SEQ ID NO:159	R0251:A05	60/222,903	08/03/00
SEQ ID NO:160	R0251:B09	60/222,903	08/03/00
SEQ ID NO:161	R0251:D01	60/222,903	08/03/00
SEQ ID NO:162	R0251:E03	60/222,903	08/03/00
SEQ ID NO:163	R0251:E06	60/222,903	08/03/00
SEQ ID NO:164	R0251:F12	60/222,903	08/03/00
SEQ ID NO:165	R0251:G06	60/222,903	08/03/00
SEQ ID NO:166	R0252:A08	60/222,903	08/03/00
SEQ ID NO:167	R0252:D02	60/222,903	08/03/00
SEQ ID NO:168	R0252:E11	60/222,903	08/03/00
SEQ ID NO:169	R0252:E04	60/222,903	08/03/00
SEQ ID NO:170	R0252:E06	60/222,903	08/03/00
SEQ ID NO:171	R0252:E07	60/222,903	08/03/00
SEQ ID NO:172	R0252:F11	60/222,903	08/03/00
SEQ ID NO:173	R0252:F02	60/222,903	08/03/00
SEQ ID NO:174	R0252:F03	60/222,903	08/03/00
SEQ ID NO:175	R0252:H01	60/222,903	08/03/00
SEQ ID NO:176	R0252:H03	60/222,903	08/03/00
SEQ ID NO:177	R0253:B04	60/222,903	08/03/00
SEQ ID NO:178	R0253:C10	60/222,903	08/03/00
SEQ ID NO:179	R0253:C04	60/222,903	08/03/00
SEQ ID NO:180	R0253:C05	60/222,903	08/03/00

SEQ ID NO:	Clone Identifier	Priority Application Number	Filing Date
SEQ ID NO:181	R0253:C06	60/222,903	08/03/00
SEQ ID NO:182	R0253:D02	60/222,903	08/03/00
SEQ ID NO:183	R0253:D08	60/222,903	08/03/00
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SEQ ID NO:185	R0253:E09	60/222,903	08/03/00
SEQ ID NO:186	R0253:F01	60/222,903	08/03/00
SEQ ID NO:187	R0253:F11	60/222,903	08/03/00
SEQ ID NO:188	R0253:F02	60/222,903	08/03/00
SEQ ID NO:189	R0253:F05	60/222,903	08/03/00
SEQ ID NO:190	R0253:F07	60/222,903	08/03/00
SEQ ID NO:191	R0253:G01	60/222,903	08/03/00
SEQ ID NO:192	R0253:G10	60/222,903	08/03/00
SEQ ID NO:193	R0253:G11	60/222,903	08/03/00
SEQ ID NO:194	R0253:G12	60/222,903	08/03/00
SEQ ID NO:195	R0253:G04	60/222,903	08/03/00
SEQ ID NO:196	R0253:G05	60/222,903	08/03/00
SEQ ID NO:197	R0253:G06	60/222,903	08/03/00
SEQ ID NO:198	R0253:H02	60/222,903	08/03/00
SEQ ID NO:199	R0253:H07	60/222,903	08/03/00
SEQ ID NO:200	R0254:F07	60/223,416	08/04/00
SEQ ID NO:201	R0254:G11	60/223,416	08/04/00
SEQ ID NO:202	R0254:G04	60/223,416	08/04/00
SEQ ID NO:203	R0254:H01	60/223,416	08/04/00
SEQ ID NO:204	R0238:C03	60/223,416	08/04/00
SEQ ID NO:205	R0255:C02	60/223,416	08/04/00
SEQ ID NO:206	R0255:F12	60/223,416	08/04/00
SEQ ID NO:207	R0258:G10	60/223,416	08/04/00
SEQ ID NO:208	R0261:A12	60/223,416	08/04/00
SEQ ID NO:209	R0261:A09	60/223,416	08/04/00
SEQ ID NO:210	R0261:B12	60/223,416	08/04/00
SEQ ID NO:211	R0261:C10	60/223,416	08/04/00
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SEQ ID NO:213	R0261:E04	60/223,416	08/04/00
SEQ ID NO:214	R0261:F05	60/223,416	08/04/00
SEQ ID NO:215	R0261:G04	60/223,416	08/04/00
SEQ ID NO:216	R0261:H03	60/223,416	08/04/00
SEQ ID NO:217	R0262:A12	60/223,416	08/04/00
SEQ ID NO:218	R0262:A02	60/223,416	08/04/00
SEQ ID NO:219	R0262:D12	60/223,416	08/04/00
SEQ ID NO:220	R0262:D04	60/223,416	08/04/00
SEQ ID NO:221	R0262:D07	60/223,416	08/04/00
SEQ ID NO:222	R0262:E02	60/223,416	08/04/00
SEQ ID NO:223	R0262:E03	60/223,416	08/04/00
SEQ ID NO:224	R0262:F06	60/223,416	08/04/00
SEQ ID NO:225	R0263:B03	60/223,416	08/04/00

SEQ ID NO:	Clone Identifier	Priority Application Number	Filing Date
SEQ ID NO:226	R0263:B09	60/223,416	08/04/00
SEQ ID NO:227	R0263:E03	60/223,416	08/04/00
SEQ ID NO:228	R0263:F08	60/223,416	08/04/00
SEQ ID NO:229	R0263:G10	60/223,416	08/04/00
SEQ ID NO:230	R0263:G02	60/223,416	08/04/00
SEQ ID NO:231	R0263:G03	60/223,416	08/04/00
SEQ ID NO:232	R0263:H10	60/223,416	08/04/00
SEQ ID NO:233	R0264:A02	60/223,416	08/04/00
SEQ ID NO:234	R0264:B11	60/223,416	08/04/00
SEQ ID NO:235	R0264:E12	60/223,416	08/04/00
SEQ ID NO:236	R0264:F11	60/223,416	08/04/00
SEQ ID NO:237	R0264:F09	60/223,416	08/04/00
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SEQ ID NO:239	R0264:G11	60/223,416	08/04/00
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SEQ ID NO:242	R0265:G01	60/223,416	08/04/00
SEQ ID NO:243	R0265:G10	60/223,416	08/04/00
SEQ ID NO:244	R0265:G11	60/223,416	08/04/00
SEQ ID NO:245	R0265:H09	60/223,416	08/04/00
SEQ ID NO:246	R0266:A11	60/223,416	08/04/00
SEQ ID NO:247	R0266:A12	60/223,416	08/04/00
SEQ ID NO:248	R0266:B01	60/223,416	08/04/00
SEQ ID NO:249	R0266:C12	60/223,416	08/04/00
SEQ ID NO:250	R0266:E01	60/223,416	08/04/00
SEQ ID NO:251	R0266:E03	60/223,416	08/04/00
SEQ ID NO:252	R0266:F03	60/223,416	08/04/00
SEQ ID NO:253	R0266:F07	60/223,416	08/04/00
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SEQ ID NO:256	R0266:H09	60/223,416	08/04/00
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SEQ ID NO:258	R0244:C02	60/223,416	08/04/00
SEQ ID NO:259	R0244:C04	60/223,416	08/04/00
SEQ ID NO:260	R0245:A02	60/223,416	08/04/00
SEQ ID NO:261	'46802.1_gaiger.ABI'	60/200,545	04/27/00
SEQ ID NO:262	'46816.1_gaiger.ABI'	60/200,545	04/27/00
SEQ ID NO:263	'46880.1_gaiger.ABI'	60/200,545	04/27/00
SEQ ID NO:264	'47011.1_gaiger.ABI'	60/200,545	04/27/00
SEQ ID NO:265	'51658.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:266	'51713.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:267	'51731.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:268	'51734.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:269	'51735.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:270	'51788.1_gaiger.ABI'	60/206,201	05/22/00

SEQ ID NO:	Clone Identifier	Priority Application Number	Filing Date
SEQ ID NO:271	'51892.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:272	'51900.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:273	'51903.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:274	1404:D07	60/218,950	07/14/00
SEQ ID NO:275	1405:C04	60/218,950	07/14/00
SEQ ID NO:276	1405:D12	60/218,950	07/14/00
SEQ ID NO:277	1405:E11	60/218,950	07/14/00
SEQ ID NO:278	'52333.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:279	'41557.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:280	'41579.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:281	'41571.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:282	'41613.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:283	'41650.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:284	'41663.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:285	'41659.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:286	'41687.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:287	'41717.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:288	'41751.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:289	'41818.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:290	'41828.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:291	'41849.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:292	'41881.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:293	'41912.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:294	'41927.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:295	'41929.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:296	'41944.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:297	'41987.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:298	'41995.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:299	'42012.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:300	'42039.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:301	'42097.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:302	'42103.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:303	'42108.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:304	R0233:A06	60/206,201	05/22/00
SEQ ID NO:305	R0233:A08	60/206,201	05/22/00
SEQ ID NO:306	R0233:C02	60/206,201	05/22/00
SEQ ID NO:307	R0233:E06	60/206,201	05/22/00
SEQ ID NO:308	R0233:F08	60/206,201	05/22/00
SEQ ID NO:309	'42324.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:310	'42335.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:311	'42325.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:312	'42401.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:313	'42469.1;gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:314	'42514.1;gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:315	'42554.1;gaiger.ABI'	60/200,779	05/22/00

SEQ ID NO:	Clone Identifier	Priority Application Number	Filing Date
SEQ ID NO:316	'42560.1;gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:317	'42588.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:318	'42595.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:319	'42609.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:320	'42703.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:321	R0234:E06	60/206,201	05/22/00
SEQ ID NO:322	R0234:F09	60/206,201	05/22/00
SEQ ID NO:323	R0235:A09	60/206,201	05/22/00
SEQ ID NO:324	R0235:D01	60/206,201	05/22/00
SEQ ID NO:325	R0236:D04	60/206,201	05/22/00
SEQ ID NO:326	R0236:F10	60/206,201	05/22/00
SEQ ID NO:327	R0236:G10	60/206,201	05/22/00
SEQ ID NO:328	R0236:G08	60/206,201	05/22/00
SEQ ID NO:329	R0249:D01	60/222,903	08/03/00
SEQ ID NO:330	R0249:G04	60/222,903	08/03/00
SEQ ID NO:331	R0250:A10	60/222,903	08/03/00
SEQ ID NO:332	R0250:E12	60/222,903	08/03/00
SEQ ID NO:333	R0250:F12	60/222,903	08/03/00
SEQ ID NO:334	R0251:B08	60/222,903	08/03/00
SEQ ID NO:335	R0252:A08	60/222,903	08/03/00
SEQ ID NO:336	R0252:F11	60/222,903	08/03/00
SEQ ID NO:337	R0252:F02	60/222,903	08/03/00
SEQ ID NO:338	R0252:F08	60/222,903	08/03/00
SEQ ID NO:339	R0252:G11	60/222,903	08/03/00
SEQ ID NO:340	R0253:E10	60/222,903	08/03/00
SEQ ID NO:341	R0253:G11	60/222,903	08/03/00
SEQ ID NO:342	R0254:A08	60/223,416	08/04/00
SEQ ID NO:343	R0254:E04	60/223,416	08/04/00
SEQ ID NO:344	R0254:F07	60/223,416	08/04/00
SEQ ID NO:345	R0237:F12	60/206,201	05/22/00
SEQ ID NO:346	R0238:B02	60/223,416	08/04/00
SEQ ID NO:347	R0238:D06	60/223,416	08/04/00
SEQ ID NO:348	R0238:F03	60/223,416	08/04/00
SEQ ID NO:349	R0239:H02	60/206,201	05/22/00
SEQ ID NO:350	R0255:F12	60/223,416	08/04/00
SEQ ID NO:351	R0258:B10	60/223,416	08/04/00
SEQ ID NO:352	R0259:C06	60/223,416	08/04/00
SEQ ID NO:353	R0261:A09	60/223,416	08/04/00
SEQ ID NO:354	R0261:B10	60/223,416	08/04/00
SEQ ID NO:355	R0261:C10	60/223,416	08/04/00
SEQ ID NO:356	R0261:D03	60/223,416	08/04/00
SEQ ID NO:357	R0261:D06	60/223,416	08/04/00
SEQ ID NO:358	R0261:E10	60/223,416	08/04/00
SEQ ID NO:359	R0261:F10	60/223,416	08/04/00
SEQ ID NO:360	R0261:G04	60/223,416	08/04/00

SEQ ID NO:	Clone Identifier	Priority Application Number	Filing Date
SEQ ID NO:361	R0262:A12	60/223,416	08/04/00
SEQ ID NO:362	R0262:A03	60/223,416	08/04/00
SEQ ID NO:363	R0262:B09	60/223,416	08/04/00
SEQ ID NO:364	R0262:C04	60/223,416	08/04/00
SEQ ID NO:365	R0262:D11	60/223,416	08/04/00
SEQ ID NO:366	R0262:D12	60/223,416	08/04/00
SEQ ID NO:367	R0262:D04	60/223,416	08/04/00
SEQ ID NO:368	R0262:D07	60/223,416	08/04/00
SEQ ID NO:369	R0262:E02	60/223,416	08/04/00
SEQ ID NO:370	R0262:G05	60/223,416	08/04/00
SEQ ID NO:371	R0263:B10	60/223,416	08/04/00
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SEQ ID NO:384	R0264:F11	60/223,416	08/04/00
SEQ ID NO:385	R0264:F09	60/223,416	08/04/00
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SEQ ID NO:393	R0265:D07	60/223,416	08/04/00
SEQ ID NO:394	R0265:E12	60/223,416	08/04/00
SEQ ID NO:395	R0265:F12	60/223,416	08/04/00
SEQ ID NO:396	R0265:H04	60/223,416	08/04/00
SEQ ID NO:397	R0265:H09	60/223,416	08/04/00
SEQ ID NO:398	R0266:A10	60/223,416	08/04/00
SEQ ID NO:399	R0266:A12	60/223,416	08/04/00
SEQ ID NO:400	R0266:B02	60/223,416	08/04/00
SEQ ID NO:401	R0266:C12	60/223,416	08/04/00
SEQ ID NO:402	R0266:E08	60/223,416	08/04/00
SEQ ID NO:403	R0266:F03	60/223,416	08/04/00
SEQ ID NO:404	R0266:F06	60/223,416	08/04/00
SEQ ID NO:405	R0266:F07	60/223,416	08/04/00

SEQ ID NO:	Clone Identifier	Priority Application Number	Filing Date
SEQ ID NO:406	R0266:G12	60/223,416	08/04/00
SEQ ID NO:407	R0266:G09	60/223,416	08/04/00
SEQ ID NO:408	R0266:H06	60/223,416	08/04/00
SEQ ID NO:409	R0242:E03	60/223,416	08/04/00
SEQ ID NO:410	R0244:C04	60/223,416	08/04/00
SEQ ID NO:411	R0244:C06	60/223,416	08/04/00
SEQ ID NO:412	R0245:A02	60/223,416	08/04/00
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SEQ ID NO:414	R0246:D10	60/223,416	08/04/00
SEQ ID NO:415	'46377.1_gaiger.ABI'	60/200,545	04/27/00
SEQ ID NO:416	'46403.1_gaiger.ABI'	60/200,545	04/27/00
SEQ ID NO:417	'46489.1_gaiger.ABI'	60/200,545	04/27/00
SEQ ID NO:418	'46872.1_gaiger.ABI'	60/200,545	04/27/00
SEQ ID NO:419	'46883.1_gaiger.ABI'	60/200,545	04/27/00
SEQ ID NO:420	'46880.1_gaiger.ABI'	60/200,545	04/27/00
SEQ ID NO:421	'46977.1_gaiger.ABI'	60/200,545	04/27/00
SEQ ID NO:422	'47011.1_gaiger.ABI'	60/200,545	04/27/00
SEQ ID NO:423	'51658.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:424	'51713.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:425	'51734.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:426	'51766.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:427	'51870.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:428	'51924.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:429	1404:A06	60/218,950	07/14/00
SEQ ID NO:430	1404:B12	60/218,950	07/14/00
SEQ ID NO:431	1404:D12	60/218,950	07/14/00
SEQ ID NO:432	1404:E11	60/218,950	07/14/00
SEQ ID NO:433	1405:A11	60/218,950	07/14/00
SEQ ID NO:434	'52280.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:435	'52345.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:436	'52373.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:437	R0238:F03	60/223,416	08/04/00
SEQ ID NO:438	R0263:E03	60/223,416	08/04/00
SEQ ID NO:439	'41557.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:440	'41650.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:441	'41663.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:442	'41659.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:443	'41667.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:444	'41729.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:445	'41751.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:446	'41818.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:447	'41828.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:448	'41847.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:449	'41849.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:450	'41927.1_gaiger.ABI'	60/190,479	03/17/00

SEQ ID NO:	Clone Identifier	Priority Application Number	Filing Date
SEQ ID NO:451	'41929.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:452	'41995.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:453	'42012.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:454	'42039.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:455	'42097.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:456	'42108.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:457	R0233:A06	60/206,201	05/22/00
SEQ ID NO:458	R0233:C02	60/206,201	05/22/00
SEQ ID NO:459	R0233:E06	60/206,201	05/22/00
SEQ ID NO:460	R0233:F08	60/206,201	05/22/00
SEQ ID NO:461	'42325.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:462	'42328.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:463	'42401.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:464	'42588.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:465	'42595.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:466	'42703.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:467	R0234:B07	60/206,201	05/22/00
SEQ ID NO:468	R0234:E06	60/206,201	05/22/00
SEQ ID NO:469	R0234:F09	60/206,201	05/22/00
SEQ ID NO:470	R0235:B03	60/206,201	05/22/00
SEQ ID NO:471	R0235:E05	60/206,201	05/22/00
SEQ ID NO:472	R0236:A06	60/206,201	05/22/00
SEQ ID NO:473	R0236:D04	60/206,201	05/22/00
SEQ ID NO:474	R0250:A10	60/222,903	08/03/00
SEQ ID NO:475	R0251:E09	60/222,903	08/03/00
SEQ ID NO:476	R0252:F11	60/222,903	08/03/00
SEQ ID NO:477	R0238:B02	60/223,416	08/04/00
SEQ ID NO:478	R0239:H02	60/206,201	05/22/00
SEQ ID NO:479	R0255:F12	60/223,416	08/04/00
SEQ ID NO:480	R0259:C06	60/223,416	08/04/00
SEQ ID NO:481	R0261:B10	60/223,416	08/04/00
SEQ ID NO:482	R0261:D06	60/223,416	08/04/00
SEQ ID NO:483	R0261:E10	60/223,416	08/04/00
SEQ ID NO:484	R0261:H08	60/223,416	08/04/00
SEQ ID NO:485	R0262:A12	60/223,416	08/04/00
SEQ ID NO:486	R0262:A03	60/223,416	08/04/00
SEQ ID NO:487	R0262:D11	60/223,416	08/04/00
SEQ ID NO:488	R0262:E03	60/223,416	08/04/00
SEQ ID NO:489	R0262:G05	60/223,416	08/04/00
SEQ ID NO:490	R0263:B11	60/223,416	08/04/00
SEQ ID NO:491	R0263:D11	60/223,416	08/04/00
SEQ ID NO:492	R0263:D07	60/223,416	08/04/00
SEQ ID NO:493	R0263:F08	60/223,416	08/04/00
SEQ ID NO:494	R0263:H02	60/223,416	08/04/00
SEQ ID NO:495	R0264:D03	60/223,416	08/04/00

SEQ ID NO:	Clone Identifier	Priority Application Number	Filing Date
SEQ ID NO:496	R0264:E12	60/223,416	08/04/00
SEQ ID NO:497	R0264:F11	60/223,416	08/04/00
SEQ ID NO:498	R0264:H03	60/223,416	08/04/00
SEQ ID NO:499	R0265:D07	60/223,416	08/04/00
SEQ ID NO:500	R0265:E12	60/223,416	08/04/00
SEQ ID NO:501	R0265:F12	60/223,416	08/04/00
SEQ ID NO:502	R0265:H04	60/223,416	08/04/00
SEQ ID NO:503	R0265:H09	60/223,416	08/04/00
SEQ ID NO:504	R0266:A10	60/223,416	08/04/00
SEQ ID NO:505	R0266:A12	60/223,416	08/04/00
SEQ ID NO:506	R0266:F03	60/223,416	08/04/00
SEQ ID NO:507	R0266:F07	60/223,416	08/04/00
SEQ ID NO:508	R0266:G12	60/223,416	08/04/00
SEQ ID NO:509	R0266:G09	60/223,416	08/04/00
SEQ ID NO:510	R0266:H06	60/223,416	08/04/00
SEQ ID NO:511	R0244:C04	60/223,416	08/04/00
SEQ ID NO:512	R0245:A02	60/223,416	08/04/00
SEQ ID NO:513	R0246:D10	60/223,416	08/04/00
SEQ ID NO:514	'46403.1_gaiger.ABI'	60/200,545	04/27/00
SEQ ID NO:515	'46458.1_gaiger.ABI'	60/200,545	04/27/00
SEQ ID NO:516	'46489.1_gaiger.ABI'	60/200,545	04/27/00
SEQ ID NO:517	'46802.1_gaiger.ABI'	60/200,545	04/27/00
SEQ ID NO:518	'46872.1_gaiger.ABI'	60/200,545	04/27/00
SEQ ID NO:519	'46880.1_gaiger.ABI'	60/200,545	04/27/00
SEQ ID NO:520	'46977.1_gaiger.ABI'	60/200,545	04/27/00
SEQ ID NO:521	'51658.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:522	'51713.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:523	'51734.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:524	'51924.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:525	1405:C04	60/218,950	07/14/00
SEQ ID NO:526	1405:E11	60/218,950	07/14/00
SEQ ID NO:527	'52246.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:528	'52333.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:529	'41557.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:530	'41579.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:531	'41571.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:532	'41573.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:533	'41628.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:534	'41635.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:535	'41663.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:536	'41667.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:537	'41751.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:538	'41944.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:539	'41986.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:540	'42101.1_gaiger.ABI'	60/190,479	03/17/00

SEQ ID NO:	Clone Identifier	Priority Application Number	Filing Date
SEQ ID NO:541	R0232:E07	60/206,201	05/22/00
SEQ ID NO:542	R0233:A06	60/206,201	05/22/00
SEQ ID NO:543	'42324.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:544	'42438.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:545	'42625.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:546	'42702.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:547	'42709.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:548	R0234:E07	60/206,201	05/22/00
SEQ ID NO:549	R0234:G11	60/206,201	05/22/00
SEQ ID NO:550	R0236:A09	60/206,201	05/22/00
SEQ ID NO:551	R0250:A05	60/222,903	08/03/00
SEQ ID NO:552	R0251:A07	60/222,903	08/03/00
SEQ ID NO:553	R0251:D01	60/222,903	08/03/00
SEQ ID NO:554	R0252:A08	60/222,903	08/03/00
SEQ ID NO:555	R0252:F11	60/222,903	08/03/00
SEQ ID NO:556	R0252:H01	60/222,903	08/03/00
SEQ ID NO:557	R0253:E09	60/222,903	08/03/00
SEQ ID NO:558	R0253:G05	60/222,903	08/03/00
SEQ ID NO:559	R0253:G06	60/222,903	08/03/00
SEQ ID NO:560	R0254:F07	60/223,416	08/04/00
SEQ ID NO:561	R0238:D06	60/223,416	08/04/00
SEQ ID NO:562	R0255:F12	60/223,416	08/04/00
SEQ ID NO:563	R0259:C04	60/223,416	08/04/00
SEQ ID NO:564	R0261:A09	60/223,416	08/04/00
SEQ ID NO:565	R0261:C10	60/223,416	08/04/00
SEQ ID NO:566	R0261:D06	60/223,416	08/04/00
SEQ ID NO:567	R0262:D04	60/223,416	08/04/00
SEQ ID NO:568	R0262:E03	60/223,416	08/04/00
SEQ ID NO:569	R0263:B11	60/223,416	08/04/00
SEQ ID NO:570	R0263:B09	60/223,416	08/04/00
SEQ ID NO:571	R0263:C08	60/223,416	08/04/00
SEQ ID NO:572	R0263:D11	60/223,416	08/04/00
SEQ ID NO:573	R0263:H10	60/223,416	08/04/00
SEQ ID NO:574	R0264:A03	60/223,416	08/04/00
SEQ ID NO:575	R0264:B11	60/223,416	08/04/00
SEQ ID NO:576	R0264:F11	60/223,416	08/04/00
SEQ ID NO:577	R0264:F05	60/223,416	08/04/00
SEQ ID NO:578	R0264:F09	60/223,416	08/04/00
SEQ ID NO:579	R0266:B02	60/223,416	08/04/00
SEQ ID NO:580	R0266:B03	60/223,416	08/04/00
SEQ ID NO:581	R0266:B04	60/223,416	08/04/00
SEQ ID NO:582	R0266:B06	60/223,416	08/04/00
SEQ ID NO:583	R0266:D05	60/223,416	08/04/00
SEQ ID NO:584	R0266:E01	60/223,416	08/04/00
SEQ ID NO:585	R0266:E03	60/223,416	08/04/00

SEQ ID NO:	Clone Identifier	Priority Application Number	Filing Date
SEQ ID NO:586	R0266:F03	60/223,416	08/04/00
SEQ ID NO:587	R0266:F09	60/223,416	08/04/00
SEQ ID NO:588	R0245:A02	60/223,416	08/04/00
SEQ ID NO:589	'46403.1_gaiger.ABI'	60/200,545	04/27/00
SEQ ID NO:590	'46458.1_gaiger.ABI'	60/200,545	04/27/00
SEQ ID NO:591	'46977.1_gaiger.ABI'	60/200,545	04/27/00
SEQ ID NO:592	'51658.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:593	'51713.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:594	'51731.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:595	'51788.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:596	'51850.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:597	'51892.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:598	'51900.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:599	'51903.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:600	'51960.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:601	1405:A09	60/218,950	07/14/00
SEQ ID NO:602	1405:D12	60/218,950	07/14/00
SEQ ID NO:603	1405:D09	60/218,950	07/14/00
SEQ ID NO:604	1405:E11	60/218,950	07/14/00
SEQ ID NO:605	'52246.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:606	'52333.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:607	1408:A09	60/218,950	07/14/00
SEQ ID NO:608	1408:B02	60/218,950	07/14/00
SEQ ID NO:609	1408:C12	60/218,950	07/14/00
SEQ ID NO:610	1408:D06	60/218,950	07/14/00
SEQ ID NO:611	'41663.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:612	'41729.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:613	'41888.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:614	'41925.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:615	'41639.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:616	'41853.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:617	'41876.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:618	'41924.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:619	'41638.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:620	'41581.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:621	'41629.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:622	'41678.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:623	'41717.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:624	'41987.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:625	R0233:F02	60/206,201	05/22/00
SEQ ID NO:626	R0232:A08	60/206,201	05/22/00
SEQ ID NO:627	R0233:B04	60/206,201	05/22/00
SEQ ID NO:628	'42041.1_gaiger.ABI'	60/190,479	03/17/00
SEQ ID NO:629	'42387.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:630	'42460.1_gaiger.ABI'	60/200,779	05/22/00

SEQ ID NO:	Clone Identifier	Priority Application Number	Filing Date
SEQ ID NO:631	'42407.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:632	'42483.1;gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:633	'42350.1_gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:634	'42530.1;gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:635	'42523.1;gaiger.ABI'	60/200,779	05/22/00
SEQ ID NO:636	R0235:D07	60/206,201	05/22/00
SEQ ID NO:637	R0235:D12	60/206,201	05/22/00
SEQ ID NO:638	R0236:H02	60/206,201	05/22/00
SEQ ID NO:639	R0251:B12	60/222,903	08/03/00
SEQ ID NO:640	R0253:D09	60/222,903	08/03/00
SEQ ID NO:641	R0254:F10	60/223,416	08/04/00
SEQ ID NO:642	R0253:G01	60/222,903	08/03/00
SEQ ID NO:643	R0254:D02	60/223,416	08/04/00
SEQ ID NO:644	R0238:B06	60/223,416	08/04/00
SEQ ID NO:645	R0255:D01	60/223,416	08/04/00
SEQ ID NO:646	R0255:C02	60/223,416	08/04/00
SEQ ID NO:647	R0261:H04	60/223,416	08/04/00
SEQ ID NO:648	R0259:C04	60/223,416	08/04/00
SEQ ID NO:649	R0259:C06	60/223,416	08/04/00
SEQ ID NO:650	R0261:H08	60/223,416	08/04/00
SEQ ID NO:651	R0261:D03	60/223,416	08/04/00
SEQ ID NO:652	R0262:C04	60/223,416	08/04/00
SEQ ID NO:653	R0264:B08	60/223,416	08/04/00
SEQ ID NO:654	R0266:D03	60/223,416	08/04/00
SEQ ID NO:655	R0265:F12	60/223,416	08/04/00
SEQ ID NO:656	R0264:C03	60/223,416	08/04/00
SEQ ID NO:657	R0264:C04	60/223,416	08/04/00
SEQ ID NO:658	R0244:C02	60/223,416	08/04/00
SEQ ID NO:659	R0245:A02	60/223,416	08/04/00
SEQ ID NO:660	'51734.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:661	'51870.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:662	'51791.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:663	'51975.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:664	'52260.1_gaiger.ABI'	60/206,201	05/22/00
SEQ ID NO:665	TCL1 DNA		
SEQ ID NO:666	TCL1 Protein		
SEQ ID NO:667	Coronin1A DNA		
SEQ ID NO:668	Coronin1A Protein		

Table 8 identifies the putative open reading frames obtained from analyses of the cDNA sequences obtained in SEQ ID NO:1-SEQ ID NO:668 as described above. Shown are the sequence identifiers, the clone name and translation frame, and the start and stop

nucleotides in the corresponding DNA sequence used to generate the polypeptide sequence of the open reading frame.

TABLE 8

5 TRANSLATION OF OPEN READING FRAMES OF IDENTIFIED CDNAS

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:669	'41567.1_gaiger.ABI'_1	frame 1	from 1 to 79
SEQ ID NO:670	'41567.1_gaiger.ABI'_2	frame 3	from 11 to 134
SEQ ID NO:671	'41567.1_gaiger.ABI'_3	frame -1	from 86 to 135
SEQ ID NO:672	'41567.1_gaiger.ABI'_4	frame -3	from 1 to 108
SEQ ID NO:673	'41557.1_gaiger.ABI'_1	frame 1	from 16 to 73
SEQ ID NO:674	'41557.1_gaiger.ABI'_2	frame 2	from 1 to 109
SEQ ID NO:675	'41557.1_gaiger.ABI'_3	frame -1	from 11 to 110
SEQ ID NO:676	'41557.1_gaiger.ABI'_4	frame -3	from 1 to 103
SEQ ID NO:677	'41571.1_gaiger.ABI'_1	frame 3	from 1 to 89
SEQ ID NO:678	'41571.1_gaiger.ABI'_2	frame -1	from 1 to 89
SEQ ID NO:679	'41571.1_gaiger.ABI'_3	frame -2	from 27 to 85
SEQ ID NO:680	'41594.1_gaiger.ABI'_1	frame 3	from 1 to 123
SEQ ID NO:681	'41594.1_gaiger.ABI'_2	frame -2	from 1 to 85
SEQ ID NO:682	'41605.1_gaiger.ABI'_1	frame 3	from 1 to 85
SEQ ID NO:683	'41605.1_gaiger.ABI'_2	frame -3	from 1 to 123
SEQ ID NO:684	'41627.1_gaiger.ABI'_1	frame 1	from 1 to 161
SEQ ID NO:685	'41627.1_gaiger.ABI'_2	frame 2	from 102 to 161
SEQ ID NO:686	'41627.1_gaiger.ABI'_3	frame 3	from 1 to 67
SEQ ID NO:687	'41627.1_gaiger.ABI'_4	frame 3	from 69 to 136
SEQ ID NO:688	'41627.1_gaiger.ABI'_5	frame -2	from 1 to 106
SEQ ID NO:689	'41627.1_gaiger.ABI'_6	frame -3	from 67 to 160
SEQ ID NO:690	'41620.1_gaiger.ABI'_1	frame 1	from 1 to 151
SEQ ID NO:691	'41620.1_gaiger.ABI'_2	frame 3	from 1 to 59
SEQ ID NO:692	'41620.1_gaiger.ABI'_3	frame -1	from 1 to 85
SEQ ID NO:693	'41620.1_gaiger.ABI'_4	frame -1	from 100 to 152
SEQ ID NO:694	'41620.1_gaiger.ABI'_5	frame -2	from 48 to 109
SEQ ID NO:695	'41620.1_gaiger.ABI'_6	frame -3	from 69 to 119
SEQ ID NO:696	'41628.1_gaiger.ABI'_1	frame 1	from 51 to 121
SEQ ID NO:697	'41628.1_gaiger.ABI'_2	frame 2	from 1 to 97
SEQ ID NO:698	'41628.1_gaiger.ABI'_3	frame -3	from 47 to 98
SEQ ID NO:699	'41635.1_gaiger.ABI'_1	frame 1	from 1 to 70

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:700	'41635.1_gaiger.ABI'_2	frame 2	from 31 to 127
SEQ ID NO:701	'41635.1_gaiger.ABI'_3	frame -1	from 56 to 127
SEQ ID NO:702	'41635.1_gaiger.ABI'_4	frame -2	from 76 to 126
SEQ ID NO:703	'41649.1_gaiger.ABI'_1	frame 1	from 17 to 77
SEQ ID NO:704	'41649.1_gaiger.ABI'_2	frame 3	from 1 to 56
SEQ ID NO:705	'41649.1_gaiger.ABI'_3	frame -2	from 12 to 87
SEQ ID NO:706	'41648.1_gaiger.ABI'_1	frame 3	from 1 to 154
SEQ ID NO:707	'41648.1_gaiger.ABI'_2	frame -1	from 1 to 67
SEQ ID NO:708	'41648.1_gaiger.ABI'_3	frame -2	from 1 to 116
SEQ ID NO:709	'41664.1_gaiger.ABI'_1	frame 3	from 1 to 125
SEQ ID NO:710	'41664.1_gaiger.ABI'_2	frame -2	from 18 to 87
SEQ ID NO:711	'41664.1_gaiger.ABI'_3	frame -3	from 1 to 53
SEQ ID NO:712	'41667.1_gaiger.ABI'_1	frame 1	from 1 to 56
SEQ ID NO:713	'41667.1_gaiger.ABI'_2	frame 2	from 1 to 56
SEQ ID NO:714	'41667.1_gaiger.ABI'_3	frame -2	from 1 to 56
SEQ ID NO:715	'41687.1_gaiger.ABI'_1	frame 1	from 35 to 154
SEQ ID NO:716	'41687.1_gaiger.ABI'_2	frame 2	from 102 to 153
SEQ ID NO:717	'41687.1_gaiger.ABI'_3	frame -1	from 50 to 109
SEQ ID NO:718	'41687.1_gaiger.ABI'_4	frame -3	from 102 to 153
SEQ ID NO:719	'41708.1_gaiger.ABI'_1	frame 1	from 1 to 53
SEQ ID NO:720	'41708.1_gaiger.ABI'_2	frame 2	from 1 to 59
SEQ ID NO:721	'41708.1_gaiger.ABI'_3	frame 3	from 1 to 68
SEQ ID NO:722	'41708.1_gaiger.ABI'_4	frame -1	from 1 to 51
SEQ ID NO:723	'41708.1_gaiger.ABI'_5	frame -2	from 17 to 68
SEQ ID NO:724	'41721.1_gaiger.ABI'_1	frame -2	from 1 to 57
SEQ ID NO:725	'41721.1_gaiger.ABI'_2	frame -3	from 1 to 97
SEQ ID NO:726	'41746.1_gaiger.ABI'_1	frame 1	from 1 to 65
SEQ ID NO:727	'41746.1_gaiger.ABI'_2	frame 2	from 1 to 60
SEQ ID NO:728	'41746.1_gaiger.ABI'_3	frame -2	from 7 to 65
SEQ ID NO:729	'41751.1_gaiger.ABI'_1	frame 1	from 27 to 82
SEQ ID NO:730	'41751.1_gaiger.ABI'_2	frame 3	from 1 to 50
SEQ ID NO:731	'41751.1_gaiger.ABI'_3	frame -2	from 1 to 70
SEQ ID NO:732	'41751.1_gaiger.ABI'_4	frame -3	from 1 to 53
SEQ ID NO:733	'41762.1_gaiger.ABI'_1	frame 1	from 1 to 76
SEQ ID NO:734	'41762.1_gaiger.ABI'_2	frame 2	from 1 to 96
SEQ ID NO:735	'41793.1_gaiger.ABI'_1	frame 3	from 1 to 85
SEQ ID NO:736	'41793.1_gaiger.ABI'_2	frame -3	from 1 to 87
SEQ ID NO:737	'41794.1_gaiger.ABI'_1	frame 1	from 1 to 125
SEQ ID NO:738	'41794.1_gaiger.ABI'_2	frame -3	from 1 to 85

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:739	'41807.1_gaiger.ABI'_1	frame 1	from 1 to 67
SEQ ID NO:740	'41807.1_gaiger.ABI'_2	frame 2	from 11 to 107
SEQ ID NO:741	'41807.1_gaiger.ABI'_3	frame -1	from 51 to 107
SEQ ID NO:742	'41802.1_gaiger.ABI'_1	frame 3	from 1 to 143
SEQ ID NO:743	'41802.1_gaiger.ABI'_2	frame -2	from 4 to 56
SEQ ID NO:744	'41802.1_gaiger.ABI'_3	frame -3	from 1 to 105
SEQ ID NO:745	'41804.1_gaiger.ABI'_1	frame 1	from 1 to 59
SEQ ID NO:746	'41804.1_gaiger.ABI'_2	frame 2	from 15 to 92
SEQ ID NO:747	'41804.1_gaiger.ABI'_3	frame 3	from 33 to 82
SEQ ID NO:748	'41804.1_gaiger.ABI'_4	frame 3	from 84 to 139
SEQ ID NO:749	'41804.1_gaiger.ABI'_5	frame -2	from 22 to 139
SEQ ID NO:750	'41804.1_gaiger.ABI'_6	frame -3	from 1 to 60
SEQ ID NO:751	'41810.1_gaiger.ABI'_1	frame 1	from 1 to 67
SEQ ID NO:752	'41810.1_gaiger.ABI'_2	frame -1	from 1 to 67
SEQ ID NO:753	'41847.1_gaiger.ABI'_1	frame -1	from 1 to 97
SEQ ID NO:754	'41847.1_gaiger.ABI'_2	frame -3	from 1 to 56
SEQ ID NO:755	'41865.1_gaiger.ABI'_1	frame 1	from 1 to 139
SEQ ID NO:756	'41865.1_gaiger.ABI'_2	frame 3	from 58 to 108
SEQ ID NO:757	'41865.1_gaiger.ABI'_3	frame -2	from 1 to 92
SEQ ID NO:758	'41859.1_gaiger.ABI'_1	frame 1	from 86 to 138
SEQ ID NO:759	'41859.1_gaiger.ABI'_2	frame 3	from 1 to 108
SEQ ID NO:760	'41859.1_gaiger.ABI'_3	frame -1	from 18 to 95
SEQ ID NO:761	'41859.1_gaiger.ABI'_4	frame -3	from 27 to 150
SEQ ID NO:762	'41878.1_gaiger.ABI'_1	frame 2	from 70 to 131
SEQ ID NO:763	'41878.1_gaiger.ABI'_2	frame -3	from 30 to 88
SEQ ID NO:764	'41869.1_gaiger.ABI'_1	frame 1	from 41 to 127
SEQ ID NO:765	'41869.1_gaiger.ABI'_2	frame 3	from 1 to 55
SEQ ID NO:766	'41869.1_gaiger.ABI'_3	frame -3	from 1 to 121
SEQ ID NO:767	'41888.1_gaiger.ABI'_1	frame 3	from 22 to 81
SEQ ID NO:768	'41907.1_gaiger.ABI'_1	frame 1	from 1 to 73
SEQ ID NO:769	'41907.1_gaiger.ABI'_2	frame 2	from 29 to 102
SEQ ID NO:770	'41907.1_gaiger.ABI'_3	frame 3	from 47 to 96
SEQ ID NO:771	'41907.1_gaiger.ABI'_4	frame -1	from 42 to 103
SEQ ID NO:772	'41907.1_gaiger.ABI'_5	frame -2	from 44 to 102
SEQ ID NO:773	'41907.1_gaiger.ABI'_6	frame -3	from 1 to 102
SEQ ID NO:774	'41908.1_gaiger.ABI'_1	frame 1	from 1 to 102
SEQ ID NO:775	'41908.1_gaiger.ABI'_2	frame 3	from 67 to 120
SEQ ID NO:776	'41908.1_gaiger.ABI'_3	frame -1	from 54 to 121
SEQ ID NO:777	'41908.1_gaiger.ABI'_4	frame -2	from 1 to 50

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:778	'41912.1_gaiger.ABI'_1	frame 2	from 1 to 138
SEQ ID NO:779	'41912.1_gaiger.ABI'_2	frame -2	from 34 to 93
SEQ ID NO:780	'41912.1_gaiger.ABI'_3	frame -3	from 60 to 125
SEQ ID NO:781	'41916.1_gaiger.ABI'_1	frame 2	from 1 to 84
SEQ ID NO:782	'41916.1_gaiger.ABI'_2	frame -1	from 1 to 84
SEQ ID NO:783	'41925.1_gaiger.ABI'_1	frame 1	from 9 to 59
SEQ ID NO:784	'41925.1_gaiger.ABI'_2	frame 2	from 1 to 59
SEQ ID NO:785	'41925.1_gaiger.ABI'_3	frame -2	from 1 to 59
SEQ ID NO:786	'41925.1_gaiger.ABI'_4	frame -3	from 1 to 58
SEQ ID NO:787	'41929.1_gaiger.ABI'_1	frame 1	from 1 to 52
SEQ ID NO:788	'41930.1_gaiger.ABI'_1	frame -1	from 1 to 55
SEQ ID NO:789	'41930.1_gaiger.ABI'_2	frame -2	from 1 to 95
SEQ ID NO:790	'41933.1_gaiger.ABI'_1	frame 1	from 1 to 90
SEQ ID NO:791	'41933.1_gaiger.ABI'_2	frame 2	from 36 to 90
SEQ ID NO:792	'41944.1_gaiger.ABI'_1	frame 1	from 1 to 56
SEQ ID NO:793	'41944.1_gaiger.ABI'_2	frame 2	from 1 to 177
SEQ ID NO:794	'41944.1_gaiger.ABI'_3	frame 3	from 37 to 92
SEQ ID NO:795	'41944.1_gaiger.ABI'_4	frame -1	from 47 to 116
SEQ ID NO:796	'41944.1_gaiger.ABI'_5	frame -1	from 125 to 177
SEQ ID NO:797	'41944.1_gaiger.ABI'_6	frame -2	from 32 to 177
SEQ ID NO:798	'41944.1_gaiger.ABI'_7	frame -3	from 120 to 177
SEQ ID NO:799	'41986.1_gaiger.ABI'_1	frame 3	from 1 to 110
SEQ ID NO:800	'41986.1_gaiger.ABI'_2	frame -1	from 1 to 110
SEQ ID NO:801	'41986.1_gaiger.ABI'_3	frame -3	from 22 to 91
SEQ ID NO:802	'42017.1_gaiger.ABI'_1	frame 2	from 78 to 130
SEQ ID NO:803	'42017.1_gaiger.ABI'_2	frame 3	from 1 to 85
SEQ ID NO:804	'42017.1_gaiger.ABI'_3	frame -3	from 1 to 129
SEQ ID NO:805	'42033.1_gaiger.ABI'_1	frame 3	from 1 to 140
SEQ ID NO:806	'42033.1_gaiger.ABI'_2	frame -2	from 1 to 71
SEQ ID NO:807	'42033.1_gaiger.ABI'_3	frame -3	from 1 to 120
SEQ ID NO:808	'42040.1_gaiger.ABI'_1	frame 3	from 1 to 80
SEQ ID NO:809	'42041.1_gaiger.ABI'_1	frame -3	from 1 to 63
SEQ ID NO:810	'42053.1_gaiger.ABI'_1	frame 3	from 1 to 123
SEQ ID NO:811	'42053.1_gaiger.ABI'_2	frame -1	from 17 to 66
SEQ ID NO:812	'42053.1_gaiger.ABI'_3	frame -3	from 1 to 85
SEQ ID NO:813	'42101.1_gaiger.ABI'_1	frame 3	from 53 to 123
SEQ ID NO:814	'42101.1_gaiger.ABI'_2	frame -2	from 1 to 124
SEQ ID NO:815	'42131.1_gaiger.ABI'_1	frame 3	from 1 to 114
SEQ ID NO:816	'42131.1_gaiger.ABI'_2	frame -1	from 8 to 77

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:817	R0232:A08_1	frame -2	from 4 to 64
SEQ ID NO:818	R0232:C10_1	frame 3	from 1 to 65
SEQ ID NO:819	R0232:C10_2	frame -2	from 1 to 61
SEQ ID NO:820	R0233:A12_1	frame 3	from 1 to 141
SEQ ID NO:821	R0233:A12_2	frame -3	from 24 to 124
SEQ ID NO:822	R0233:A06_1	frame 1	from 12 to 77
SEQ ID NO:823	R0233:A06_2	frame 3	from 2 to 76
SEQ ID NO:824	R0233:A06_3	frame -3	from 1 to 59
SEQ ID NO:825	R0233:A08_1	frame 1	from 1 to 59
SEQ ID NO:826	R0233:A08_2	frame -1	from 1 to 63
SEQ ID NO:827	R0233:B10_1	frame 3	from 1 to 85
SEQ ID NO:828	R0233:B10_2	frame -3	from 1 to 85
SEQ ID NO:829	R0233:B04_1	frame 2	from 76 to 136
SEQ ID NO:830	R0233:B04_2	frame -3	from 1 to 103
SEQ ID NO:831	R0233:C04_1	frame 3	from 1 to 83
SEQ ID NO:832	R0233:C04_2	frame -3	from 1 to 119
SEQ ID NO:833	R0233:D01_1	frame 3	from 1 to 85
SEQ ID NO:834	R0233:D01_2	frame -1	from 2 to 122
SEQ ID NO:835	R0233:D02_1	frame 3	from 1 to 127
SEQ ID NO:836	R0233:D02_2	frame -1	from 1 to 127
SEQ ID NO:837	R0233:F10_1	frame 3	from 1 to 85
SEQ ID NO:838	R0233:F10_2	frame -3	from 1 to 123
SEQ ID NO:839	R0233:F05_1	frame 3	from 1 to 85
SEQ ID NO:840	R0233:F05_2	frame -2	from 58 to 111
SEQ ID NO:841	R0233:F05_3	frame -3	from 1 to 110
SEQ ID NO:842	R0233:F07_1	frame 3	from 1 to 85
SEQ ID NO:843	R0233:F07_2	frame -1	from 1 to 125
SEQ ID NO:844	'42324.1_gaiger.ABI'_1	frame 1	from 1 to 94
SEQ ID NO:845	'42324.1_gaiger.ABI'_2	frame 2	from 1 to 57
SEQ ID NO:846	'42324.1_gaiger.ABI'_3	frame 3	from 38 to 130
SEQ ID NO:847	'42324.1_gaiger.ABI'_4	frame -1	from 10 to 130
SEQ ID NO:848	'42324.1_gaiger.ABI'_5	frame -2	from 1 to 54
SEQ ID NO:849	'42324.1_gaiger.ABI'_6	frame -2	from 72 to 130
SEQ ID NO:850	'42324.1_gaiger.ABI'_7	frame -3	from 1 to 67
SEQ ID NO:851	'42324.1_gaiger.ABI'_8	frame -3	from 76 to 130
SEQ ID NO:852	'42349.1_gaiger.ABI'_1	frame 3	from 1 to 146
SEQ ID NO:853	'42349.1_gaiger.ABI'_2	frame -2	from 1 to 137
SEQ ID NO:854	'42379.1_gaiger.ABI'_1	frame 3	from 1 to 59
SEQ ID NO:855	'42379.1_gaiger.ABI'_2	frame -2	from 1 to 59

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:856	'42396.1_gaiger.ABI'_1	frame -1	from 1 to 50
SEQ ID NO:857	'42396.1_gaiger.ABI'_2	frame -2	from 22 to 82
SEQ ID NO:858	'42424.1_gaiger.ABI'_1	frame 3	from 1 to 85
SEQ ID NO:859	'42424.1_gaiger.ABI'_2	frame -3	from 1 to 123
SEQ ID NO:860	'42438.1_gaiger.ABI'_1	frame 1	from 1 to 123
SEQ ID NO:861	'42438.1_gaiger.ABI'_2	frame -3	from 53 to 123
SEQ ID NO:862	'42447.1_gaiger.ABI'_1	frame 1	from 1 to 57
SEQ ID NO:863	'42447.1_gaiger.ABI'_2	frame 2	from 33 to 97
SEQ ID NO:864	'42447.1_gaiger.ABI'_3	frame 3	from 1 to 72
SEQ ID NO:865	'42447.1_gaiger.ABI'_4	frame -2	from 26 to 97
SEQ ID NO:866	'42524.1;gaiger.ABI'_1	frame 2	from 1 to 69
SEQ ID NO:867	'42524.1;gaiger.ABI'_2	frame 3	from 1 to 59
SEQ ID NO:868	'42555.1;gaiger.ABI'_1	frame 3	from 1 to 115
SEQ ID NO:869	'42555.1;gaiger.ABI'_2	frame -2	from 35 to 131
SEQ ID NO:870	'42555.1;gaiger.ABI'_3	frame -3	from 1 to 75
SEQ ID NO:871	'42560.1;gaiger.ABI'_1	frame 1	from 1 to 67
SEQ ID NO:872	'42560.1;gaiger.ABI'_2	frame -3	from 1 to 66
SEQ ID NO:873	'42594.1_gaiger.ABI'_1	frame 2	from 56 to 118
SEQ ID NO:874	'42594.1_gaiger.ABI'_2	frame -1	from 42 to 118
SEQ ID NO:875	'42602.1_gaiger.ABI'_1	frame 1	from 1 to 97
SEQ ID NO:876	'42602.1_gaiger.ABI'_2	frame 3	from 1 to 76
SEQ ID NO:877	'42665.1_gaiger.ABI'_1	frame 1	from 1 to 94
SEQ ID NO:878	'42665.1_gaiger.ABI'_2	frame 3	from 35 to 94
SEQ ID NO:879	'42665.1_gaiger.ABI'_3	frame -1	from 35 to 94
SEQ ID NO:880	'42665.1_gaiger.ABI'_4	frame -3	from 12 to 73
SEQ ID NO:881	'42703.1_gaiger.ABI'_1	frame 2	from 25 to 95
SEQ ID NO:882	'42703.1_gaiger.ABI'_2	frame -2	from 10 to 82
SEQ ID NO:883	'42709.1_gaiger.ABI'_1	frame 2	from 1 to 118
SEQ ID NO:884	'42709.1_gaiger.ABI'_2	frame -3	from 53 to 118
SEQ ID NO:885	'42756.1_gaiger.ABI'_1	frame 3	from 1 to 109
SEQ ID NO:886	'42756.1_gaiger.ABI'_2	frame -2	from 1 to 85
SEQ ID NO:887	'42756.1_gaiger.ABI'_3	frame -3	from 1 to 51
SEQ ID NO:888	R0234:A06_1	frame 3	from 1 to 118
SEQ ID NO:889	R0234:A06_2	frame -2	from 1 to 80
SEQ ID NO:890	R0234:A07_1	frame 1	from 1 to 62
SEQ ID NO:891	R0234:A07_2	frame 2	from 6 to 102
SEQ ID NO:892	R0234:A07_3	frame -1	from 51 to 102
SEQ ID NO:893	R0234:B03_1	frame 3	from 1 to 68
SEQ ID NO:894	R0234:B03_2	frame -3	from 2 to 63

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:895	R0234:B06_1	frame 3	from 1 to 85
SEQ ID NO:896	R0234:B06_2	frame -3	from 1 to 123
SEQ ID NO:897	R0234:B09_1	frame 1	from 1 to 115
SEQ ID NO:898	R0234:B09_2	frame -3	from 53 to 115
SEQ ID NO:899	R0234:C02_1	frame 3	from 1 to 85
SEQ ID NO:900	R0234:C02_2	frame 3	from 87 to 139
SEQ ID NO:901	R0234:C02_3	frame -3	from 1 to 139
SEQ ID NO:902	R0234:C06_1	frame 3	from 1 to 85
SEQ ID NO:903	R0234:C06_2	frame -2	from 1 to 107
SEQ ID NO:904	R0234:D08_1	frame 3	from 1 to 55
SEQ ID NO:905	R0234:D08_2	frame -1	from 1 to 55
SEQ ID NO:906	R0234:E01_1	frame 3	from 1 to 101
SEQ ID NO:907	R0234:E01_2	frame -3	from 1 to 101
SEQ ID NO:908	R0234:E12_1	frame 2	from 78 to 134
SEQ ID NO:909	R0234:E12_2	frame 3	from 1 to 189
SEQ ID NO:910	R0234:E12_3	frame -2	from 8 to 120
SEQ ID NO:911	R0234:E12_4	frame -3	from 28 to 77
SEQ ID NO:912	R0234:E12_5	frame -3	from 105 to 189
SEQ ID NO:913	R0234:E02_1	frame 3	from 1 to 85
SEQ ID NO:914	R0234:E02_2	frame -3	from 1 to 111
SEQ ID NO:915	R0234:E04_1	frame 1	from 40 to 114
SEQ ID NO:916	R0234:E04_2	frame 3	from 1 to 54
SEQ ID NO:917	R0234:E04_3	frame -1	from 1 to 109
SEQ ID NO:918	R0234:E05_1	frame 3	from 1 to 85
SEQ ID NO:919	R0234:E05_2	frame -1	from 1 to 52
SEQ ID NO:920	R0234:E05_3	frame -2	from 1 to 121
SEQ ID NO:921	R0234:F02_1	frame 3	from 1 to 109
SEQ ID NO:922	R0234:F02_2	frame -2	from 1 to 109
SEQ ID NO:923	R0234:F04_1	frame 3	from 1 to 83
SEQ ID NO:924	R0234:F04_2	frame -2	from 1 to 122
SEQ ID NO:925	R0234:G01_1	frame 3	from 1 to 84
SEQ ID NO:926	R0234:G11_1	frame 3	from 1 to 121
SEQ ID NO:927	R0234:G11_2	frame -2	from 51 to 121
SEQ ID NO:928	R0234:G12_1	frame 2	from 1 to 150
SEQ ID NO:929	R0234:G12_2	frame -2	from 61 to 113
SEQ ID NO:930	R0234:G12_3	frame -3	from 24 to 124
SEQ ID NO:931	R0234:G02_1	frame 3	from 1 to 123
SEQ ID NO:932	R0234:G02_2	frame -3	from 1 to 85
SEQ ID NO:933	R0234:G04_1	frame 2	from 1 to 150

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:934	R0234:G04_2	frame -3	from 24 to 124
SEQ ID NO:935	R0234:G09_1	frame 1	from 1 to 61
SEQ ID NO:936	R0234:G09_2	frame 1	from 74 to 187
SEQ ID NO:937	R0234:G09_3	frame 2	from 123 to 186
SEQ ID NO:938	R0234:G09_4	frame 3	from 1 to 82
SEQ ID NO:939	R0234:G09_5	frame 3	from 84 to 171
SEQ ID NO:940	R0234:G09_6	frame -2	from 90 to 155
SEQ ID NO:941	R0234:G09_7	frame -3	from 29 to 164
SEQ ID NO:942	R0234:H01_1	frame 3	from 1 to 84
SEQ ID NO:943	R0234:H06_1	frame 3	from 1 to 85
SEQ ID NO:944	R0234:H06_2	frame -1	from 1 to 121
SEQ ID NO:945	R0235:B01_1	frame 3	from 1 to 119
SEQ ID NO:946	R0235:B01_2	frame -1	from 8 to 128
SEQ ID NO:947	R0235:B01_3	frame -3	from 3 to 58
SEQ ID NO:948	R0235:B11_1	frame 3	from 1 to 62
SEQ ID NO:949	R0235:B04_1	frame 3	from 1 to 101
SEQ ID NO:950	R0235:B04_2	frame -1	from 1 to 102
SEQ ID NO:951	R0235:B05_1	frame 3	from 1 to 67
SEQ ID NO:952	R0235:B05_2	frame -1	from 1 to 67
SEQ ID NO:953	R0235:B07_1	frame 3	from 1 to 83
SEQ ID NO:954	R0235:B09_1	frame 1	from 1 to 58
SEQ ID NO:955	R0235:B09_2	frame 2	from 2 to 78
SEQ ID NO:956	R0235:B09_3	frame 3	from 34 to 88
SEQ ID NO:957	R0235:C07_1	frame 3	from 1 to 69
SEQ ID NO:958	R0235:C07_2	frame -2	from 1 to 69
SEQ ID NO:959	R0235:C09_1	frame -1	from 1 to 97
SEQ ID NO:960	R0235:C09_2	frame -3	from 1 to 56
SEQ ID NO:961	R0235:D11_1	frame 1	from 1 to 87
SEQ ID NO:962	R0235:D11_2	frame 2	from 74 to 136
SEQ ID NO:963	R0235:D11_3	frame 3	from 1 to 76
SEQ ID NO:964	R0235:D11_4	frame -1	from 15 to 85
SEQ ID NO:965	R0235:D11_5	frame -2	from 6 to 94
SEQ ID NO:966	R0235:E10_1	frame 3	from 1 to 66
SEQ ID NO:967	R0235:E12_1	frame 3	from 1 to 51
SEQ ID NO:968	R0235:E12_2	frame -1	from 1 to 51
SEQ ID NO:969	R0235:E02_1	frame 3	from 1 to 52
SEQ ID NO:970	R0235:F01_1	frame 3	from 1 to 66
SEQ ID NO:971	R0235:F02_1	frame 3	from 1 to 56
SEQ ID NO:972	R0235:F02_2	frame -2	from 11 to 65

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:973	R0235:F06_1	frame 3	from 24 to 124
SEQ ID NO:974	R0235:F06_2	frame -2	from 1 to 150
SEQ ID NO:975	R0235:F09_1	frame 3	from 1 to 53
SEQ ID NO:976	R0235:F09_2	frame -1	from 1 to 53
SEQ ID NO:977	R0235:G07_1	frame 3	from 1 to 97
SEQ ID NO:978	R0235:G07_2	frame -2	from 1 to 59
SEQ ID NO:979	R0235:H06_1	frame 3	from 1 to 83
SEQ ID NO:980	R0235:H06_2	frame -3	from 1 to 60
SEQ ID NO:981	R0235:H08_1	frame 3	from 1 to 123
SEQ ID NO:982	R0235:H08_2	frame -3	from 1 to 123
SEQ ID NO:983	R0236:A06_1	frame 2	from 1 to 150
SEQ ID NO:984	R0236:A06_2	frame -2	from 25 to 125
SEQ ID NO:985	R0236:A09_1	frame 3	from 1 to 122
SEQ ID NO:986	R0236:A09_2	frame -1	from 54 to 122
SEQ ID NO:987	R0236:C01_1	frame 3	from 1 to 118
SEQ ID NO:988	R0236:C01_2	frame -2	from 1 to 80
SEQ ID NO:989	R0236:F12_1	frame 1	from 17 to 79
SEQ ID NO:990	R0236:F12_2	frame 3	from 1 to 56
SEQ ID NO:991	R0236:F05_1	frame 3	from 1 to 123
SEQ ID NO:992	R0236:F05_2	frame -3	from 1 to 85
SEQ ID NO:993	R0236:F06_1	frame 3	from 1 to 123
SEQ ID NO:994	R0236:F06_2	frame -3	from 1 to 85
SEQ ID NO:995	R0236:G08_1	frame 2	from 1 to 88
SEQ ID NO:996	R0236:G08_2	frame 3	from 34 to 88
SEQ ID NO:997	R0249:A11_1	frame 3	from 1 to 83
SEQ ID NO:998	R0249:A11_2	frame -3	from 1 to 121
SEQ ID NO:999	R0249:B04_1	frame -2	from 1 to 56
SEQ ID NO:1000	R0249:B04_2	frame -3	from 1 to 96
SEQ ID NO:1001	R0249:B06_1	frame -1	from 1 to 81
SEQ ID NO:1002	R0249:D11_1	frame 2	from 1 to 170
SEQ ID NO:1003	R0249:D11_2	frame 3	from 41 to 101
SEQ ID NO:1004	R0249:D11_3	frame 3	from 103 to 153
SEQ ID NO:1005	R0249:D11_4	frame -1	from 1 to 59
SEQ ID NO:1006	R0249:D11_5	frame -1	from 79 to 139
SEQ ID NO:1007	R0249:D11_6	frame -3	from 65 to 170
SEQ ID NO:1008	R0249:E11_1	frame 3	from 1 to 59
SEQ ID NO:1009	R0249:E11_2	frame -3	from 1 to 59
SEQ ID NO:1010	R0249:E06_1	frame 3	from 1 to 85
SEQ ID NO:1011	R0249:E06_2	frame -3	from 1 to 123

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:1012	R0249:H09_1	frame 3	from 1 to 83
SEQ ID NO:1013	R0249:H09_2	frame -2	from 1 to 83
SEQ ID NO:1014	R0250:C09_1	frame 1	from 1 to 55
SEQ ID NO:1015	R0250:C09_2	frame 1	from 117 to 166
SEQ ID NO:1016	R0250:C09_3	frame 3	from 30 to 88
SEQ ID NO:1017	R0250:C09_4	frame 3	from 90 to 165
SEQ ID NO:1018	R0250:C09_5	frame -1	from 74 to 125
SEQ ID NO:1019	R0250:C09_6	frame -3	from 1 to 165
SEQ ID NO:1020	R0250:D10_1	frame 3	from 1 to 85
SEQ ID NO:1021	R0250:D10_2	frame -3	from 1 to 123
SEQ ID NO:1022	R0250:D03_1	frame 1	from 17 to 66
SEQ ID NO:1023	R0250:D03_2	frame 3	from 1 to 80
SEQ ID NO:1024	R0250:D03_3	frame -2	from 1 to 80
SEQ ID NO:1025	R0250:E09_1	frame 3	from 1 to 101
SEQ ID NO:1026	R0250:E09_2	frame -3	from 1 to 63
SEQ ID NO:1027	R0250:F09_1	frame 2	from 62 to 136
SEQ ID NO:1028	R0250:F09_2	frame 3	from 69 to 145
SEQ ID NO:1029	R0250:F09_3	frame -1	from 1 to 82
SEQ ID NO:1030	R0250:F09_4	frame -1	from 84 to 167
SEQ ID NO:1031	R0250:F09_5	frame -2	from 1 to 60
SEQ ID NO:1032	R0250:G01_1	frame 1	from 17 to 87
SEQ ID NO:1033	R0250:G01_2	frame 2	from 1 to 77
SEQ ID NO:1034	R0250:G01_3	frame 2	from 126 to 179
SEQ ID NO:1035	R0250:G01_4	frame -1	from 111 to 160
SEQ ID NO:1036	R0250:G01_5	frame -2	from 33 to 101
SEQ ID NO:1037	R0250:G01_6	frame -3	from 1 to 61
SEQ ID NO:1038	R0250:G01_7	frame -3	from 63 to 121
SEQ ID NO:1039	R0250:G01_8	frame -3	from 123 to 178
SEQ ID NO:1040	R0251:A12_1	frame 3	from 1 to 85
SEQ ID NO:1041	R0251:A12_2	frame -3	from 1 to 123
SEQ ID NO:1042	R0251:A05_1	frame 3	from 1 to 96
SEQ ID NO:1043	R0251:A05_2	frame -1	from 1 to 96
SEQ ID NO:1044	R0251:B09_1	frame 3	from 1 to 85
SEQ ID NO:1045	R0251:B09_2	frame -3	from 1 to 90
SEQ ID NO:1046	R0251:D01_1	frame 2	from 1 to 124
SEQ ID NO:1047	R0251:D01_2	frame -3	from 53 to 123
SEQ ID NO:1048	R0251:E03_1	frame 3	from 1 to 95
SEQ ID NO:1049	R0251:E03_2	frame -2	from 1 to 57
SEQ ID NO:1050	R0251:E06_1	frame 3	from 1 to 98

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:1051	R0251:E06_2	frame -2	from 1 to 60
SEQ ID NO:1052	R0251:F12_1	frame 1	from 51 to 110
SEQ ID NO:1053	R0251:F12_2	frame -1	from 32 to 111
SEQ ID NO:1054	R0251:F12_3	frame -2	from 35 to 131
SEQ ID NO:1055	R0251:G06_1	frame -1	from 1 to 97
SEQ ID NO:1056	R0251:G06_2	frame -3	from 1 to 56
SEQ ID NO:1057	R0252:A08_1	frame 1	from 1 to 64
SEQ ID NO:1058	R0252:A08_2	frame 2	from 12 to 64
SEQ ID NO:1059	R0252:A08_3	frame -1	from 1 to 51
SEQ ID NO:1060	R0252:A08_4	frame -2	from 1 to 64
SEQ ID NO:1061	R0252:D02_1	frame 3	from 1 to 85
SEQ ID NO:1062	R0252:D02_2	frame -3	from 1 to 123
SEQ ID NO:1063	R0252:E04_1	frame 1	from 1 to 59
SEQ ID NO:1064	R0252:E04_2	frame 2	from 57 to 107
SEQ ID NO:1065	R0252:E04_3	frame 3	from 35 to 154
SEQ ID NO:1066	R0252:E04_4	frame -1	from 22 to 110
SEQ ID NO:1067	R0252:E04_5	frame -3	from 1 to 60
SEQ ID NO:1068	R0252:E04_6	frame -3	from 91 to 154
SEQ ID NO:1069	R0252:E06_1	frame 1	from 1 to 59
SEQ ID NO:1070	R0252:E06_2	frame 2	from 57 to 107
SEQ ID NO:1071	R0252:E06_3	frame 3	from 35 to 142
SEQ ID NO:1072	R0252:E06_4	frame -2	from 79 to 142
SEQ ID NO:1073	R0252:E06_5	frame -3	from 9 to 97
SEQ ID NO:1074	R0252:E07_1	frame 1	from 1 to 59
SEQ ID NO:1075	R0252:E07_2	frame 2	from 57 to 107
SEQ ID NO:1076	R0252:E07_3	frame 2	from 109 to 184
SEQ ID NO:1077	R0252:E07_4	frame 3	from 35 to 183
SEQ ID NO:1078	R0252:E07_5	frame -1	from 51 to 139
SEQ ID NO:1079	R0252:E07_6	frame -3	from 28 to 89
SEQ ID NO:1080	R0252:E07_7	frame -3	from 120 to 183
SEQ ID NO:1081	R0252:F11_1	frame 1	from 1 to 94
SEQ ID NO:1082	R0252:F11_2	frame 3	from 1 to 61
SEQ ID NO:1083	R0252:F11_3	frame -2	from 12 to 69
SEQ ID NO:1084	R0252:F11_4	frame -3	from 1 to 139
SEQ ID NO:1085	R0252:F02_1	frame 1	from 1 to 66
SEQ ID NO:1086	R0252:F02_2	frame 2	from 57 to 107
SEQ ID NO:1087	R0252:F02_3	frame 2	from 109 to 160
SEQ ID NO:1088	R0252:F02_4	frame 3	from 35 to 159
SEQ ID NO:1089	R0252:F02_5	frame -1	from 27 to 115

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:1090	R0252:F02_6	frame -3	from 4 to 65
SEQ ID NO:1091	R0252:F02_7	frame -3	from 96 to 159
SEQ ID NO:1092	R0252:H01_1	frame 2	from 1 to 123
SEQ ID NO:1093	R0252:H01_2	frame -3	from 53 to 123
SEQ ID NO:1094	R0252:H03_1	frame 3	from 1 to 85
SEQ ID NO:1095	R0252:H03_2	frame -3	from 1 to 123
SEQ ID NO:1096	R0253:B04_1	frame 3	from 1 to 85
SEQ ID NO:1097	R0253:B04_2	frame -3	from 1 to 102
SEQ ID NO:1098	R0253:C04_1	frame 3	from 1 to 85
SEQ ID NO:1099	R0253:C04_2	frame -2	from 1 to 108
SEQ ID NO:1100	R0253:C05_1	frame 3	from 1 to 56
SEQ ID NO:1101	R0253:C05_2	frame -1	from 1 to 54
SEQ ID NO:1102	R0253:C05_3	frame -2	from 9 to 63
SEQ ID NO:1103	R0253:C06_1	frame 3	from 1 to 56
SEQ ID NO:1104	R0253:D02_1	frame 3	from 1 to 85
SEQ ID NO:1105	R0253:D02_2	frame -3	from 1 to 123
SEQ ID NO:1106	R0253:D08_1	frame 2	from 1 to 194
SEQ ID NO:1107	R0253:D08_2	frame 3	from 102 to 153
SEQ ID NO:1108	R0253:D08_3	frame -1	from 1 to 55
SEQ ID NO:1109	R0253:D08_4	frame -1	from 117 to 182
SEQ ID NO:1110	R0253:D08_5	frame -3	from 30 to 88
SEQ ID NO:1111	R0253:D08_6	frame -3	from 90 to 149
SEQ ID NO:1112	R0253:E06_1	frame 1	from 1 to 51
SEQ ID NO:1113	R0253:E06_2	frame 2	from 1 to 51
SEQ ID NO:1114	R0253:F11_1	frame 1	from 1 to 79
SEQ ID NO:1115	R0253:F11_2	frame 3	from 26 to 79
SEQ ID NO:1116	R0253:F11_3	frame -3	from 1 to 59
SEQ ID NO:1117	R0253:F07_1	frame 3	from 1 to 85
SEQ ID NO:1118	R0253:F07_2	frame -3	from 1 to 93
SEQ ID NO:1119	R0253:G11_1	frame 2	from 1 to 194
SEQ ID NO:1120	R0253:G11_2	frame 3	from 102 to 153
SEQ ID NO:1121	R0253:G11_3	frame -1	from 1 to 55
SEQ ID NO:1122	R0253:G11_4	frame -1	from 117 to 182
SEQ ID NO:1123	R0253:G11_5	frame -3	from 30 to 88
SEQ ID NO:1124	R0253:G11_6	frame -3	from 90 to 149
SEQ ID NO:1125	R0253:G12_1	frame 1	from 1 to 94
SEQ ID NO:1126	R0253:G12_2	frame 3	from 1 to 53
SEQ ID NO:1127	R0253:G05_1	frame 3	from 53 to 123
SEQ ID NO:1128	R0253:G05_2	frame -2	from 1 to 124

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:1129	R0253:H02_1	frame 2	from 1 to 63
SEQ ID NO:1130	R0253:H07_1	frame 2	from 1 to 73
SEQ ID NO:1131	R0253:H07_2	frame 3	from 1 to 57
SEQ ID NO:1132	R0254:F07_1	frame 1	from 69 to 153
SEQ ID NO:1133	R0254:F07_2	frame -1	from 87 to 142
SEQ ID NO:1134	R0254:F07_3	frame -2	from 47 to 116
SEQ ID NO:1135	R0254:F07_4	frame -3	from 1 to 82
SEQ ID NO:1136	R0254:F07_5	frame -3	from 99 to 154
SEQ ID NO:1137	R0254:G11_1	frame 3	from 1 to 85
SEQ ID NO:1138	R0254:G11_2	frame -3	from 1 to 123
SEQ ID NO:1139	R0254:G04_1	frame 3	from 1 to 123
SEQ ID NO:1140	R0254:G04_2	frame -3	from 1 to 85
SEQ ID NO:1141	R0254:H01_1	frame 3	from 1 to 85
SEQ ID NO:1142	R0254:H01_2	frame -3	from 1 to 123
SEQ ID NO:1143	R0238:C03_1	frame 2	from 6 to 120
SEQ ID NO:1144	R0238:C03_2	frame 3	from 103 to 157
SEQ ID NO:1145	R0238:C03_3	frame -1	from 28 to 78
SEQ ID NO:1146	R0255:C02_1	frame 1	from 1 to 60
SEQ ID NO:1147	R0255:C02_2	frame 3	from 23 to 96
SEQ ID NO:1148	R0255:C02_3	frame -1	from 35 to 108
SEQ ID NO:1149	R0255:F12_1	frame 3	from 1 to 57
SEQ ID NO:1150	R0255:F12_2	frame -2	from 1 to 78
SEQ ID NO:1151	R0258:G10_1	frame 1	from 7 to 121
SEQ ID NO:1152	R0258:G10_2	frame 2	from 104 to 158
SEQ ID NO:1153	R0258:G10_3	frame -1	from 34 to 84
SEQ ID NO:1154	R0261:A12_1	frame 2	from 2 to 60
SEQ ID NO:1155	R0261:A12_2	frame 3	from 1 to 110
SEQ ID NO:1156	R0261:A12_3	frame -1	from 1 to 145
SEQ ID NO:1157	R0261:A12_4	frame -3	from 13 to 144
SEQ ID NO:1158	R0261:A09_1	frame 1	from 1 to 174
SEQ ID NO:1159	R0261:A09_2	frame 2	from 34 to 89
SEQ ID NO:1160	R0261:A09_3	frame 3	from 1 to 52
SEQ ID NO:1161	R0261:A09_4	frame -1	from 121 to 174
SEQ ID NO:1162	R0261:A09_5	frame -2	from 47 to 116
SEQ ID NO:1163	R0261:A09_6	frame -2	from 125 to 174
SEQ ID NO:1164	R0261:A09_7	frame -3	from 32 to 174
SEQ ID NO:1165	R0261:B12_1	frame 1	from 51 to 113
SEQ ID NO:1166	R0261:B12_2	frame -2	from 2 to 51
SEQ ID NO:1167	R0261:C10_1	frame 2	from 6 to 120

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:1168	R0261:C10_2	frame 3	from 103 to 157
SEQ ID NO:1169	R0261:C10_3	frame -1	from 25 to 75
SEQ ID NO:1170	R0261:D06_1	frame 2	from 1 to 117
SEQ ID NO:1171	R0261:D06_2	frame -2	from 1 to 117
SEQ ID NO:1172	R0261:D06_3	frame -3	from 35 to 117
SEQ ID NO:1173	R0261:E04_1	frame 2	from 1 to 170
SEQ ID NO:1174	R0261:E04_2	frame -2	from 32 to 122
SEQ ID NO:1175	R0261:E04_3	frame -3	from 36 to 144
SEQ ID NO:1176	R0261:F05_1	frame 2	from 61 to 111
SEQ ID NO:1177	R0261:F05_2	frame -1	from 1 to 78
SEQ ID NO:1178	R0261:F05_3	frame -1	from 105 to 157
SEQ ID NO:1179	R0261:F05_4	frame -2	from 61 to 115
SEQ ID NO:1180	R0261:G04_1	frame 2	from 13 to 111
SEQ ID NO:1181	R0261:G04_2	frame 3	from 91 to 147
SEQ ID NO:1182	R0261:G04_3	frame -1	from 83 to 169
SEQ ID NO:1183	R0261:G04_4	frame -2	from 4 to 56
SEQ ID NO:1184	R0261:G04_5	frame -3	from 123 to 181
SEQ ID NO:1185	R0261:H03_1	frame 2	from 6 to 120
SEQ ID NO:1186	R0261:H03_2	frame 3	from 103 to 157
SEQ ID NO:1187	R0261:H03_3	frame -1	from 33 to 83
SEQ ID NO:1188	R0262:A12_1	frame -1	from 35 to 132
SEQ ID NO:1189	R0262:A02_1	frame 1	from 1 to 142
SEQ ID NO:1190	R0262:A02_2	frame 2	from 18 to 81
SEQ ID NO:1191	R0262:A02_3	frame 3	from 1 to 86
SEQ ID NO:1192	R0262:A02_4	frame -2	from 1 to 73
SEQ ID NO:1193	R0262:A02_5	frame -3	from 1 to 52
SEQ ID NO:1194	R0262:D12_1	frame 2	from 4 to 118
SEQ ID NO:1195	R0262:D04_1	frame 1	from 26 to 95
SEQ ID NO:1196	R0262:D04_2	frame 3	from 32 to 94
SEQ ID NO:1197	R0262:D04_3	frame -2	from 16 to 65
SEQ ID NO:1198	R0262:D04_4	frame -3	from 1 to 92
SEQ ID NO:1199	R0262:D07_1	frame 1	from 102 to 156
SEQ ID NO:1200	R0262:D07_2	frame 3	from 4 to 118
SEQ ID NO:1201	R0262:D07_3	frame -1	from 20 to 70
SEQ ID NO:1202	R0262:E02_1	frame 1	from 7 to 121
SEQ ID NO:1203	R0262:E02_2	frame 2	from 104 to 158
SEQ ID NO:1204	R0262:E02_3	frame -2	from 27 to 77
SEQ ID NO:1205	R0262:E03_1	frame 1	from 127 to 176
SEQ ID NO:1206	R0262:E03_2	frame 2	from 26 to 159

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:1207	R0262:E03_3	frame 3	from 1 to 67
SEQ ID NO:1208	R0262:E03_4	frame -1	from 9 to 68
SEQ ID NO:1209	R0262:E03_5	frame -2	from 113 to 176
SEQ ID NO:1210	R0262:E03_6	frame -3	from 107 to 159
SEQ ID NO:1211	R0262:F06_1	frame 1	from 1 to 99
SEQ ID NO:1212	R0262:F06_2	frame 3	from 13 to 98
SEQ ID NO:1213	R0262:F06_3	frame -2	from 1 to 64
SEQ ID NO:1214	R0263:B03_1	frame 1	from 1 to 84
SEQ ID NO:1215	R0263:B03_2	frame 3	from 13 to 83
SEQ ID NO:1216	R0263:B09_1	frame 2	from 1 to 199
SEQ ID NO:1217	R0263:B09_2	frame -1	from 1 to 76
SEQ ID NO:1218	R0263:B09_3	frame -1	from 78 to 199
SEQ ID NO:1219	R0263:B09_4	frame -2	from 140 to 195
SEQ ID NO:1220	R0263:E03_1	frame 3	from 50 to 111
SEQ ID NO:1221	R0263:E03_2	frame -1	from 119 to 204
SEQ ID NO:1222	R0263:F08_1	frame 3	from 1 to 95
SEQ ID NO:1223	R0263:G10_1	frame 1	from 7 to 121
SEQ ID NO:1224	R0263:G10_2	frame 1	from 148 to 198
SEQ ID NO:1225	R0263:G10_3	frame 2	from 14 to 77
SEQ ID NO:1226	R0263:G10_4	frame 2	from 104 to 158
SEQ ID NO:1227	R0263:G10_5	frame -1	from 37 to 87
SEQ ID NO:1228	R0263:G02_1	frame 1	from 54 to 126
SEQ ID NO:1229	R0263:G02_2	frame 2	from 1 to 70
SEQ ID NO:1230	R0263:G02_3	frame -2	from 109 to 190
SEQ ID NO:1231	R0263:G02_4	frame -3	from 34 to 105
SEQ ID NO:1232	R0263:G03_1	frame 1	from 90 to 139
SEQ ID NO:1233	R0263:G03_2	frame 2	from 13 to 106
SEQ ID NO:1234	R0263:G03_3	frame -1	from 3 to 55
SEQ ID NO:1235	R0263:G03_4	frame -2	from 122 to 180
SEQ ID NO:1236	R0263:G03_5	frame -3	from 77 to 167
SEQ ID NO:1237	R0263:H10_1	frame 1	from 1 to 55
SEQ ID NO:1238	R0263:H10_2	frame 1	from 99 to 152
SEQ ID NO:1239	R0263:H10_3	frame 3	from 1 to 147
SEQ ID NO:1240	R0263:H10_4	frame -1	from 6 to 140
SEQ ID NO:1241	R0263:H10_5	frame -3	from 1 to 151
SEQ ID NO:1242	R0264:A02_1	frame 1	from 1 to 85
SEQ ID NO:1243	R0264:A02_2	frame 3	from 13 to 84
SEQ ID NO:1244	R0264:A02_3	frame -3	from 1 to 50
SEQ ID NO:1245	R0264:B11_1	frame 2	from 6 to 120

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:1246	R0264:B11_2	frame 3	from 103 to 157
SEQ ID NO:1247	R0264:B11_3	frame -1	from 30 to 80
SEQ ID NO:1248	R0264:E12_1	frame 3	from 50 to 111
SEQ ID NO:1249	R0264:E12_2	frame -1	from 78 to 163
SEQ ID NO:1250	R0264:F11_1	frame 1	from 13 to 81
SEQ ID NO:1251	R0264:F11_2	frame -1	from 1 to 102
SEQ ID NO:1252	R0264:F11_3	frame -2	from 25 to 101
SEQ ID NO:1253	R0264:F11_4	frame -3	from 42 to 101
SEQ ID NO:1254	R0264:F09_1	frame 1	from 7 to 121
SEQ ID NO:1255	R0264:F09_2	frame 2	from 104 to 158
SEQ ID NO:1256	R0264:F09_3	frame -3	from 25 to 75
SEQ ID NO:1257	R0264:G01_1	frame 2	from 61 to 124
SEQ ID NO:1258	R0264:G01_2	frame 3	from 24 to 82
SEQ ID NO:1259	R0264:G01_3	frame -1	from 80 to 150
SEQ ID NO:1260	R0264:G01_4	frame -2	from 1 to 94
SEQ ID NO:1261	R0264:G11_1	frame 1	from 1 to 164
SEQ ID NO:1262	R0264:G11_2	frame 2	from 74 to 145
SEQ ID NO:1263	R0264:G11_3	frame -2	from 1 to 120
SEQ ID NO:1264	R0264:G11_4	frame -3	from 50 to 163
SEQ ID NO:1265	R0264:G04_1	frame 2	from 6 to 93
SEQ ID NO:1266	R0265:F07_1	frame 1	from 1 to 75
SEQ ID NO:1267	R0265:F07_2	frame 1	from 102 to 154
SEQ ID NO:1268	R0265:F07_3	frame 2	from 58 to 112
SEQ ID NO:1269	R0265:F07_4	frame 2	from 116 to 167
SEQ ID NO:1270	R0265:F07_5	frame -2	from 61 to 111
SEQ ID NO:1271	R0265:G01_1	frame 1	from 1 to 112
SEQ ID NO:1272	R0265:G01_2	frame 3	from 3 to 61
SEQ ID NO:1273	R0265:G01_3	frame -1	from 1 to 146
SEQ ID NO:1274	R0265:G01_4	frame -3	from 13 to 146
SEQ ID NO:1275	R0265:G10_1	frame 1	from 1 to 115
SEQ ID NO:1276	R0265:G10_2	frame 3	from 13 to 114
SEQ ID NO:1277	R0265:G10_3	frame -2	from 1 to 80
SEQ ID NO:1278	R0265:G11_1	frame 1	from 59 to 122
SEQ ID NO:1279	R0265:G11_2	frame 3	from 25 to 103
SEQ ID NO:1280	R0265:G11_3	frame -1	from 14 to 91
SEQ ID NO:1281	R0265:H09_1	frame 1	from 1 to 191
SEQ ID NO:1282	R0265:H09_2	frame -1	from 1 to 51
SEQ ID NO:1283	R0265:H09_3	frame -1	from 91 to 141
SEQ ID NO:1284	R0265:H09_4	frame -2	from 98 to 152

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:1285	R0266:A11_1	frame 1	from 1 to 107
SEQ ID NO:1286	R0266:A11_2	frame 3	from 1 to 56
SEQ ID NO:1287	R0266:A11_3	frame -1	from 1 to 141
SEQ ID NO:1288	R0266:A11_4	frame -3	from 13 to 125
SEQ ID NO:1289	R0266:A12_1	frame 1	from 1 to 106
SEQ ID NO:1290	R0266:A12_2	frame 1	from 133 to 185
SEQ ID NO:1291	R0266:A12_3	frame 2	from 89 to 143
SEQ ID NO:1292	R0266:A12_4	frame 2	from 147 to 197
SEQ ID NO:1293	R0266:A12_5	frame -3	from 51 to 101
SEQ ID NO:1294	R0266:B01_1	frame 1	from 20 to 93
SEQ ID NO:1295	R0266:B01_2	frame 2	from 1 to 56
SEQ ID NO:1296	R0266:B01_3	frame -3	from 31 to 104
SEQ ID NO:1297	R0266:C12_1	frame 1	from 7 to 121
SEQ ID NO:1298	R0266:C12_2	frame 1	from 148 to 200
SEQ ID NO:1299	R0266:C12_3	frame 2	from 104 to 158
SEQ ID NO:1300	R0266:C12_4	frame -3	from 41 to 93
SEQ ID NO:1301	R0266:E01_1	frame 3	from 1 to 125
SEQ ID NO:1302	R0266:E01_2	frame -1	from 75 to 133
SEQ ID NO:1303	R0266:E01_3	frame -2	from 34 to 133
SEQ ID NO:1304	R0266:E03_1	frame 3	from 81 to 130
SEQ ID NO:1305	R0266:E03_2	frame -1	from 1 to 131
SEQ ID NO:1306	R0266:E03_3	frame -3	from 1 to 53
SEQ ID NO:1307	R0266:F03_1	frame 1	from 64 to 141
SEQ ID NO:1308	R0266:F03_2	frame 2	from 8 to 141
SEQ ID NO:1309	R0266:F03_3	frame 3	from 39 to 104
SEQ ID NO:1310	R0266:F03_4	frame -2	from 1 to 141
SEQ ID NO:1311	R0266:F07_1	frame -3	from 37 to 97
SEQ ID NO:1312	R0266:F07_2	frame -3	from 138 to 188
SEQ ID NO:1313	R0266:G10_1	frame 3	from 24 to 124
SEQ ID NO:1314	R0266:G10_2	frame -2	from 1 to 150
SEQ ID NO:1315	R0266:G09_1	frame 1	from 7 to 121
SEQ ID NO:1316	R0266:G09_2	frame 2	from 104 to 158
SEQ ID NO:1317	R0266:G09_3	frame -2	from 28 to 78
SEQ ID NO:1318	R0266:H09_1	frame 1	from 1 to 68
SEQ ID NO:1319	R0266:H09_2	frame 3	from 48 to 148
SEQ ID NO:1320	R0266:H09_3	frame -2	from 1 to 137
SEQ ID NO:1321	R0243:F07_1	frame 1	from 19 to 77
SEQ ID NO:1322	R0243:F07_2	frame 2	from 13 to 76
SEQ ID NO:1323	R0243:F07_3	frame 3	from 20 to 76

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:1324	R0243:F07_4	frame -1	from 15 to 65
SEQ ID NO:1325	R0244:C02_1	frame 1	from 1 to 64
SEQ ID NO:1326	R0244:C02_2	frame -1	from 8 to 107
SEQ ID NO:1327	R0244:C02_3	frame -2	from 19 to 70
SEQ ID NO:1328	R0244:C04_1	frame 1	from 19 to 77
SEQ ID NO:1329	R0244:C04_2	frame 2	from 13 to 76
SEQ ID NO:1330	R0244:C04_3	frame 3	from 20 to 76
SEQ ID NO:1331	R0244:C04_4	frame -1	from 15 to 65
SEQ ID NO:1332	R0245:A02_1	frame 2	from 12 to 61
SEQ ID NO:1333	R0245:A02_2	frame -3	from 42 to 92
SEQ ID NO:1334	'46802.1_gaiger.ABI'_1	frame 1	from 1 to 90
SEQ ID NO:1335	'46802.1_gaiger.ABI'_2	frame -1	from 1 to 52
SEQ ID NO:1336	'46816.1_gaiger.ABI'_1	frame 2	from 1 to 166
SEQ ID NO:1337	'46816.1_gaiger.ABI'_2	frame -2	from 16 to 91
SEQ ID NO:1338	'46816.1_gaiger.ABI'_3	frame -2	from 94 to 166
SEQ ID NO:1339	'46816.1_gaiger.ABI'_4	frame -3	from 99 to 166
SEQ ID NO:1340	'46880.1_gaiger.ABI'_1	frame 2	from 36 to 95
SEQ ID NO:1341	'46880.1_gaiger.ABI'_2	frame 3	from 1 to 95
SEQ ID NO:1342	'46880.1_gaiger.ABI'_3	frame -1	from 32 to 81
SEQ ID NO:1343	'47011.1_gaiger.ABI'_1	frame 1	from 1 to 102
SEQ ID NO:1344	'47011.1_gaiger.ABI'_2	frame 3	from 42 to 101
SEQ ID NO:1345	'47011.1_gaiger.ABI'_3	frame -1	from 32 to 81
SEQ ID NO:1346	'51658.1_gaiger.ABI'_1	frame 2	from 5 to 80
SEQ ID NO:1347	'51658.1_gaiger.ABI'_2	frame 3	from 10 to 77
SEQ ID NO:1348	'51734.1_gaiger.ABI'_1	frame 1	from 12 to 98
SEQ ID NO:1349	'51734.1_gaiger.ABI'_2	frame 3	from 22 to 76
SEQ ID NO:1350	'51734.1_gaiger.ABI'_3	frame -2	from 18 to 137
SEQ ID NO:1351	'51735.1_gaiger.ABI'_1	frame 1	from 30 to 153
SEQ ID NO:1352	'51735.1_gaiger.ABI'_2	frame 3	from 1 to 69
SEQ ID NO:1353	'51735.1_gaiger.ABI'_3	frame -2	from 44 to 123
SEQ ID NO:1354	'51788.1_gaiger.ABI'_1	frame 1	from 1 to 59
SEQ ID NO:1355	'51788.1_gaiger.ABI'_2	frame -2	from 1 to 68
SEQ ID NO:1356	'51892.1_gaiger.ABI'_1	frame 1	from 1 to 158
SEQ ID NO:1357	'51892.1_gaiger.ABI'_2	frame 2	from 2 to 69
SEQ ID NO:1358	'51892.1_gaiger.ABI'_3	frame -1	from 76 to 139
SEQ ID NO:1359	'51892.1_gaiger.ABI'_4	frame -2	from 35 to 137
SEQ ID NO:1360	'51900.1_gaiger.ABI'_1	frame 2	from 1 to 123
SEQ ID NO:1361	'51900.1_gaiger.ABI'_2	frame 3	from 3 to 70
SEQ ID NO:1362	'51900.1_gaiger.ABI'_3	frame -2	from 78 to 141

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:1363	'51900.1_gaiger.ABI'_4	frame -3	from 36 to 139
SEQ ID NO:1364	1404:D07_1	frame 1	from 3 to 150
SEQ ID NO:1365	1404:D07_2	frame 2	from 8 to 75
SEQ ID NO:1366	1404:D07_3	frame -1	from 13 to 115
SEQ ID NO:1367	1404:D07_4	frame -3	from 53 to 116
SEQ ID NO:1368	1405:C04_1	frame 2	from 1 to 50
SEQ ID NO:1369	1405:C04_2	frame 3	from 10 to 102
SEQ ID NO:1370	1405:C04_3	frame -2	from 76 to 140
SEQ ID NO:1371	1405:D12_1	frame 1	from 4 to 71
SEQ ID NO:1372	1405:D12_2	frame 3	from 1 to 143
SEQ ID NO:1373	1405:D12_3	frame -1	from 52 to 115
SEQ ID NO:1374	1405:D12_4	frame -2	from 11 to 113
SEQ ID NO:1375	1405:E11_1	frame 1	from 87 to 159
SEQ ID NO:1376	1405:E11_2	frame 3	from 92 to 143
SEQ ID NO:1377	1405:E11_3	frame -2	from 48 to 111
SEQ ID NO:1378	1405:E11_4	frame -3	from 1 to 55
SEQ ID NO:1379	'52333.1_gaiger.ABI'_1	frame 1	from 1 to 69
SEQ ID NO:1380	'52333.1_gaiger.ABI'_2	frame 2	from 1 to 66
SEQ ID NO:1381	'41557.1_gaiger.ABI'_1	frame 1	from 16 to 73
SEQ ID NO:1382	'41557.1_gaiger.ABI'_2	frame 2	from 1 to 109
SEQ ID NO:1383	'41557.1_gaiger.ABI'_3	frame -1	from 11 to 110
SEQ ID NO:1384	'41557.1_gaiger.ABI'_4	frame -3	from 1 to 103
SEQ ID NO:1385	'41579.1_gaiger.ABI'_1	frame 3	from 43 to 97
SEQ ID NO:1386	'41579.1_gaiger.ABI'_2	frame -2	from 1 to 97
SEQ ID NO:1387	'41579.1_gaiger.ABI'_3	frame -3	from 43 to 97
SEQ ID NO:1388	'41571.1_gaiger.ABI'_1	frame 3	from 1 to 89
SEQ ID NO:1389	'41571.1_gaiger.ABI'_2	frame -1	from 1 to 89
SEQ ID NO:1390	'41571.1_gaiger.ABI'_3	frame -2	from 27 to 85
SEQ ID NO:1391	'41613.1_gaiger.ABI'_1	frame 3	from 1 to 136
SEQ ID NO:1392	'41613.1_gaiger.ABI'_2	frame -1	from 40 to 163
SEQ ID NO:1393	'41613.1_gaiger.ABI'_3	frame -2	from 49 to 100
SEQ ID NO:1394	'41613.1_gaiger.ABI'_4	frame -3	from 3 to 61
SEQ ID NO:1395	'41650.1_gaiger.ABI'_1	frame 1	from 22 to 109
SEQ ID NO:1396	'41650.1_gaiger.ABI'_2	frame 2	from 1 to 157
SEQ ID NO:1397	'41650.1_gaiger.ABI'_3	frame 3	from 1 to 156
SEQ ID NO:1398	'41650.1_gaiger.ABI'_4	frame -1	from 25 to 99
SEQ ID NO:1399	'41650.1_gaiger.ABI'_5	frame -2	from 47 to 157
SEQ ID NO:1400	'41650.1_gaiger.ABI'_6	frame -3	from 53 to 156

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:1401	'41663.1_gaiger.ABI'_1	frame -2	from 64 to 116
SEQ ID NO:1402	'41663.1_gaiger.ABI'_2	frame -3	from 1 to 67
SEQ ID NO:1403	'41687.1_gaiger.ABI'_1	frame 1	from 35 to 154
SEQ ID NO:1404	'41687.1_gaiger.ABI'_2	frame 2	from 102 to 153
SEQ ID NO:1405	'41687.1_gaiger.ABI'_3	frame -1	from 50 to 109
SEQ ID NO:1406	'41687.1_gaiger.ABI'_4	frame -3	from 102 to 153
SEQ ID NO:1407	'41717.1_gaiger.ABI'_1	frame 1	from 55 to 129
SEQ ID NO:1408	'41717.1_gaiger.ABI'_2	frame 2	from 1 to 63
SEQ ID NO:1409	'41717.1_gaiger.ABI'_3	frame -3	from 1 to 68
SEQ ID NO:1410	'41751.1_gaiger.ABI'_1	frame 1	from 27 to 82
SEQ ID NO:1411	'41751.1_gaiger.ABI'_2	frame 3	from 1 to 50
SEQ ID NO:1412	'41751.1_gaiger.ABI'_3	frame -2	from 1 to 70
SEQ ID NO:1413	'41751.1_gaiger.ABI'_4	frame -3	from 1 to 53
SEQ ID NO:1414	'41818.1_gaiger.ABI'_1	frame 2	from 1 to 69
SEQ ID NO:1415	'41818.1_gaiger.ABI'_2	frame -1	from 30 to 93
SEQ ID NO:1416	'41818.1_gaiger.ABI'_3	frame -3	from 1 to 92
SEQ ID NO:1417	'41828.1_gaiger.ABI'_1	frame -3	from 1 to 77
SEQ ID NO:1418	'41849.1_gaiger.ABI'_1	frame 1	from 1 to 75
SEQ ID NO:1419	'41849.1_gaiger.ABI'_2	frame 3	from 4 to 77
SEQ ID NO:1420	'41849.1_gaiger.ABI'_3	frame -1	from 12 to 77
SEQ ID NO:1421	'41881.1_gaiger.ABI'_1	frame -1	from 1 to 127
SEQ ID NO:1422	'41881.1_gaiger.ABI'_2	frame -2	from 73 to 126
SEQ ID NO:1423	'41881.1_gaiger.ABI'_3	frame -3	from 1 to 76
SEQ ID NO:1424	'41912.1_gaiger.ABI'_1	frame 2	from 1 to 138
SEQ ID NO:1425	'41912.1_gaiger.ABI'_2	frame -2	from 34 to 93
SEQ ID NO:1426	'41912.1_gaiger.ABI'_3	frame -3	from 60 to 125
SEQ ID NO:1427	'41927.1_gaiger.ABI'_1	frame 3	from 20 to 74
SEQ ID NO:1428	'41929.1_gaiger.ABI'_1	frame 1	from 1 to 52
SEQ ID NO:1429	'41944.1_gaiger.ABI'_1	frame 1	from 1 to 56
SEQ ID NO:1430	'41944.1_gaiger.ABI'_2	frame 2	from 1 to 177
SEQ ID NO:1431	'41944.1_gaiger.ABI'_3	frame 3	from 37 to 92
SEQ ID NO:1432	'41944.1_gaiger.ABI'_4	frame -1	from 47 to 116
SEQ ID NO:1433	'41944.1_gaiger.ABI'_5	frame -1	from 125 to 177
SEQ ID NO:1434	'41944.1_gaiger.ABI'_6	frame -2	from 32 to 177
SEQ ID NO:1435	'41944.1_gaiger.ABI'_7	frame -3	from 120 to 177
SEQ ID NO:1436	'41987.1_gaiger.ABI'_1	frame 1	from 48 to 116
SEQ ID NO:1437	'41987.1_gaiger.ABI'_2	frame 2	from 1 to 50
SEQ ID NO:1438	'41987.1_gaiger.ABI'_3	frame 2	from 96 to 154
SEQ ID NO:1439	'41987.1_gaiger.ABI'_4	frame 3	from 53 to 120

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:1440	'41987.1_gaiger.ABI'_5	frame 3	from 122 to 175
SEQ ID NO:1441	'41987.1_gaiger.ABI'_6	frame -1	from 37 to 136
SEQ ID NO:1442	'41987.1_gaiger.ABI'_7	frame -2	from 1 to 72
SEQ ID NO:1443	'41995.1_gaiger.ABI'_1	frame 1	from 1 to 115
SEQ ID NO:1444	'41995.1_gaiger.ABI'_2	frame 3	from 60 to 109
SEQ ID NO:1445	'41995.1_gaiger.ABI'_3	frame -2	from 1 to 114
SEQ ID NO:1446	'41995.1_gaiger.ABI'_4	frame -3	from 35 to 108
SEQ ID NO:1447	'42012.1_gaiger.ABI'_1	frame 2	from 1 to 60
SEQ ID NO:1448	'42012.1_gaiger.ABI'_2	frame -3	from 1 to 60
SEQ ID NO:1449	'42039.1_gaiger.ABI'_1	frame 2	from 70 to 127
SEQ ID NO:1450	'42039.1_gaiger.ABI'_2	frame 3	from 1 to 146
SEQ ID NO:1451	'42039.1_gaiger.ABI'_3	frame -2	from 39 to 100
SEQ ID NO:1452	'42097.1_gaiger.ABI'_1	frame 1	from 24 to 132
SEQ ID NO:1453	'42097.1_gaiger.ABI'_2	frame -1	from 52 to 132
SEQ ID NO:1454	'42097.1_gaiger.ABI'_3	frame -3	from 34 to 92
SEQ ID NO:1455	'42103.1_gaiger.ABI'_1	frame 1	from 1 to 153
SEQ ID NO:1456	'42103.1_gaiger.ABI'_2	frame 2	from 24 to 83
SEQ ID NO:1457	'42103.1_gaiger.ABI'_3	frame 2	from 85 to 182
SEQ ID NO:1458	'42103.1_gaiger.ABI'_4	frame -2	from 27 to 99
SEQ ID NO:1459	'42103.1_gaiger.ABI'_5	frame -2	from 113 to 174
SEQ ID NO:1460	'42103.1_gaiger.ABI'_6	frame -3	from 38 to 126
SEQ ID NO:1461	'42108.1_gaiger.ABI'_1	frame -2	from 4 to 77
SEQ ID NO:1462	R0233:A06_1	frame 1	from 12 to 77
SEQ ID NO:1463	R0233:A06_2	frame 3	from 2 to 76
SEQ ID NO:1464	R0233:A06_3	frame -3	from 1 to 59
SEQ ID NO:1465	R0233:A08_1	frame 1	from 1 to 59
SEQ ID NO:1466	R0233:A08_2	frame -1	from 1 to 63
SEQ ID NO:1467	R0233:C02_1	frame 3	from 26 to 90
SEQ ID NO:1468	R0233:C02_2	frame -2	from 1 to 107
SEQ ID NO:1469	R0233:C02_3	frame -3	from 1 to 74
SEQ ID NO:1470	R0233:E06_1	frame 1	from 84 to 146
SEQ ID NO:1471	R0233:E06_2	frame 3	from 1 to 181
SEQ ID NO:1472	R0233:E06_3	frame -2	from 49 to 157
SEQ ID NO:1473	R0233:F08_1	frame 1	from 11 to 110
SEQ ID NO:1474	R0233:F08_2	frame 3	from 1 to 103
SEQ ID NO:1475	R0233:F08_3	frame -1	from 16 to 73
SEQ ID NO:1476	R0233:F08_4	frame -2	from 1 to 109
SEQ ID NO:1477	'42324.1_gaiger.ABI'_1	frame 1	from 1 to 94

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:1478	'42324.1_gaiger.ABI'_2	frame 2	from 1 to 57
SEQ ID NO:1479	'42324.1_gaiger.ABI'_3	frame 3	from 38 to 130
SEQ ID NO:1480	'42324.1_gaiger.ABI'_4	frame -1	from 10 to 130
SEQ ID NO:1481	'42324.1_gaiger.ABI'_5	frame -2	from 1 to 54
SEQ ID NO:1482	'42324.1_gaiger.ABI'_6	frame -2	from 72 to 130
SEQ ID NO:1483	'42324.1_gaiger.ABI'_7	frame -3	from 1 to 67
SEQ ID NO:1484	'42324.1_gaiger.ABI'_8	frame -3	from 76 to 130
SEQ ID NO:1485	'42469.1_gaiger.ABI'_1	frame 3	from 11 to 90
SEQ ID NO:1486	'42514.1_gaiger.ABI'_1	frame 2	from 14 to 89
SEQ ID NO:1487	'42514.1_gaiger.ABI'_2	frame -2	from 10 to 76
SEQ ID NO:1488	'42554.1_gaiger.ABI'_1	frame 1	from 1 to 67
SEQ ID NO:1489	'42554.1_gaiger.ABI'_2	frame 2	from 6 to 63
SEQ ID NO:1490	'42554.1_gaiger.ABI'_3	frame -1	from 7 to 67
SEQ ID NO:1491	'42554.1_gaiger.ABI'_4	frame -2	from 1 to 56
SEQ ID NO:1492	'42560.1_gaiger.ABI'_1	frame 1	from 1 to 67
SEQ ID NO:1493	'42560.1_gaiger.ABI'_2	frame -3	from 1 to 66
SEQ ID NO:1494	'42588.1_gaiger.ABI'_1	frame 1	from 1 to 60
SEQ ID NO:1495	'42588.1_gaiger.ABI'_2	frame 2	from 1 to 60
SEQ ID NO:1496	'42588.1_gaiger.ABI'_3	frame 3	from 1 to 60
SEQ ID NO:1497	'42588.1_gaiger.ABI'_4	frame -1	from 1 to 60
SEQ ID NO:1498	'42588.1_gaiger.ABI'_5	frame -2	from 1 to 53
SEQ ID NO:1499	'42609.1_gaiger.ABI'_1	frame 1	from 1 to 51
SEQ ID NO:1500	'42609.1_gaiger.ABI'_2	frame 2	from 1 to 79
SEQ ID NO:1501	'42609.1_gaiger.ABI'_3	frame -1	from 10 to 80
SEQ ID NO:1502	'42609.1_gaiger.ABI'_4	frame -3	from 2 to 68
SEQ ID NO:1503	'42703.1_gaiger.ABI'_1	frame 2	from 25 to 95
SEQ ID NO:1504	'42703.1_gaiger.ABI'_2	frame -2	from 10 to 82
SEQ ID NO:1505	R0234:E06_1	frame 3	from 4 to 77
SEQ ID NO:1506	R0234:E06_2	frame -1	from 1 to 66
SEQ ID NO:1507	R0235:A09_1	frame 3	from 1 to 98
SEQ ID NO:1508	R0235:A09_2	frame -1	from 15 to 76
SEQ ID NO:1509	R0235:A09_3	frame -2	from 2 to 98
SEQ ID NO:1510	R0235:A09_4	frame -3	from 1 to 54
SEQ ID NO:1511	R0235:D01_1	frame 1	from 1 to 137
SEQ ID NO:1512	R0235:D01_2	frame 3	from 1 to 67
SEQ ID NO:1513	R0235:D01_3	frame -1	from 1 to 137
SEQ ID NO:1514	R0235:D01_4	frame -2	from 1 to 61
SEQ ID NO:1515	R0236:D04_1	frame 1	from 1 to 87
SEQ ID NO:1516	R0236:D04_2	frame 2	from 1 to 113

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:1517	R0236:D04_3	frame -1	from 1 to 79
SEQ ID NO:1518	R0236:F10_1	frame 1	from 1 to 51
SEQ ID NO:1519	R0236:F10_2	frame 2	from 1 to 79
SEQ ID NO:1520	R0236:F10_3	frame -1	from 10 to 80
SEQ ID NO:1521	R0236:F10_4	frame -3	from 1 to 68
SEQ ID NO:1522	R0236:G10_1	frame 2	from 1 to 117
SEQ ID NO:1523	R0236:G10_2	frame -3	from 42 to 109
SEQ ID NO:1524	R0236:G08_1	frame 2	from 1 to 88
SEQ ID NO:1525	R0236:G08_2	frame 3	from 34 to 88
SEQ ID NO:1526	R0249:D01_1	frame 1	from 25 to 76
SEQ ID NO:1527	R0249:D01_2	frame 2	from 1 to 75
SEQ ID NO:1528	R0249:D01_3	frame -1	from 1 to 76
SEQ ID NO:1529	R0249:D01_4	frame -2	from 1 to 52
SEQ ID NO:1530	R0249:G04_1	frame 1	from 1 to 96
SEQ ID NO:1531	R0249:G04_2	frame 2	from 30 to 83
SEQ ID NO:1532	R0249:G04_3	frame 3	from 13 to 71
SEQ ID NO:1533	R0249:G04_4	frame 3	from 120 to 174
SEQ ID NO:1534	R0249:G04_5	frame -3	from 1 to 66
SEQ ID NO:1535	R0250:A10_1	frame 1	from 127 to 180
SEQ ID NO:1536	R0250:A10_2	frame -1	from 1 to 55
SEQ ID NO:1537	R0250:A10_3	frame -2	from 20 to 80
SEQ ID NO:1538	R0250:A10_4	frame -3	from 1 to 96
SEQ ID NO:1539	R0250:E12_1	frame 1	from 1 to 115
SEQ ID NO:1540	R0250:E12_2	frame 3	from 60 to 109
SEQ ID NO:1541	R0250:E12_3	frame -2	from 1 to 114
SEQ ID NO:1542	R0250:E12_4	frame -3	from 35 to 108
SEQ ID NO:1543	R0250:F12_1	frame 1	from 1 to 55
SEQ ID NO:1544	R0250:F12_2	frame 2	from 20 to 80
SEQ ID NO:1545	R0250:F12_3	frame 3	from 1 to 96
SEQ ID NO:1546	R0250:F12_4	frame -1	from 127 to 180
SEQ ID NO:1547	R0251:B08_1	frame 1	from 121 to 172
SEQ ID NO:1548	R0251:B08_2	frame -2	from 61 to 122
SEQ ID NO:1549	R0251:B08_3	frame -3	from 9 to 70
SEQ ID NO:1550	R0251:B08_4	frame -3	from 72 to 133
SEQ ID NO:1551	R0252:A08_1	frame 1	from 1 to 64
SEQ ID NO:1552	R0252:A08_2	frame 2	from 12 to 64
SEQ ID NO:1553	R0252:A08_3	frame -1	from 1 to 51
SEQ ID NO:1554	R0252:A08_4	frame -2	from 1 to 64
SEQ ID NO:1555	R0252:F11_1	frame 1	from 1 to 94

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:1556	R0252:F11_2	frame 3	from 1 to 61
SEQ ID NO:1557	R0252:F11_3	frame -2	from 12 to 69
SEQ ID NO:1558	R0252:F11_4	frame -3	from 1 to 139
SEQ ID NO:1559	R0252:F02_1	frame 1	from 1 to 66
SEQ ID NO:1560	R0252:F02_2	frame 2	from 57 to 107
SEQ ID NO:1561	R0252:F02_3	frame 2	from 109 to 160
SEQ ID NO:1562	R0252:F02_4	frame 3	from 35 to 159
SEQ ID NO:1563	R0252:F02_5	frame -1	from 27 to 115
SEQ ID NO:1564	R0252:F02_6	frame -3	from 4 to 65
SEQ ID NO:1565	R0252:F02_7	frame -3	from 96 to 159
SEQ ID NO:1566	R0252:G11_1	frame 1	from 1 to 131
SEQ ID NO:1567	R0252:G11_2	frame 2	from 51 to 105
SEQ ID NO:1568	R0252:G11_3	frame -1	from 13 to 131
SEQ ID NO:1569	R0252:G11_4	frame -2	from 61 to 113
SEQ ID NO:1570	R0253:E10_1	frame 2	from 46 to 118
SEQ ID NO:1571	R0253:E10_2	frame -1	from 84 to 139
SEQ ID NO:1572	R0253:G11_1	frame 2	from 1 to 194
SEQ ID NO:1573	R0253:G11_2	frame 3	from 102 to 153
SEQ ID NO:1574	R0253:G11_3	frame -1	from 1 to 55
SEQ ID NO:1575	R0253:G11_4	frame -1	from 117 to 182
SEQ ID NO:1576	R0253:G11_5	frame -3	from 30 to 88
SEQ ID NO:1577	R0253:G11_6	frame -3	from 90 to 149
SEQ ID NO:1578	R0254:A08_1	frame 3	from 1 to 85
SEQ ID NO:1579	R0254:A08_2	frame -1	from 47 to 98
SEQ ID NO:1580	R0254:E04_1	frame 2	from 12 to 65
SEQ ID NO:1581	R0254:E04_2	frame 3	from 49 to 135
SEQ ID NO:1582	R0254:F07_1	frame 1	from 69 to 153
SEQ ID NO:1583	R0254:F07_2	frame -1	from 87 to 142
SEQ ID NO:1584	R0254:F07_3	frame -2	from 47 to 116
SEQ ID NO:1585	R0254:F07_4	frame -3	from 1 to 82
SEQ ID NO:1586	R0254:F07_5	frame -3	from 99 to 154
SEQ ID NO:1587	R0237:F12_1	frame 2	from 64 to 115
SEQ ID NO:1588	R0237:F12_2	frame 3	from 1 to 99
SEQ ID NO:1589	R0237:F12_3	frame -1	from 1 to 145
SEQ ID NO:1590	R0237:F12_4	frame -2	from 19 to 134
SEQ ID NO:1591	R0238:B02_1	frame 3	from 50 to 111
SEQ ID NO:1592	R0238:B02_2	frame -2	from 102 to 187
SEQ ID NO:1593	R0239:H02_1	frame 3	from 1 to 97
SEQ ID NO:1594	R0255:F12_1	frame 3	from 1 to 57

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:1595	R0255:F12_2	frame -2	from 1 to 78
SEQ ID NO:1596	R0258:B10_1	frame 2	from 1 to 130
SEQ ID NO:1597	R0258:B10_2	frame 3	from 1 to 73
SEQ ID NO:1598	R0258:B10_3	frame -2	from 86 to 142
SEQ ID NO:1599	R0258:B10_4	frame -3	from 1 to 69
SEQ ID NO:1600	R0259:C06_1	frame -1	from 36 to 100
SEQ ID NO:1601	R0259:C06_2	frame -2	from 124 to 187
SEQ ID NO:1602	R0261:A09_1	frame 1	from 1 to 174
SEQ ID NO:1603	R0261:A09_2	frame 2	from 34 to 89
SEQ ID NO:1604	R0261:A09_3	frame 3	from 1 to 52
SEQ ID NO:1605	R0261:A09_4	frame -1	from 121 to 174
SEQ ID NO:1606	R0261:A09_5	frame -2	from 47 to 116
SEQ ID NO:1607	R0261:A09_6	frame -2	from 125 to 174
SEQ ID NO:1608	R0261:A09_7	frame -3	from 32 to 174
SEQ ID NO:1609	R0261:B10_1	frame 1	from 1 to 79
SEQ ID NO:1610	R0261:B10_2	frame -1	from 1 to 87
SEQ ID NO:1611	R0261:B10_3	frame -2	from 1 to 113
SEQ ID NO:1612	R0261:C10_1	frame 2	from 6 to 120
SEQ ID NO:1613	R0261:C10_2	frame 3	from 103 to 157
SEQ ID NO:1614	R0261:C10_3	frame -1	from 25 to 75
SEQ ID NO:1615	R0261:D03_1	frame 1	from 44 to 179
SEQ ID NO:1616	R0261:D03_2	frame 2	from 12 to 90
SEQ ID NO:1617	R0261:D03_3	frame 2	from 92 to 164
SEQ ID NO:1618	R0261:D03_4	frame 3	from 40 to 96
SEQ ID NO:1619	R0261:D03_5	frame 3	from 98 to 186
SEQ ID NO:1620	R0261:D03_6	frame -1	from 37 to 160
SEQ ID NO:1621	R0261:D03_7	frame -2	from 22 to 144
SEQ ID NO:1622	R0261:D06_1	frame 2	from 1 to 117
SEQ ID NO:1623	R0261:D06_2	frame -2	from 1 to 117
SEQ ID NO:1624	R0261:D06_3	frame -3	from 35 to 117
SEQ ID NO:1625	R0261:E10_1	frame 1	from 1 to 67
SEQ ID NO:1626	R0261:F10_1	frame 1	from 103 to 154
SEQ ID NO:1627	R0261:F10_2	frame 2	from 5 to 106
SEQ ID NO:1628	R0261:F10_3	frame 3	from 24 to 109
SEQ ID NO:1629	R0261:F10_4	frame -1	from 93 to 154
SEQ ID NO:1630	R0261:G04_1	frame 2	from 13 to 111
SEQ ID NO:1631	R0261:G04_2	frame 3	from 91 to 147
SEQ ID NO:1632	R0261:G04_3	frame -1	from 83 to 169
SEQ ID NO:1633	R0261:G04_4	frame -2	from 4 to 56

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:1634	R0261:G04_5	frame -3	from 123 to 181
SEQ ID NO:1635	R0262:A12_1	frame -1	from 35 to 132
SEQ ID NO:1636	R0262:A03_1	frame 2	from 1 to 66
SEQ ID NO:1637	R0262:A03_2	frame -1	from 1 to 84
SEQ ID NO:1638	R0262:A03_3	frame -3	from 1 to 64
SEQ ID NO:1639	R0262:B09_1	frame 1	from 1 to 59
SEQ ID NO:1640	R0262:B09_2	frame 2	from 57 to 107
SEQ ID NO:1641	R0262:B09_3	frame 2	from 109 to 190
SEQ ID NO:1642	R0262:B09_4	frame 3	from 35 to 189
SEQ ID NO:1643	R0262:B09_5	frame -1	from 1 to 55
SEQ ID NO:1644	R0262:B09_6	frame -1	from 57 to 145
SEQ ID NO:1645	R0262:B09_7	frame -3	from 34 to 95
SEQ ID NO:1646	R0262:B09_8	frame -3	from 126 to 189
SEQ ID NO:1647	R0262:C04_1	frame 1	from 18 to 75
SEQ ID NO:1648	R0262:C04_2	frame 2	from 7 to 77
SEQ ID NO:1649	R0262:C04_3	frame -2	from 67 to 139
SEQ ID NO:1650	R0262:C04_4	frame -3	from 1 to 88
SEQ ID NO:1651	R0262:D11_1	frame 1	from 22 to 90
SEQ ID NO:1652	R0262:D11_2	frame 2	from 1 to 57
SEQ ID NO:1653	R0262:D11_3	frame 2	from 59 to 124
SEQ ID NO:1654	R0262:D11_4	frame -2	from 1 to 67
SEQ ID NO:1655	R0262:D11_5	frame -3	from 26 to 124
SEQ ID NO:1656	R0262:D12_1	frame 2	from 4 to 118
SEQ ID NO:1657	R0262:D04_1	frame 1	from 26 to 95
SEQ ID NO:1658	R0262:D04_2	frame 3	from 32 to 94
SEQ ID NO:1659	R0262:D04_3	frame -2	from 16 to 65
SEQ ID NO:1660	R0262:D04_4	frame -3	from 1 to 92
SEQ ID NO:1661	R0262:D07_1	frame 1	from 102 to 156
SEQ ID NO:1662	R0262:D07_2	frame 3	from 4 to 118
SEQ ID NO:1663	R0262:D07_3	frame -1	from 20 to 70
SEQ ID NO:1664	R0262:E02_1	frame 1	from 7 to 121
SEQ ID NO:1665	R0262:E02_2	frame 2	from 104 to 158
SEQ ID NO:1666	R0262:E02_3	frame -2	from 27 to 77
SEQ ID NO:1667	R0262:G05_1	frame 3	from 50 to 111
SEQ ID NO:1668	R0262:G05_2	frame -1	from 49 to 134
SEQ ID NO:1669	R0263:B10_1	frame 2	from 46 to 115
SEQ ID NO:1670	R0263:B10_2	frame -2	from 12 to 61
SEQ ID NO:1671	R0263:B06_1	frame 3	from 1 to 115
SEQ ID NO:1672	R0263:B06_2	frame -1	from 52 to 116

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:1673	R0263:B06_3	frame -2	from 2 to 78
SEQ ID NO:1674	R0263:B06_4	frame -3	from 15 to 87
SEQ ID NO:1675	R0263:B09_1	frame 2	from 1 to 199
SEQ ID NO:1676	R0263:B09_2	frame -1	from 1 to 76
SEQ ID NO:1677	R0263:B09_3	frame -1	from 78 to 199
SEQ ID NO:1678	R0263:B09_4	frame -2	from 140 to 195
SEQ ID NO:1679	R0263:D11_1	frame 1	from 12 to 98
SEQ ID NO:1680	R0263:D11_2	frame 3	from 22 to 76
SEQ ID NO:1681	R0263:D11_3	frame -2	from 4 to 126
SEQ ID NO:1682	R0263:D07_1	frame 1	from 1 to 191
SEQ ID NO:1683	R0263:D07_2	frame -1	from 1 to 51
SEQ ID NO:1684	R0263:D07_3	frame -1	from 91 to 141
SEQ ID NO:1685	R0263:D07_4	frame -2	from 98 to 152
SEQ ID NO:1686	R0263:E03_1	frame 3	from 50 to 111
SEQ ID NO:1687	R0263:E03_2	frame -1	from 119 to 204
SEQ ID NO:1688	R0263:F08_1	frame 3	from 1 to 95
SEQ ID NO:1689	R0263:G03_1	frame 1	from 90 to 139
SEQ ID NO:1690	R0263:G03_2	frame 2	from 13 to 106
SEQ ID NO:1691	R0263:G03_3	frame -1	from 3 to 55
SEQ ID NO:1692	R0263:G03_4	frame -2	from 122 to 180
SEQ ID NO:1693	R0263:G03_5	frame -3	from 77 to 167
SEQ ID NO:1694	R0263:H10_1	frame 1	from 1 to 55
SEQ ID NO:1695	R0263:H10_2	frame 1	from 99 to 152
SEQ ID NO:1696	R0263:H10_3	frame 3	from 1 to 147
SEQ ID NO:1697	R0263:H10_4	frame -1	from 6 to 140
SEQ ID NO:1698	R0263:H10_5	frame -3	from 1 to 151
SEQ ID NO:1699	R0263:H02_1	frame 1	from 4 to 63
SEQ ID NO:1700	R0263:H02_2	frame 1	from 65 to 121
SEQ ID NO:1701	R0263:H02_3	frame 2	from 1 to 50
SEQ ID NO:1702	R0263:H02_4	frame 2	from 52 to 104
SEQ ID NO:1703	R0263:H02_5	frame -1	from 13 to 77
SEQ ID NO:1704	R0263:H02_6	frame -1	from 98 to 161
SEQ ID NO:1705	R0263:H02_7	frame -2	from 3 to 54
SEQ ID NO:1706	R0263:H02_8	frame -2	from 56 to 122
SEQ ID NO:1707	R0264:B11_1	frame 2	from 6 to 120
SEQ ID NO:1708	R0264:B11_2	frame 3	from 103 to 157
SEQ ID NO:1709	R0264:B11_3	frame -1	from 30 to 80
SEQ ID NO:1710	R0264:D03_1	frame 1	from 100 to 157
SEQ ID NO:1711	R0264:D03_2	frame 3	from 16 to 91

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:1712	R0264:D03_3	frame 3	from 94 to 156
SEQ ID NO:1713	R0264:D03_4	frame -2	from 1 to 156
SEQ ID NO:1714	R0264:E12_1	frame 3	from 50 to 111
SEQ ID NO:1715	R0264:E12_2	frame -1	from 78 to 163
SEQ ID NO:1716	R0264:F11_1	frame 1	from 13 to 81
SEQ ID NO:1717	R0264:F11_2	frame -1	from 1 to 102
SEQ ID NO:1718	R0264:F11_3	frame -2	from 25 to 101
SEQ ID NO:1719	R0264:F11_4	frame -3	from 42 to 101
SEQ ID NO:1720	R0264:F09_1	frame 1	from 7 to 121
SEQ ID NO:1721	R0264:F09_2	frame 2	from 104 to 158
SEQ ID NO:1722	R0264:F09_3	frame -3	from 25 to 75
SEQ ID NO:1723	R0264:G03_1	frame 1	from 1 to 62
SEQ ID NO:1724	R0264:G03_2	frame -1	from 1 to 62
SEQ ID NO:1725	R0264:G03_3	frame -2	from 2 to 61
SEQ ID NO:1726	R0264:G04_1	frame 2	from 6 to 93
SEQ ID NO:1727	R0264:G06_1	frame 1	from 50 to 106
SEQ ID NO:1728	R0264:G09_1	frame 2	from 46 to 110
SEQ ID NO:1729	R0264:G09_2	frame -2	from 1 to 56
SEQ ID NO:1730	R0264:H04_1	frame 1	from 58 to 130
SEQ ID NO:1731	R0264:H04_2	frame 3	from 78 to 129
SEQ ID NO:1732	R0264:H04_3	frame -1	from 67 to 130
SEQ ID NO:1733	R0264:H04_4	frame -3	from 44 to 95
SEQ ID NO:1734	R0265:A09_1	frame 1	from 1 to 59
SEQ ID NO:1735	R0265:A09_2	frame 2	from 54 to 107
SEQ ID NO:1736	R0265:A09_3	frame 3	from 35 to 153
SEQ ID NO:1737	R0265:A09_4	frame -2	from 1 to 59
SEQ ID NO:1738	R0265:A09_5	frame -2	from 90 to 153
SEQ ID NO:1739	R0265:A09_6	frame -3	from 20 to 108
SEQ ID NO:1740	R0265:D10_1	frame 1	from 118 to 175
SEQ ID NO:1741	R0265:D10_2	frame 3	from 7 to 100
SEQ ID NO:1742	R0265:D10_3	frame -2	from 77 to 169
SEQ ID NO:1743	R0265:D07_1	frame 3	from 50 to 111
SEQ ID NO:1744	R0265:D07_2	frame -1	from 70 to 185
SEQ ID NO:1745	R0265:E12_1	frame 1	from 1 to 87
SEQ ID NO:1746	R0265:E12_2	frame 2	from 1 to 113
SEQ ID NO:1747	R0265:E12_3	frame -1	from 1 to 79
SEQ ID NO:1748	R0265:F12_1	frame 1	from 75 to 126
SEQ ID NO:1749	R0265:F12_2	frame 2	from 46 to 160
SEQ ID NO:1750	R0265:F12_3	frame -1	from 36 to 87

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:1751	R0265:F12_4	frame -3	from 78 to 133
SEQ ID NO:1752	R0265:H04_1	frame 2	from 64 to 149
SEQ ID NO:1753	R0265:H04_2	frame -3	from 50 to 111
SEQ ID NO:1754	R0265:H09_1	frame 1	from 1 to 191
SEQ ID NO:1755	R0265:H09_2	frame -1	from 1 to 51
SEQ ID NO:1756	R0265:H09_3	frame -1	from 91 to 141
SEQ ID NO:1757	R0265:H09_4	frame -2	from 98 to 152
SEQ ID NO:1758	R0266:A10_1	frame 1	from 1 to 87
SEQ ID NO:1759	R0266:A10_2	frame 2	from 1 to 113
SEQ ID NO:1760	R0266:A10_3	frame -1	from 1 to 79
SEQ ID NO:1761	R0266:A12_1	frame 1	from 1 to 106
SEQ ID NO:1762	R0266:A12_2	frame 1	from 133 to 185
SEQ ID NO:1763	R0266:A12_3	frame 2	from 89 to 143
SEQ ID NO:1764	R0266:A12_4	frame 2	from 147 to 197
SEQ ID NO:1765	R0266:A12_5	frame -3	from 51 to 101
SEQ ID NO:1766	R0266:B02_1	frame 1	from 68 to 168
SEQ ID NO:1767	R0266:B02_2	frame 2	from 44 to 167
SEQ ID NO:1768	R0266:B02_3	frame -1	from 1 to 100
SEQ ID NO:1769	R0266:C12_1	frame 1	from 7 to 121
SEQ ID NO:1770	R0266:C12_2	frame 1	from 148 to 200
SEQ ID NO:1771	R0266:C12_3	frame 2	from 104 to 158
SEQ ID NO:1772	R0266:C12_4	frame -3	from 41 to 93
SEQ ID NO:1773	R0266:E08_1	frame 1	from 1 to 54
SEQ ID NO:1774	R0266:E08_2	frame 3	from 1 to 63
SEQ ID NO:1775	R0266:E08_3	frame 3	from 128 to 195
SEQ ID NO:1776	R0266:E08_4	frame -1	from 51 to 122
SEQ ID NO:1777	R0266:E08_5	frame -1	from 124 to 175
SEQ ID NO:1778	R0266:E08_6	frame -3	from 9 to 68
SEQ ID NO:1779	R0266:E08_7	frame -3	from 83 to 134
SEQ ID NO:1780	R0266:F03_1	frame 1	from 64 to 141
SEQ ID NO:1781	R0266:F03_2	frame 2	from 8 to 141
SEQ ID NO:1782	R0266:F03_3	frame 3	from 39 to 104
SEQ ID NO:1783	R0266:F03_4	frame -2	from 1 to 141
SEQ ID NO:1784	R0266:F06_1	frame 1	from 23 to 75
SEQ ID NO:1785	R0266:F06_2	frame 3	from 150 to 200
SEQ ID NO:1786	R0266:F06_3	frame -1	from 109 to 175
SEQ ID NO:1787	R0266:F06_4	frame -2	from 143 to 200
SEQ ID NO:1788	R0266:F07_1	frame -3	from 37 to 97
SEQ ID NO:1789	R0266:F07_2	frame -3	from 138 to 188

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:1790	R0266:G12_1	frame 1	from 1 to 192
SEQ ID NO:1791	R0266:G12_2	frame 2	from 94 to 168
SEQ ID NO:1792	R0266:G12_3	frame -2	from 65 to 128
SEQ ID NO:1793	R0266:G12_4	frame -3	from 17 to 120
SEQ ID NO:1794	R0266:G12_5	frame -3	from 122 to 192
SEQ ID NO:1795	R0266:G09_1	frame 1	from 7 to 121
SEQ ID NO:1796	R0266:G09_2	frame 2	from 104 to 158
SEQ ID NO:1797	R0266:G09_3	frame -2	from 28 to 78
SEQ ID NO:1798	R0242:E03_1	frame 1	from 1 to 54
SEQ ID NO:1799	R0242:E03_2	frame 2	from 38 to 93
SEQ ID NO:1800	R0244:C04_1	frame 1	from 19 to 77
SEQ ID NO:1801	R0244:C04_2	frame 2	from 13 to 76
SEQ ID NO:1802	R0244:C04_3	frame 3	from 20 to 76
SEQ ID NO:1803	R0244:C04_4	frame -1	from 15 to 65
SEQ ID NO:1804	R0244:C06_1	frame 2	from 38 to 111
SEQ ID NO:1805	R0244:C06_2	frame -1	from 58 to 134
SEQ ID NO:1806	R0244:C06_3	frame -2	from 14 to 98
SEQ ID NO:1807	R0245:A02_1	frame 2	from 12 to 61
SEQ ID NO:1808	R0245:A02_2	frame -3	from 42 to 92
SEQ ID NO:1809	R0245:D12_1	frame 2	from 1 to 92
SEQ ID NO:1810	R0245:D12_2	frame -3	from 4 to 53
SEQ ID NO:1811	R0246:D10_1	frame 3	from 30 to 95
SEQ ID NO:1812	R0246:D10_2	frame -1	from 1 to 83
SEQ ID NO:1813	R0246:D10_3	frame -2	from 14 to 95
SEQ ID NO:1814	R0246:D10_4	frame -3	from 1 to 53
SEQ ID NO:1815	'46377.1_gaiger.ABI'_1	frame 1	from 1 to 116
SEQ ID NO:1816	'46377.1_gaiger.ABI'_2	frame -1	from 16 to 66
SEQ ID NO:1817	'46377.1_gaiger.ABI'_3	frame -2	from 23 to 77
SEQ ID NO:1818	'46403.1_gaiger.ABI'_1	frame 1	from 1 to 63
SEQ ID NO:1819	'46403.1_gaiger.ABI'_2	frame 2	from 25 to 94
SEQ ID NO:1820	'46403.1_gaiger.ABI'_3	frame -3	from 19 to 94
SEQ ID NO:1821	'46489.1;gaiger.ABI'_1	frame 1	from 1 to 70
SEQ ID NO:1822	'46489.1;gaiger.ABI'_2	frame -1	from 1 to 70
SEQ ID NO:1823	'46489.1;gaiger.ABI'_3	frame -2	from 1 to 64
SEQ ID NO:1824	'46872.1_gaiger.ABI'_1	frame 3	from 4 to 77
SEQ ID NO:1825	'46872.1_gaiger.ABI'_2	frame -1	from 1 to 66
SEQ ID NO:1826	'46883.1_gaiger.ABI'_1	frame -1	from 1 to 76
SEQ ID NO:1827	'46880.1_gaiger.ABI'_1	frame 2	from 36 to 95
SEQ ID NO:1828	'46880.1_gaiger.ABI'_2	frame 3	from 1 to 95

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:1829	'46880.1_gaiger.ABI'_3	frame -1	from 32 to 81
SEQ ID NO:1830	'46977.1_gaiger.ABI'_1	frame -2	from 1 to 62
SEQ ID NO:1831	'46977.1_gaiger.ABI'_2	frame -3	from 1 to 94
SEQ ID NO:1832	'47011.1_gaiger.ABI'_1	frame 1	from 1 to 102
SEQ ID NO:1833	'47011.1_gaiger.ABI'_2	frame 3	from 42 to 101
SEQ ID NO:1834	'47011.1_gaiger.ABI'_3	frame -1	from 32 to 81
SEQ ID NO:1835	'51658.1_gaiger.ABI'_1	frame 2	from 5 to 80
SEQ ID NO:1836	'51658.1_gaiger.ABI'_2	frame 3	from 10 to 77
SEQ ID NO:1837	'51734.1_gaiger.ABI'_1	frame 1	from 12 to 98
SEQ ID NO:1838	'51734.1_gaiger.ABI'_2	frame 3	from 22 to 76
SEQ ID NO:1839	'51734.1_gaiger.ABI'_3	frame -2	from 18 to 137
SEQ ID NO:1840	'51870.1_gaiger.ABI'_1	frame 3	from 33 to 107
SEQ ID NO:1841	'51870.1_gaiger.ABI'_2	frame -2	from 27 to 85
SEQ ID NO:1842	'51870.1_gaiger.ABI'_3	frame -3	from 65 to 115
SEQ ID NO:1843	1404:A06_1	frame 1	from 29 to 102
SEQ ID NO:1844	1404:A06_2	frame -3	from 10 to 59
SEQ ID NO:1845	1404:B12_1	frame 2	from 1 to 93
SEQ ID NO:1846	1404:B12_2	frame -2	from 76 to 131
SEQ ID NO:1847	1404:E11_1	frame 3	from 1 to 64
SEQ ID NO:1848	1404:E11_2	frame 3	from 106 to 158
SEQ ID NO:1849	1404:E11_3	frame -2	from 28 to 81
SEQ ID NO:1850	1405:A11_1	frame 2	from 1 to 188
SEQ ID NO:1851	1405:A11_2	frame -1	from 20 to 69
SEQ ID NO:1852	1405:A11_3	frame -2	from 34 to 99
SEQ ID NO:1853	1405:A11_4	frame -3	from 1 to 71
SEQ ID NO:1854	'52280.1_gaiger.ABI'_1	frame 2	from 1 to 80
SEQ ID NO:1855	'52280.1_gaiger.ABI'_2	frame 3	from 16 to 127
SEQ ID NO:1856	'52280.1_gaiger.ABI'_3	frame -2	from 1 to 127
SEQ ID NO:1857	'52280.1_gaiger.ABI'_4	frame -3	from 1 to 51
SEQ ID NO:1858	'52345.1_gaiger.ABI'_1	frame 3	from 74 to 126
SEQ ID NO:1859	'52345.1_gaiger.ABI'_2	frame -2	from 85 to 141
SEQ ID NO:1860	R0263:E03_1	frame 3	from 50 to 111
SEQ ID NO:1861	R0263:E03_2	frame -1	from 119 to 204
SEQ ID NO:1862	'41557.1_gaiger.ABI'_1	frame 1	from 16 to 73
SEQ ID NO:1863	'41557.1_gaiger.ABI'_2	frame 2	from 1 to 109
SEQ ID NO:1864	'41557.1_gaiger.ABI'_3	frame -1	from 11 to 110
SEQ ID NO:1865	'41557.1_gaiger.ABI'_4	frame -3	from 1 to 103
SEQ ID NO:1866	'41650.1_gaiger.ABI'_1	frame 1	from 22 to 109

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:1867	'41650.1_gaiger.ABI'_2	frame 2	from 1 to 157
SEQ ID NO:1868	'41650.1_gaiger.ABI'_3	frame 3	from 1 to 156
SEQ ID NO:1869	'41650.1_gaiger.ABI'_4	frame -1	from 25 to 99
SEQ ID NO:1870	'41650.1_gaiger.ABI'_5	frame -2	from 47 to 157
SEQ ID NO:1871	'41650.1_gaiger.ABI'_6	frame -3	from 53 to 156
SEQ ID NO:1872	'41663.1_gaiger.ABI'_1	frame -2	from 64 to 116
SEQ ID NO:1873	'41663.1_gaiger.ABI'_2	frame -3	from 1 to 67
SEQ ID NO:1874	'41667.1_gaiger.ABI'_1	frame 1	from 1 to 56
SEQ ID NO:1875	'41667.1_gaiger.ABI'_2	frame 2	from 1 to 56
SEQ ID NO:1876	'41667.1_gaiger.ABI'_3	frame -2	from 1 to 56
SEQ ID NO:1877	'41729.1_gaiger.ABI'_1	frame 1	from 64 to 114
SEQ ID NO:1878	'41751.1_gaiger.ABI'_1	frame 1	from 27 to 82
SEQ ID NO:1879	'41751.1_gaiger.ABI'_2	frame 3	from 1 to 50
SEQ ID NO:1880	'41751.1_gaiger.ABI'_3	frame -2	from 1 to 70
SEQ ID NO:1881	'41751.1_gaiger.ABI'_4	frame -3	from 1 to 53
SEQ ID NO:1882	'41818.1_gaiger.ABI'_1	frame 2	from 1 to 69
SEQ ID NO:1883	'41818.1_gaiger.ABI'_2	frame -1	from 30 to 93
SEQ ID NO:1884	'41818.1_gaiger.ABI'_3	frame -3	from 1 to 92
SEQ ID NO:1885	'41828.1_gaiger.ABI'_1	frame -3	from 1 to 77
SEQ ID NO:1886	'41847.1_gaiger.ABI'_1	frame -1	from 1 to 97
SEQ ID NO:1887	'41847.1_gaiger.ABI'_2	frame -3	from 1 to 56
SEQ ID NO:1888	'41849.1_gaiger.ABI'_1	frame 1	from 1 to 75
SEQ ID NO:1889	'41849.1_gaiger.ABI'_2	frame 3	from 4 to 77
SEQ ID NO:1890	'41849.1_gaiger.ABI'_3	frame -1	from 12 to 77
SEQ ID NO:1891	'41927.1_gaiger.ABI'_1	frame 3	from 20 to 74
SEQ ID NO:1892	'41929.1_gaiger.ABI'_1	frame 1	from 1 to 52
SEQ ID NO:1893	'41995.1_gaiger.ABI'_1	frame 1	from 1 to 115
SEQ ID NO:1894	'41995.1_gaiger.ABI'_2	frame 3	from 60 to 109
SEQ ID NO:1895	'41995.1_gaiger.ABI'_3	frame -2	from 1 to 114
SEQ ID NO:1896	'41995.1_gaiger.ABI'_4	frame -3	from 35 to 108
SEQ ID NO:1897	'42012.1_gaiger.ABI'_1	frame 2	from 1 to 60
SEQ ID NO:1898	'42012.1_gaiger.ABI'_2	frame -3	from 1 to 60
SEQ ID NO:1899	'42039.1_gaiger.ABI'_1	frame 2	from 70 to 127
SEQ ID NO:1900	'42039.1_gaiger.ABI'_2	frame 3	from 1 to 146
SEQ ID NO:1901	'42039.1_gaiger.ABI'_3	frame -2	from 39 to 100
SEQ ID NO:1902	'42097.1_gaiger.ABI'_1	frame 1	from 24 to 132
SEQ ID NO:1903	'42097.1_gaiger.ABI'_2	frame -1	from 52 to 132
SEQ ID NO:1904	'42097.1_gaiger.ABI'_3	frame -3	from 34 to 92
SEQ ID NO:1905	'42108.1_gaiger.ABI'_1	frame -2	from 4 to 77

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:1906	R0233:A06_1	frame 1	from 12 to 77
SEQ ID NO:1907	R0233:A06_2	frame 3	from 2 to 76
SEQ ID NO:1908	R0233:A06_3	frame -3	from 1 to 59
SEQ ID NO:1909	R0233:C02_1	frame 3	from 26 to 90
SEQ ID NO:1910	R0233:C02_2	frame -2	from 1 to 107
SEQ ID NO:1911	R0233:C02_3	frame -3	from 1 to 74
SEQ ID NO:1912	R0233:E06_1	frame 1	from 84 to 146
SEQ ID NO:1913	R0233:E06_2	frame 3	from 1 to 181
SEQ ID NO:1914	R0233:E06_3	frame -2	from 49 to 157
SEQ ID NO:1915	R0233:F08_1	frame 1	from 11 to 110
SEQ ID NO:1916	R0233:F08_2	frame 3	from 1 to 103
SEQ ID NO:1917	R0233:F08_3	frame -1	from 16 to 73
SEQ ID NO:1918	R0233:F08_4	frame -2	from 1 to 109
SEQ ID NO:1919	'42328.1_gaiger.ABI'_1	frame 2	from 26 to 103
SEQ ID NO:1920	'42328.1_gaiger.ABI'_2	frame -2	from 1 to 103
SEQ ID NO:1921	'42588.1_gaiger.ABI'_1	frame 1	from 1 to 60
SEQ ID NO:1922	'42588.1_gaiger.ABI'_2	frame 2	from 1 to 60
SEQ ID NO:1923	'42588.1_gaiger.ABI'_3	frame 3	from 1 to 60
SEQ ID NO:1924	'42588.1_gaiger.ABI'_4	frame -1	from 1 to 60
SEQ ID NO:1925	'42588.1_gaiger.ABI'_5	frame -2	from 1 to 53
SEQ ID NO:1926	'42703.1_gaiger.ABI'_1	frame 2	from 25 to 95
SEQ ID NO:1927	'42703.1_gaiger.ABI'_2	frame -2	from 10 to 82
SEQ ID NO:1928	R0234:B07_1	frame 1	from 84 to 146
SEQ ID NO:1929	R0234:B07_2	frame 3	from 1 to 181
SEQ ID NO:1930	R0234:B07_3	frame -2	from 49 to 157
SEQ ID NO:1931	R0234:E06_1	frame 3	from 4 to 77
SEQ ID NO:1932	R0234:E06_2	frame -1	from 1 to 66
SEQ ID NO:1933	R0235:B03_1	frame 1	from 84 to 146
SEQ ID NO:1934	R0235:B03_2	frame 3	from 1 to 169
SEQ ID NO:1935	R0235:B03_3	frame -1	from 38 to 146
SEQ ID NO:1936	R0235:E05_1	frame 2	from 2 to 57
SEQ ID NO:1937	R0235:E05_2	frame 2	from 67 to 145
SEQ ID NO:1938	R0235:E05_3	frame -1	from 74 to 187
SEQ ID NO:1939	R0235:E05_4	frame -2	from 64 to 121
SEQ ID NO:1940	R0236:A06_1	frame 2	from 1 to 150
SEQ ID NO:1941	R0236:A06_2	frame -2	from 25 to 125
SEQ ID NO:1942	R0236:D04_1	frame 1	from 1 to 87
SEQ ID NO:1943	R0236:D04_2	frame 2	from 1 to 113
SEQ ID NO:1944	R0236:D04_3	frame -1	from 1 to 79

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:1945	R0250:A10_1	frame 1	from 127 to 180
SEQ ID NO:1946	R0250:A10_2	frame -1	from 1 to 55
SEQ ID NO:1947	R0250:A10_3	frame -2	from 20 to 80
SEQ ID NO:1948	R0250:A10_4	frame -3	from 1 to 96
SEQ ID NO:1949	R0251:E09_1	frame 3	from 26 to 90
SEQ ID NO:1950	R0251:E09_2	frame -2	from 1 to 107
SEQ ID NO:1951	R0251:E09_3	frame -3	from 1 to 74
SEQ ID NO:1952	R0252:F11_1	frame 1	from 1 to 94
SEQ ID NO:1953	R0252:F11_2	frame 3	from 1 to 61
SEQ ID NO:1954	R0252:F11_3	frame -2	from 12 to 69
SEQ ID NO:1955	R0252:F11_4	frame -3	from 1 to 139
SEQ ID NO:1956	R0238:B02_1	frame 3	from 50 to 111
SEQ ID NO:1957	R0238:B02_2	frame -2	from 102 to 187
SEQ ID NO:1958	R0239:H02_1	frame 3	from 1 to 97
SEQ ID NO:1959	R0255:F12_1	frame 3	from 1 to 57
SEQ ID NO:1960	R0255:F12_2	frame -2	from 1 to 78
SEQ ID NO:1961	R0259:C06_1	frame -1	from 36 to 100
SEQ ID NO:1962	R0259:C06_2	frame -2	from 124 to 187
SEQ ID NO:1963	R0261:B10_1	frame 1	from 1 to 79
SEQ ID NO:1964	R0261:B10_2	frame -1	from 1 to 87
SEQ ID NO:1965	R0261:B10_3	frame -2	from 1 to 113
SEQ ID NO:1966	R0261:D06_1	frame 2	from 1 to 117
SEQ ID NO:1967	R0261:D06_2	frame -2	from 1 to 117
SEQ ID NO:1968	R0261:D06_3	frame -3	from 35 to 117
SEQ ID NO:1969	R0261:E10_1	frame 1	from 1 to 67
SEQ ID NO:1970	R0261:H08_1	frame 1	from 29 to 102
SEQ ID NO:1971	R0261:H08_2	frame 2	from 1 to 101
SEQ ID NO:1972	R0261:H08_3	frame 3	from 1 to 101
SEQ ID NO:1973	R0261:H08_4	frame -2	from 1 to 74
SEQ ID NO:1974	R0261:H08_5	frame -3	from 38 to 101
SEQ ID NO:1975	R0262:A12_1	frame -1	from 35 to 132
SEQ ID NO:1976	R0262:A03_1	frame 2	from 1 to 66
SEQ ID NO:1977	R0262:A03_2	frame -1	from 1 to 84
SEQ ID NO:1978	R0262:A03_3	frame -3	from 1 to 64
SEQ ID NO:1979	R0262:D11_1	frame 1	from 22 to 90
SEQ ID NO:1980	R0262:D11_2	frame 2	from 1 to 57
SEQ ID NO:1981	R0262:D11_3	frame 2	from 59 to 124
SEQ ID NO:1982	R0262:D11_4	frame -2	from 1 to 67
SEQ ID NO:1983	R0262:D11_5	frame -3	from 26 to 124

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:1984	R0262:E03_1	frame 1	from 127 to 176
SEQ ID NO:1985	R0262:E03_2	frame 2	from 26 to 159
SEQ ID NO:1986	R0262:E03_3	frame 3	from 1 to 67
SEQ ID NO:1987	R0262:E03_4	frame -1	from 9 to 68
SEQ ID NO:1988	R0262:E03_5	frame -2	from 113 to 176
SEQ ID NO:1989	R0262:E03_6	frame -3	from 107 to 159
SEQ ID NO:1990	R0262:G05_1	frame 3	from 50 to 111
SEQ ID NO:1991	R0262:G05_2	frame -1	from 49 to 134
SEQ ID NO:1992	R0263:B11_1	frame 2	from 1 to 185
SEQ ID NO:1993	R0263:B11_2	frame 3	from 42 to 106
SEQ ID NO:1994	R0263:B11_3	frame -1	from 74 to 185
SEQ ID NO:1995	R0263:D11_1	frame 1	from 12 to 98
SEQ ID NO:1996	R0263:D11_2	frame 3	from 22 to 76
SEQ ID NO:1997	R0263:D11_3	frame -2	from 4 to 126
SEQ ID NO:1998	R0263:D07_1	frame 1	from 1 to 191
SEQ ID NO:1999	R0263:D07_2	frame -1	from 1 to 51
SEQ ID NO:2000	R0263:D07_3	frame -1	from 91 to 141
SEQ ID NO:2001	R0263:D07_4	frame -2	from 98 to 152
SEQ ID NO:2002	R0263:F08_1	frame 3	from 1 to 95
SEQ ID NO:2003	R0263:H02_1	frame 1	from 4 to 63
SEQ ID NO:2004	R0263:H02_2	frame 1	from 65 to 121
SEQ ID NO:2005	R0263:H02_3	frame 2	from 1 to 50
SEQ ID NO:2006	R0263:H02_4	frame 2	from 52 to 104
SEQ ID NO:2007	R0263:H02_5	frame -1	from 13 to 77
SEQ ID NO:2008	R0263:H02_6	frame -1	from 98 to 161
SEQ ID NO:2009	R0263:H02_7	frame -2	from 3 to 54
SEQ ID NO:2010	R0263:H02_8	frame -2	from 56 to 122
SEQ ID NO:2011	R0264:D03_1	frame 1	from 100 to 157
SEQ ID NO:2012	R0264:D03_2	frame 3	from 16 to 91
SEQ ID NO:2013	R0264:D03_3	frame 3	from 94 to 156
SEQ ID NO:2014	R0264:D03_4	frame -2	from 1 to 156
SEQ ID NO:2015	R0264:E12_1	frame 3	from 50 to 111
SEQ ID NO:2016	R0264:E12_2	frame -1	from 78 to 163
SEQ ID NO:2017	R0264:F11_1	frame 1	from 13 to 81
SEQ ID NO:2018	R0264:F11_2	frame -1	from 1 to 102
SEQ ID NO:2019	R0264:F11_3	frame -2	from 25 to 101
SEQ ID NO:2020	R0264:F11_4	frame -3	from 42 to 101
SEQ ID NO:2021	R0264:H03_1	frame 1	from 1 to 115
SEQ ID NO:2022	R0264:H03_2	frame 3	from 60 to 109

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:2023	R0264:H03_3	frame -2	from 1 to 114
SEQ ID NO:2024	R0264:H03_4	frame -3	from 35 to 108
SEQ ID NO:2025	R0265:D07_1	frame 3	from 50 to 111
SEQ ID NO:2026	R0265:D07_2	frame -1	from 70 to 185
SEQ ID NO:2027	R0265:E12_1	frame 1	from 1 to 87
SEQ ID NO:2028	R0265:E12_2	frame 2	from 1 to 113
SEQ ID NO:2029	R0265:E12_3	frame -1	from 1 to 79
SEQ ID NO:2030	R0265:F12_1	frame 1	from 75 to 126
SEQ ID NO:2031	R0265:F12_2	frame 2	from 46 to 160
SEQ ID NO:2032	R0265:F12_3	frame -1	from 36 to 87
SEQ ID NO:2033	R0265:F12_4	frame -3	from 78 to 133
SEQ ID NO:2034	R0265:H04_1	frame 2	from 64 to 149
SEQ ID NO:2035	R0265:H04_2	frame -3	from 50 to 111
SEQ ID NO:2036	R0265:H09_1	frame 1	from 1 to 191
SEQ ID NO:2037	R0265:H09_2	frame -1	from 1 to 51
SEQ ID NO:2038	R0265:H09_3	frame -1	from 91 to 141
SEQ ID NO:2039	R0265:H09_4	frame -2	from 98 to 152
SEQ ID NO:2040	R0266:A10_1	frame 1	from 1 to 87
SEQ ID NO:2041	R0266:A10_2	frame 2	from 1 to 113
SEQ ID NO:2042	R0266:A10_3	frame -1	from 1 to 79
SEQ ID NO:2043	R0266:A12_1	frame 1	from 1 to 106
SEQ ID NO:2044	R0266:A12_2	frame 1	from 133 to 185
SEQ ID NO:2045	R0266:A12_3	frame 2	from 89 to 143
SEQ ID NO:2046	R0266:A12_4	frame 2	from 147 to 197
SEQ ID NO:2047	R0266:A12_5	frame -3	from 51 to 101
SEQ ID NO:2048	R0266:F03_1	frame 1	from 64 to 141
SEQ ID NO:2049	R0266:F03_2	frame 2	from 8 to 141
SEQ ID NO:2050	R0266:F03_3	frame 3	from 39 to 104
SEQ ID NO:2051	R0266:F03_4	frame -2	from 1 to 141
SEQ ID NO:2052	R0266:F07_1	frame -3	from 37 to 97
SEQ ID NO:2053	R0266:F07_2	frame -3	from 138 to 188
SEQ ID NO:2054	R0266:G12_1	frame 1	from 1 to 192
SEQ ID NO:2055	R0266:G12_2	frame 2	from 94 to 168
SEQ ID NO:2056	R0266:G12_3	frame -2	from 65 to 128
SEQ ID NO:2057	R0266:G12_4	frame -3	from 17 to 120
SEQ ID NO:2058	R0266:G12_5	frame -3	from 122 to 192
SEQ ID NO:2059	R0266:G09_1	frame 1	from 7 to 121
SEQ ID NO:2060	R0266:G09_2	frame 2	from 104 to 158
SEQ ID NO:2061	R0266:G09_3	frame -2	from 28 to 78

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:2062	R0244:C04_1	frame 1	from 19 to 77
SEQ ID NO:2063	R0244:C04_2	frame 2	from 13 to 76
SEQ ID NO:2064	R0244:C04_3	frame 3	from 20 to 76
SEQ ID NO:2065	R0244:C04_4	frame -1	from 15 to 65
SEQ ID NO:2066	R0245:A02_1	frame 2	from 12 to 61
SEQ ID NO:2067	R0245:A02_2	frame -3	from 42 to 92
SEQ ID NO:2068	R0246:D10_1	frame 3	from 30 to 95
SEQ ID NO:2069	R0246:D10_2	frame -1	from 1 to 83
SEQ ID NO:2070	R0246:D10_3	frame -2	from 14 to 95
SEQ ID NO:2071	R0246:D10_4	frame -3	from 1 to 53
SEQ ID NO:2072	'46403.1_gaiger.ABI'_1	frame 1	from 1 to 63
SEQ ID NO:2073	'46403.1_gaiger.ABI'_2	frame 2	from 25 to 94
SEQ ID NO:2074	'46403.1_gaiger.ABI'_3	frame -3	from 19 to 94
SEQ ID NO:2075	'46458.1_gaiger.ABI'_1	frame -3	from 1 to 67
SEQ ID NO:2076	'46489.1;gaiger.ABI'_1	frame 1	from 1 to 70
SEQ ID NO:2077	'46489.1;gaiger.ABI'_2	frame -1	from 1 to 70
SEQ ID NO:2078	'46489.1;gaiger.ABI'_3	frame -2	from 1 to 64
SEQ ID NO:2079	'46802.1_gaiger.ABI'_1	frame 1	from 1 to 90
SEQ ID NO:2080	'46802.1_gaiger.ABI'_2	frame -1	from 1 to 52
SEQ ID NO:2081	'46872.1_gaiger.ABI'_1	frame 3	from 4 to 77
SEQ ID NO:2082	'46872.1_gaiger.ABI'_2	frame -1	from 1 to 66
SEQ ID NO:2083	'46880.1_gaiger.ABI'_1	frame 2	from 36 to 95
SEQ ID NO:2084	'46880.1_gaiger.ABI'_2	frame 3	from 1 to 95
SEQ ID NO:2085	'46880.1_gaiger.ABI'_3	frame -1	from 32 to 81
SEQ ID NO:2086	'46977.1_gaiger.ABI'_1	frame -2	from 1 to 62
SEQ ID NO:2087	'46977.1_gaiger.ABI'_2	frame -3	from 1 to 94
SEQ ID NO:2088	'51658.1_gaiger.ABI'_1	frame 2	from 5 to 80
SEQ ID NO:2089	'51658.1_gaiger.ABI'_2	frame 3	from 10 to 77
SEQ ID NO:2090	'51734.1_gaiger.ABI'_1	frame 1	from 12 to 98
SEQ ID NO:2091	'51734.1_gaiger.ABI'_2	frame 3	from 22 to 76
SEQ ID NO:2092	'51734.1_gaiger.ABI'_3	frame -2	from 18 to 137
SEQ ID NO:2093	1405:C04_1	frame 2	from 1 to 50
SEQ ID NO:2094	1405:C04_2	frame 3	from 10 to 102
SEQ ID NO:2095	1405:C04_3	frame -2	from 76 to 140
SEQ ID NO:2096	1405:E11_1	frame 1	from 87 to 159
SEQ ID NO:2097	1405:E11_2	frame 3	from 92 to 143
SEQ ID NO:2098	1405:E11_3	frame -2	from 48 to 111
SEQ ID NO:2099	1405:E11_4	frame -3	from 1 to 55
SEQ ID NO:2100	'52246.1_gaiger.ABI'_1	frame 1	from 12 to 98

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:2101	'52246.1_gaiger.ABI'_2	frame 3	from 22 to 76
SEQ ID NO:2102	'52246.1_gaiger.ABI'_3	frame 3	from 78 to 127
SEQ ID NO:2103	'52246.1_gaiger.ABI'_4	frame -2	from 5 to 127
SEQ ID NO:2104	'52333.1_gaiger.ABI'_1	frame 1	from 1 to 69
SEQ ID NO:2105	'52333.1_gaiger.ABI'_2	frame 2	from 1 to 66
SEQ ID NO:2106	'41557.1_gaiger.ABI'_1	frame 1	from 16 to 73
SEQ ID NO:2107	'41557.1_gaiger.ABI'_2	frame 2	from 1 to 109
SEQ ID NO:2108	'41557.1_gaiger.ABI'_3	frame -1	from 11 to 110
SEQ ID NO:2109	'41557.1_gaiger.ABI'_4	frame -3	from 1 to 103
SEQ ID NO:2110	'41579.1_gaiger.ABI'_1	frame 3	from 43 to 97
SEQ ID NO:2111	'41579.1_gaiger.ABI'_2	frame -2	from 1 to 97
SEQ ID NO:2112	'41579.1_gaiger.ABI'_3	frame -3	from 43 to 97
SEQ ID NO:2113	'41571.1_gaiger.ABI'_1	frame 3	from 1 to 89
SEQ ID NO:2114	'41571.1_gaiger.ABI'_2	frame -1	from 1 to 89
SEQ ID NO:2115	'41571.1_gaiger.ABI'_3	frame -2	from 27 to 85
SEQ ID NO:2116	'41628.1_gaiger.ABI'_1	frame 1	from 51 to 121
SEQ ID NO:2117	'41628.1_gaiger.ABI'_2	frame 2	from 1 to 97
SEQ ID NO:2118	'41628.1_gaiger.ABI'_3	frame -3	from 47 to 98
SEQ ID NO:2119	'41635.1_gaiger.ABI'_1	frame 1	from 1 to 70
SEQ ID NO:2120	'41635.1_gaiger.ABI'_2	frame 2	from 31 to 127
SEQ ID NO:2121	'41635.1_gaiger.ABI'_3	frame -1	from 56 to 127
SEQ ID NO:2122	'41635.1_gaiger.ABI'_4	frame -2	from 76 to 126
SEQ ID NO:2123	'41663.1_gaiger.ABI'_1	frame -2	from 64 to 116
SEQ ID NO:2124	'41663.1_gaiger.ABI'_2	frame -3	from 1 to 67
SEQ ID NO:2125	'41667.1_gaiger.ABI'_1	frame 1	from 1 to 56
SEQ ID NO:2126	'41667.1_gaiger.ABI'_2	frame 2	from 1 to 56
SEQ ID NO:2127	'41667.1_gaiger.ABI'_3	frame -2	from 1 to 56
SEQ ID NO:2128	'41751.1_gaiger.ABI'_1	frame 1	from 27 to 82
SEQ ID NO:2129	'41751.1_gaiger.ABI'_2	frame 3	from 1 to 50
SEQ ID NO:2130	'41751.1_gaiger.ABI'_3	frame -2	from 1 to 70
SEQ ID NO:2131	'41751.1_gaiger.ABI'_4	frame -3	from 1 to 53
SEQ ID NO:2132	'41944.1_gaiger.ABI'_1	frame 1	from 1 to 56
SEQ ID NO:2133	'41944.1_gaiger.ABI'_2	frame 2	from 1 to 177
SEQ ID NO:2134	'41944.1_gaiger.ABI'_3	frame 3	from 37 to 92
SEQ ID NO:2135	'41944.1_gaiger.ABI'_4	frame -1	from 47 to 116
SEQ ID NO:2136	'41944.1_gaiger.ABI'_5	frame -1	from 125 to 177
SEQ ID NO:2137	'41944.1_gaiger.ABI'_6	frame -2	from 32 to 177
SEQ ID NO:2138	'41944.1_gaiger.ABI'_7	frame -3	from 120 to 177

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:2139	'41986.1_gaiger.ABI'_1	frame 3	from 1 to 110
SEQ ID NO:2140	'41986.1_gaiger.ABI'_2	frame -1	from 1 to 110.
SEQ ID NO:2141	'41986.1_gaiger.ABI'_3	frame -3	from 22 to 91
SEQ ID NO:2142	'42101.1_gaiger.ABI'_1	frame 3	from 53 to 123
SEQ ID NO:2143	'42101.1_gaiger.ABI'_2	frame -2	from 1 to 124
SEQ ID NO:2144	R0232:E07_1	frame 2	from 1 to 51
SEQ ID NO:2145	R0232:E07_2	frame -1	from 1 to 51
SEQ ID NO:2146	R0233:A06_1	frame 1	from 12 to 77
SEQ ID NO:2147	R0233:A06_2	frame 3	from 2 to 76
SEQ ID NO:2148	R0233:A06_3	frame -3	from 1 to 59
SEQ ID NO:2149	'42324.1_gaiger.ABI'_1	frame 1	from 1 to 94
SEQ ID NO:2150	'42324.1_gaiger.ABI'_2	frame 2	from 1 to 57
SEQ ID NO:2151	'42324.1_gaiger.ABI'_3	frame 3	from 38 to 130
SEQ ID NO:2152	'42324.1_gaiger.ABI'_4	frame -1	from 10 to 130
SEQ ID NO:2153	'42324.1_gaiger.ABI'_5	frame -2	from 1 to 54
SEQ ID NO:2154	'42324.1_gaiger.ABI'_6	frame -2	from 72 to 130
SEQ ID NO:2155	'42324.1_gaiger.ABI'_7	frame -3	from 1 to 67
SEQ ID NO:2156	'42324.1_gaiger.ABI'_8	frame -3	from 76 to 130
SEQ ID NO:2157	'42438.1_gaiger.ABI'_1	frame 1	from 1 to 123
SEQ ID NO:2158	'42438.1_gaiger.ABI'_2	frame -3	from 53 to 123
SEQ ID NO:2159	'42625.1_gaiger.ABI'_1	frame 1	from 1 to 62
SEQ ID NO:2160	'42702.1_gaiger.ABI'_1	frame 1	from 1 to 53
SEQ ID NO:2161	'42702.1_gaiger.ABI'_2	frame 2	from 19 to 101
SEQ ID NO:2162	'42702.1_gaiger.ABI'_3	frame 3	from 35 to 149
SEQ ID NO:2163	'42702.1_gaiger.ABI'_4	frame -1	from 4 to 168
SEQ ID NO:2164	'42702.1_gaiger.ABI'_5	frame -2	from 28 to 118
SEQ ID NO:2165	'42702.1_gaiger.ABI'_6	frame -2	from 120 to 185
SEQ ID NO:2166	'42702.1_gaiger.ABI'_7	frame -3	from 104 to 185
SEQ ID NO:2167	'42709.1_gaiger.ABI'_1	frame 2	from 1 to 118
SEQ ID NO:2168	'42709.1_gaiger.ABI'_2	frame -3	from 53 to 118
SEQ ID NO:2169	R0234:E07_1	frame 2	from 1 to 86
SEQ ID NO:2170	R0234:E07_2	frame 3	from 27 to 86
SEQ ID NO:2171	R0234:E07_3	frame -1	from 1 to 51
SEQ ID NO:2172	R0234:G11_1	frame 3	from 1 to 121
SEQ ID NO:2173	R0234:G11_2	frame -2	from 51 to 121
SEQ ID NO:2174	R0236:A09_1	frame 3	from 1 to 122
SEQ ID NO:2175	R0236:A09_2	frame -1	from 54 to 122
SEQ ID NO:2176	R0250:A05_1	frame 1	from 22 to 85
SEQ ID NO:2177	R0250:A05_2	frame 3	from 1 to 179

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:2178	R0250:A05_3	frame -1	from 96 to 159
SEQ ID NO:2179	R0250:A05_4	frame -2	from 34 to 85
SEQ ID NO:2180	R0250:A05_5	frame -2	from 87 to 150
SEQ ID NO:2181	R0251:A07_1	frame 1	from 43 to 176
SEQ ID NO:2182	R0251:A07_2	frame 2	from 48 to 176
SEQ ID NO:2183	R0251:A07_3	frame -2	from 1 to 129
SEQ ID NO:2184	R0251:A07_4	frame -3	from 80 to 134
SEQ ID NO:2185	R0251:D01_1	frame 2	from 1 to 124
SEQ ID NO:2186	R0251:D01_2	frame -3	from 53 to 123
SEQ ID NO:2187	R0252:A08_1	frame 1	from 1 to 64
SEQ ID NO:2188	R0252:A08_2	frame 2	from 12 to 64
SEQ ID NO:2189	R0252:A08_3	frame -1	from 1 to 51
SEQ ID NO:2190	R0252:A08_4	frame -2	from 1 to 64
SEQ ID NO:2191	R0252:F11_1	frame 1	from 1 to 94
SEQ ID NO:2192	R0252:F11_2	frame 3	from 1 to 61
SEQ ID NO:2193	R0252:F11_3	frame -2	from 12 to 69
SEQ ID NO:2194	R0252:F11_4	frame -3	from 1 to 139
SEQ ID NO:2195	R0252:H01_1	frame 2	from 1 to 123
SEQ ID NO:2196	R0252:H01_2	frame -3	from 53 to 123
SEQ ID NO:2197	R0253:G05_1	frame 3	from 53 to 123
SEQ ID NO:2198	R0253:G05_2	frame -2	from 1 to 124
SEQ ID NO:2199	R0254:F07_1	frame 1	from 69 to 153
SEQ ID NO:2200	R0254:F07_2	frame -1	from 87 to 142
SEQ ID NO:2201	R0254:F07_3	frame -2	from 47 to 116
SEQ ID NO:2202	R0254:F07_4	frame -3	from 1 to 82
SEQ ID NO:2203	R0254:F07_5	frame -3	from 99 to 154
SEQ ID NO:2204	R0255:F12_1	frame 3	from 1 to 57
SEQ ID NO:2205	R0255:F12_2	frame -2	from 1 to 78
SEQ ID NO:2206	R0259:C04_1	frame 1	from 16 to 78
SEQ ID NO:2207	R0259:C04_2	frame -2	from 53 to 139
SEQ ID NO:2208	R0261:A09_1	frame 1	from 1 to 174
SEQ ID NO:2209	R0261:A09_2	frame 2	from 34 to 89
SEQ ID NO:2210	R0261:A09_3	frame 3	from 1 to 52
SEQ ID NO:2211	R0261:A09_4	frame -1	from 121 to 174
SEQ ID NO:2212	R0261:A09_5	frame -2	from 47 to 116
SEQ ID NO:2213	R0261:A09_6	frame -2	from 125 to 174
SEQ ID NO:2214	R0261:A09_7	frame -3	from 32 to 174
SEQ ID NO:2215	R0261:C10_1	frame 2	from 6 to 120
SEQ ID NO:2216	R0261:C10_2	frame 3	from 103 to 157

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:2217	R0261:C10_3	frame -1	from 25 to 75
SEQ ID NO:2218	R0261:D06_1	frame 2	from 1 to 117
SEQ ID NO:2219	R0261:D06_2	frame -2	from 1 to 117
SEQ ID NO:2220	R0261:D06_3	frame -3	from 35 to 117
SEQ ID NO:2221	R0262:D04_1	frame 1	from 26 to 95
SEQ ID NO:2222	R0262:D04_2	frame 3	from 32 to 94
SEQ ID NO:2223	R0262:D04_3	frame -2	from 16 to 65
SEQ ID NO:2224	R0262:D04_4	frame -3	from 1 to 92
SEQ ID NO:2225	R0262:E03_1	frame 1	from 127 to 176
SEQ ID NO:2226	R0262:E03_2	frame 2	from 26 to 159
SEQ ID NO:2227	R0262:E03_3	frame 3	from 1 to 67
SEQ ID NO:2228	R0262:E03_4	frame -1	from 9 to 68
SEQ ID NO:2229	R0262:E03_5	frame -2	from 113 to 176
SEQ ID NO:2230	R0262:E03_6	frame -3	from 107 to 159
SEQ ID NO:2231	R0263:B11_1	frame 2	from 1 to 185
SEQ ID NO:2232	R0263:B11_2	frame 3	from 42 to 106
SEQ ID NO:2233	R0263:B11_3	frame -1	from 74 to 185
SEQ ID NO:2234	R0263:B09_1	frame 2	from 1 to 199
SEQ ID NO:2235	R0263:B09_2	frame -1	from 1 to 76
SEQ ID NO:2236	R0263:B09_3	frame -1	from 78 to 199
SEQ ID NO:2237	R0263:B09_4	frame -2	from 140 to 195
SEQ ID NO:2238	R0263:C08_1	frame 1	from 1 to 50
SEQ ID NO:2239	R0263:C08_2	frame 1	from 52 to 101
SEQ ID NO:2240	R0263:C08_3	frame 1	from 161 to 215
SEQ ID NO:2241	R0263:C08_4	frame 2	from 55 to 129
SEQ ID NO:2242	R0263:C08_5	frame 3	from 45 to 147
SEQ ID NO:2243	R0263:C08_6	frame -1	from 113 to 188
SEQ ID NO:2244	R0263:C08_7	frame -2	from 1 to 194
SEQ ID NO:2245	R0263:D11_1	frame 1	from 12 to 98
SEQ ID NO:2246	R0263:D11_2	frame 3	from 22 to 76
SEQ ID NO:2247	R0263:D11_3	frame -2	from 1 to 119
SEQ ID NO:2248	R0263:H10_1	frame 1	from 1 to 55
SEQ ID NO:2249	R0263:H10_2	frame 1	from 99 to 152
SEQ ID NO:2250	R0263:H10_3	frame 3	from 1 to 147
SEQ ID NO:2251	R0263:H10_4	frame -1	from 6 to 140
SEQ ID NO:2252	R0263:H10_5	frame -3	from 1 to 151
SEQ ID NO:2253	R0264:A03_1	frame 2	from 18 to 77
SEQ ID NO:2254	R0264:A03_2	frame 3	from 59 to 128
SEQ ID NO:2255	R0264:A03_3	frame -2	from 53 to 129

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:2256	R0264:B11_1	frame 2	from 6 to 120
SEQ ID NO:2257	R0264:B11_2	frame 3	from 103 to 157
SEQ ID NO:2258	R0264:B11_3	frame -1	from 30 to 80
SEQ ID NO:2259	R0264:F11_1	frame 1	from 13 to 81
SEQ ID NO:2260	R0264:F11_2	frame -1	from 1 to 102
SEQ ID NO:2261	R0264:F11_3	frame -2	from 25 to 101
SEQ ID NO:2262	R0264:F11_4	frame -3	from 42 to 101
SEQ ID NO:2263	R0264:F05_1	frame 2	from 18 to 77
SEQ ID NO:2264	R0264:F05_2	frame 3	from 59 to 113
SEQ ID NO:2265	R0264:F05_3	frame -1	from 38 to 114
SEQ ID NO:2266	R0264:F09_1	frame 1	from 7 to 121
SEQ ID NO:2267	R0264:F09_2	frame 2	from 104 to 158
SEQ ID NO:2268	R0264:F09_3	frame -3	from 25 to 75
SEQ ID NO:2269	R0266:B02_1	frame 1	from 68 to 168
SEQ ID NO:2270	R0266:B02_2	frame 2	from 44 to 167
SEQ ID NO:2271	R0266:B02_3	frame -1	from 1 to 100
SEQ ID NO:2272	R0266:B03_1	frame 2	from 47 to 100
SEQ ID NO:2273	R0266:B03_2	frame 3	from 13 to 84
SEQ ID NO:2274	R0266:B03_3	frame -1	from 47 to 101
SEQ ID NO:2275	R0266:B03_4	frame -2	from 27 to 100
SEQ ID NO:2276	R0266:B04_1	frame 1	from 53 to 121
SEQ ID NO:2277	R0266:B04_2	frame 3	from 1 to 120
SEQ ID NO:2278	R0266:B04_3	frame -2	from 1 to 100
SEQ ID NO:2279	R0266:B04_4	frame -3	from 7 to 106
SEQ ID NO:2280	R0266:B06_1	frame 1	from 28 to 102
SEQ ID NO:2281	R0266:B06_2	frame 1	from 104 to 154
SEQ ID NO:2282	R0266:B06_3	frame 2	from 1 to 57
SEQ ID NO:2283	R0266:B06_4	frame 3	from 1 to 68
SEQ ID NO:2284	R0266:B06_5	frame -1	from 7 to 72
SEQ ID NO:2285	R0266:B06_6	frame -1	from 111 to 169
SEQ ID NO:2286	R0266:B06_7	frame -2	from 1 to 50
SEQ ID NO:2287	R0266:B06_8	frame -3	from 50 to 136
SEQ ID NO:2288	R0266:D05_1	frame 1	from 71 to 158
SEQ ID NO:2289	R0266:D05_2	frame -1	from 96 to 148
SEQ ID NO:2290	R0266:D05_3	frame -2	from 56 to 106
SEQ ID NO:2291	R0266:D05_4	frame -3	from 63 to 143
SEQ ID NO:2292	R0266:E01_1	frame 3	from 1 to 125
SEQ ID NO:2293	R0266:E01_2	frame -1	from 75 to 133
SEQ ID NO:2294	R0266:E01_3	frame -2	from 34 to 133

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:2295	R0266:E03_1	frame 3	from 81 to 130
SEQ ID NO:2296	R0266:E03_2	frame -1	from 1 to 131
SEQ ID NO:2297	R0266:E03_3	frame -3	from 1 to 53
SEQ ID NO:2298	R0266:F03_1	frame 1	from 64 to 141
SEQ ID NO:2299	R0266:F03_2	frame 2	from 8 to 141
SEQ ID NO:2300	R0266:F03_3	frame 3	from 39 to 104
SEQ ID NO:2301	R0266:F03_4	frame -2	from 1 to 141
SEQ ID NO:2302	R0266:F09_1	frame 1	from 1 to 50
SEQ ID NO:2303	R0266:F09_2	frame 1	from 52 to 101
SEQ ID NO:2304	R0266:F09_3	frame 2	from 55 to 129
SEQ ID NO:2305	R0266:F09_4	frame 2	from 139 to 198
SEQ ID NO:2306	R0266:F09_5	frame 3	from 45 to 147
SEQ ID NO:2307	R0266:F09_6	frame -1	from 1 to 177
SEQ ID NO:2308	R0266:F09_7	frame -2	from 29 to 97
SEQ ID NO:2309	R0266:F09_8	frame -3	from 95 to 170
SEQ ID NO:2310	R0245:A02_1	frame 2	from 12 to 61
SEQ ID NO:2311	R0245:A02_2	frame -3	from 42 to 92
SEQ ID NO:2312	'46403.1_gaiger.ABI'_1	frame 1	from 1 to 63
SEQ ID NO:2313	'46403.1_gaiger.ABI'_2	frame 2	from 25 to 94
SEQ ID NO:2314	'46403.1_gaiger.ABI'_3	frame -3	from 19 to 94
SEQ ID NO:2315	'46458.1_gaiger.ABI'_1	frame -3	from 1 to 67
SEQ ID NO:2316	'46977.1_gaiger.ABI'_1	frame -2	from 1 to 62
SEQ ID NO:2317	'46977.1_gaiger.ABI'_2	frame -3	from 1 to 94
SEQ ID NO:2318	'51658.1_gaiger.ABI'_1	frame 2	from 5 to 80
SEQ ID NO:2319	'51658.1_gaiger.ABI'_2	frame 3	from 10 to 77
SEQ ID NO:2320	'51788.1_gaiger.ABI'_1	frame 1	from 1 to 59
SEQ ID NO:2321	'51788.1_gaiger.ABI'_2	frame -2	from 1 to 68
SEQ ID NO:2322	'51850.1_gaiger.ABI'_1	frame 2	from 1 to 58
SEQ ID NO:2323	'51850.1_gaiger.ABI'_2	frame 3	from 47 to 106
SEQ ID NO:2324	'51850.1_gaiger.ABI'_3	frame -3	from 1 to 67
SEQ ID NO:2325	'51892.1_gaiger.ABI'_1	frame 1	from 1 to 158
SEQ ID NO:2326	'51892.1_gaiger.ABI'_2	frame 2	from 2 to 69
SEQ ID NO:2327	'51892.1_gaiger.ABI'_3	frame -1	from 76 to 139
SEQ ID NO:2328	'51892.1_gaiger.ABI'_4	frame -2	from 35 to 137
SEQ ID NO:2329	'51900.1_gaiger.ABI'_1	frame 2	from 1 to 123
SEQ ID NO:2330	'51900.1_gaiger.ABI'_2	frame 3	from 3 to 70
SEQ ID NO:2331	'51900.1_gaiger.ABI'_3	frame -2	from 78 to 141
SEQ ID NO:2332	'51900.1_gaiger.ABI'_4	frame -3	from 36 to 139
SEQ ID NO:2333	'51960.1_gaiger.ABI'_1	frame 3	from 61 to 133

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:2334	1405:A09_1	frame 1	from 66 to 131
SEQ ID NO:2335	1405:A09_2	frame -1	from 19 to 77
SEQ ID NO:2336	1405:A09_3	frame -3	from 1 to 68
SEQ ID NO:2337	1405:A09_4	frame -3	from 117 to 174
SEQ ID NO:2338	1405:D12_1	frame 1	from 4 to 71
SEQ ID NO:2339	1405:D12_2	frame 3	from 1 to 143
SEQ ID NO:2340	1405:D12_3	frame -1	from 52 to 115
SEQ ID NO:2341	1405:D12_4	frame -2	from 11 to 113
SEQ ID NO:2342	1405:D09_1	frame 1	from 9 to 170
SEQ ID NO:2343	1405:D09_2	frame 2	from 1 to 55
SEQ ID NO:2344	1405:D09_3	frame 2	from 104 to 169
SEQ ID NO:2345	1405:D09_4	frame -1	from 1 to 98
SEQ ID NO:2346	1405:D09_5	frame -2	from 5 to 104
SEQ ID NO:2347	1405:E11_1	frame 1	from 87 to 159
SEQ ID NO:2348	1405:E11_2	frame 3	from 92 to 143
SEQ ID NO:2349	1405:E11_3	frame -2	from 48 to 111
SEQ ID NO:2350	1405:E11_4	frame -3	from 1 to 55
SEQ ID NO:2351	'52246.1_gaiger.ABI'_1	frame 1	from 12 to 98
SEQ ID NO:2352	'52246.1_gaiger.ABI'_2	frame 3	from 22 to 76
SEQ ID NO:2353	'52246.1_gaiger.ABI'_3	frame 3	from 78 to 127
SEQ ID NO:2354	'52246.1_gaiger.ABI'_4	frame -2	from 5 to 127
SEQ ID NO:2355	'52333.1_gaiger.ABI'_1	frame 1	from 1 to 69
SEQ ID NO:2356	'52333.1_gaiger.ABI'_2	frame 2	from 1 to 66
SEQ ID NO:2357	1408:A09_1	frame 2	from 1 to 156
SEQ ID NO:2358	1408:A09_2	frame 3	from 1 to 67
SEQ ID NO:2359	1408:A09_3	frame -2	from 94 to 157
SEQ ID NO:2360	1408:A09_4	frame -3	from 53 to 155
SEQ ID NO:2361	1408:B02_1	frame 2	from 8 to 187
SEQ ID NO:2362	1408:B02_2	frame -1	from 9 to 80
SEQ ID NO:2363	1408:B02_3	frame -1	from 82 to 175
SEQ ID NO:2364	1408:B02_4	frame -3	from 29 to 78
SEQ ID NO:2365	1408:B02_5	frame -3	from 118 to 187
SEQ ID NO:2366	1408:C12_1	frame 2	from 122 to 175
SEQ ID NO:2367	1408:C12_2	frame 3	from 1 to 187
SEQ ID NO:2368	1408:C12_3	frame -2	from 1 to 71
SEQ ID NO:2369	1408:C12_4	frame -3	from 1 to 84
SEQ ID NO:2370	1408:C12_5	frame -3	from 86 to 137
SEQ ID NO:2371	1408:D06_1	frame 1	from 127 to 180
SEQ ID NO:2372	1408:D06_2	frame 2	from 1 to 161

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:2373	1408:D06_3	frame 3	from 35 to 166
SEQ ID NO:2374	1408:D06_4	frame -1	from 61 to 183
SEQ ID NO:2375	1408:D06_5	frame -3	from 7 to 63
SEQ ID NO:2376	'41663.1_gaiger.ABI'_1	frame -2	from 64 to 116
SEQ ID NO:2377	'41663.1_gaiger.ABI'_2	frame -3	from 1 to 67
SEQ ID NO:2378	'41729.1_gaiger.ABI'_1	frame 1	from 64 to 114
SEQ ID NO:2379	'41888.1_gaiger.ABI'_1	frame 3	from 22 to 81
SEQ ID NO:2380	'41925.1_gaiger.ABI'_1	frame 1	from 9 to 59
SEQ ID NO:2381	'41925.1_gaiger.ABI'_2	frame 2	from 1 to 59
SEQ ID NO:2382	'41925.1_gaiger.ABI'_3	frame -2	from 1 to 59
SEQ ID NO:2383	'41925.1_gaiger.ABI'_4	frame -3	from 1 to 58
SEQ ID NO:2384	'41639.1_gaiger.ABI'_1	frame 1	from 1 to 135
SEQ ID NO:2385	'41639.1_gaiger.ABI'_2	frame 2	from 86 to 135
SEQ ID NO:2386	'41639.1_gaiger.ABI'_3	frame 3	from 1 to 134
SEQ ID NO:2387	'41639.1_gaiger.ABI'_4	frame -1	from 1 to 84
SEQ ID NO:2388	'41639.1_gaiger.ABI'_5	frame -1	from 86 to 135
SEQ ID NO:2389	'41639.1_gaiger.ABI'_6	frame -3	from 39 to 124
SEQ ID NO:2390	'41853.1_gaiger.ABI'_1	frame 1	from 13 to 90
SEQ ID NO:2391	'41853.1_gaiger.ABI'_2	frame 2	from 28 to 78
SEQ ID NO:2392	'41853.1_gaiger.ABI'_3	frame 3	from 1 to 50
SEQ ID NO:2393	'41853.1_gaiger.ABI'_4	frame 3	from 66 to 147
SEQ ID NO:2394	'41853.1_gaiger.ABI'_5	frame -3	from 35 to 112
SEQ ID NO:2395	'41924.1_gaiger.ABI'_1	frame 2	from 1 to 64
SEQ ID NO:2396	'41924.1_gaiger.ABI'_2	frame -2	from 27 to 83
SEQ ID NO:2397	'41638.1_gaiger.ABI'_1	frame 1	from 8 to 81
SEQ ID NO:2398	'41638.1_gaiger.ABI'_2	frame 3	from 6 to 62
SEQ ID NO:2399	'41638.1_gaiger.ABI'_3	frame -2	from 1 to 58
SEQ ID NO:2400	'41629.1_gaiger.ABI'_1	frame 1	from 1 to 59
SEQ ID NO:2401	'41629.1_gaiger.ABI'_2	frame 2	from 38 to 87
SEQ ID NO:2402	'41629.1_gaiger.ABI'_3	frame -3	from 42 to 91
SEQ ID NO:2403	'41678.1_gaiger.ABI'_1	frame -2	from 1 to 60
SEQ ID NO:2404	'41717.1_gaiger.ABI'_1	frame 1	from 55 to 129
SEQ ID NO:2405	'41717.1_gaiger.ABI'_2	frame 2	from 1 to 63
SEQ ID NO:2406	'41717.1_gaiger.ABI'_3	frame -3	from 1 to 68
SEQ ID NO:2407	'41987.1_gaiger.ABI'_1	frame 1	from 48 to 116
SEQ ID NO:2408	'41987.1_gaiger.ABI'_2	frame 2	from 1 to 50
SEQ ID NO:2409	'41987.1_gaiger.ABI'_3	frame 2	from 96 to 154
SEQ ID NO:2410	'41987.1_gaiger.ABI'_4	frame 3	from 53 to 120

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:2411	'41987.1_gaiger.ABI'_5	frame 3	from 122 to 175
SEQ ID NO:2412	'41987.1_gaiger.ABI'_6	frame -1	from 37 to 136
SEQ ID NO:2413	'41987.1_gaiger.ABI'_7	frame -2	from 1 to 72
SEQ ID NO:2414	R0233:F02_1	frame 2	from 119 to 190
SEQ ID NO:2415	R0233:F02_2	frame 3	from 1 to 76
SEQ ID NO:2416	R0233:F02_3	frame -1	from 31 to 82
SEQ ID NO:2417	R0233:F02_4	frame -1	from 112 to 190
SEQ ID NO:2418	R0232:A08_1	frame -2	from 4 to 64
SEQ ID NO:2419	R0233:B04_1	frame 2	from 76 to 136
SEQ ID NO:2420	R0233:B04_2	frame -3	from 1 to 103
SEQ ID NO:2421	'42041.1_gaiger.ABI'_1	frame -3	from 1 to 63
SEQ ID NO:2422	'42407.1_gaiger.ABI'_1	frame 1	from 32 to 83
SEQ ID NO:2423	'42407.1_gaiger.ABI'_2	frame 3	from 1 to 90
SEQ ID NO:2424	'42407.1_gaiger.ABI'_3	frame -1	from 32 to 87
SEQ ID NO:2425	'42407.1_gaiger.ABI'_4	frame -2	from 10 to 100
SEQ ID NO:2426	'42483.1;gaiger.ABI'_1	frame 3	from 4 to 81
SEQ ID NO:2427	'42483.1;gaiger.ABI'_2	frame -2	from 12 to 75
SEQ ID NO:2428	'42483.1;gaiger.ABI'_3	frame -3	from 1 to 51
SEQ ID NO:2429	'42350.1_gaiger.ABI'_1	frame -1	from 12 to 90
SEQ ID NO:2430	'42530.1;gaiger.ABI'_1	frame 1	from 7 to 73
SEQ ID NO:2431	'42530.1;gaiger.ABI'_2	frame -3	from 3 to 72
SEQ ID NO:2432	'42523.1;gaiger.ABI'_1	frame 2	from 19 to 74
SEQ ID NO:2433	'42523.1;gaiger.ABI'_2	frame 3	from 2 to 51
SEQ ID NO:2434	'42523.1;gaiger.ABI'_3	frame -2	from 1 to 58
SEQ ID NO:2435	R0235:D07_1	frame 3	from 33 to 110
SEQ ID NO:2436	R0235:D07_2	frame -2	from 64 to 113
SEQ ID NO:2437	R0235:D07_3	frame -3	from 34 to 150
SEQ ID NO:2438	R0235:D12_1	frame -2	from 18 to 71
SEQ ID NO:2439	R0235:D12_2	frame -3	from 14 to 71
SEQ ID NO:2440	R0236:H02_1	frame 1	from 1 to 70
SEQ ID NO:2441	R0236:H02_2	frame 2	from 1 to 111
SEQ ID NO:2442	R0236:H02_3	frame 2	from 113 to 165
SEQ ID NO:2443	R0236:H02_4	frame 3	from 1 to 138
SEQ ID NO:2444	R0236:H02_5	frame -2	from 10 to 110
SEQ ID NO:2445	R0236:H02_6	frame -3	from 105 to 165
SEQ ID NO:2446	R0251:B12_1	frame 3	from 1 to 196
SEQ ID NO:2447	R0251:B12_2	frame -2	from 15 to 128
SEQ ID NO:2448	R0251:B12_3	frame -2	from 130 to 196
SEQ ID NO:2449	R0253:D09_1	frame 2	from 1 to 65

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:2450	R0253:D09_2	frame 2	from 67 to 116
SEQ ID NO:2451	R0253:D09_3	frame 3	from 31 to 115
SEQ ID NO:2452	R0253:D09_4	frame -1	from 1 to 116
SEQ ID NO:2453	R0253:D09_5	frame -3	from 13 to 66
SEQ ID NO:2454	R0254:F10_1	frame 3	from 54 to 103
SEQ ID NO:2455	R0254:D02_1	frame 1	from 1 to 53
SEQ ID NO:2456	R0254:D02_2	frame 1	from 55 to 135
SEQ ID NO:2457	R0254:D02_3	frame 2	from 109 to 158
SEQ ID NO:2458	R0254:D02_4	frame -2	from 1 to 193
SEQ ID NO:2459	R0254:D02_5	frame -3	from 33 to 90
SEQ ID NO:2460	R0238:B06_1	frame 3	from 31 to 139
SEQ ID NO:2461	R0238:B06_2	frame -1	from 1 to 51
SEQ ID NO:2462	R0238:B06_3	frame -2	from 69 to 119
SEQ ID NO:2463	R0238:B06_4	frame -3	from 4 to 70
SEQ ID NO:2464	R0255:D01_1	frame 1	from 9 to 90
SEQ ID NO:2465	R0255:D01_2	frame 1	from 104 to 168
SEQ ID NO:2466	R0255:D01_3	frame 2	from 88 to 168
SEQ ID NO:2467	R0255:D01_4	frame -1	from 1 to 79
SEQ ID NO:2468	R0255:D01_5	frame -1	from 81 to 130
SEQ ID NO:2469	R0255:D01_6	frame -2	from 1 to 59
SEQ ID NO:2470	R0255:D01_7	frame -2	from 62 to 168
SEQ ID NO:2471	R0255:D01_8	frame -3	from 35 to 91
SEQ ID NO:2472	R0255:D01_9	frame -3	from 93 to 156
SEQ ID NO:2473	R0255:C02_1	frame 1	from 1 to 60
SEQ ID NO:2474	R0255:C02_2	frame 3	from 23 to 96
SEQ ID NO:2475	R0255:C02_3	frame -1	from 35 to 108
SEQ ID NO:2476	R0261:H04_1	frame 1	from 100 to 159
SEQ ID NO:2477	R0261:H04_2	frame 3	from 1 to 126
SEQ ID NO:2478	R0261:H04_3	frame -1	from 1 to 97
SEQ ID NO:2479	R0261:H04_4	frame -2	from 1 to 75
SEQ ID NO:2480	R0261:H04_5	frame -2	from 77 to 128
SEQ ID NO:2481	R0261:H04_6	frame -3	from 6 to 158
SEQ ID NO:2482	R0259:C04_1	frame 1	from 16 to 78
SEQ ID NO:2483	R0259:C04_2	frame -2	from 53 to 139
SEQ ID NO:2484	R0259:C06_1	frame -1	from 36 to 100
SEQ ID NO:2485	R0259:C06_2	frame -2	from 124 to 187
SEQ ID NO:2486	R0261:H08_1	frame 1	from 29 to 102
SEQ ID NO:2487	R0261:H08_2	frame 2	from 1 to 101
SEQ ID NO:2488	R0261:H08_3	frame 3	from 1 to 101

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:2489	R0261:H08_4	frame -2	from 1 to 74
SEQ ID NO:2490	R0261:H08_5	frame -3	from 38 to 101
SEQ ID NO:2491	R0261:D03_1	frame 1	from 44 to 179
SEQ ID NO:2492	R0261:D03_2	frame 2	from 12 to 90
SEQ ID NO:2493	R0261:D03_3	frame 2	from 92 to 164
SEQ ID NO:2494	R0261:D03_4	frame 3	from 40 to 96
SEQ ID NO:2495	R0261:D03_5	frame 3	from 98 to 186
SEQ ID NO:2496	R0261:D03_6	frame -1	from 37 to 160
SEQ ID NO:2497	R0261:D03_7	frame -2	from 22 to 144
SEQ ID NO:2498	R0262:C04_1	frame 1	from 18 to 75
SEQ ID NO:2499	R0262:C04_2	frame 2	from 7 to 77
SEQ ID NO:2500	R0262:C04_3	frame -2	from 67 to 139
SEQ ID NO:2501	R0262:C04_4	frame -3	from 1 to 88
SEQ ID NO:2502	R0264:B08_1	frame 1	from 1 to 59
SEQ ID NO:2503	R0266:D03_1	frame 1	from 1 to 171
SEQ ID NO:2504	R0266:D03_2	frame 2	from 94 to 193
SEQ ID NO:2505	R0266:D03_3	frame 3	from 131 to 185
SEQ ID NO:2506	R0266:D03_4	frame -1	from 89 to 160
SEQ ID NO:2507	R0266:D03_5	frame -3	from 2 to 59
SEQ ID NO:2508	R0266:D03_6	frame -3	from 141 to 193
SEQ ID NO:2509	R0265:F12_1	frame 1	from 75 to 126
SEQ ID NO:2510	R0265:F12_2	frame 2	from 46 to 160
SEQ ID NO:2511	R0265:F12_3	frame -1	from 36 to 87
SEQ ID NO:2512	R0265:F12_4	frame -3	from 78 to 133
SEQ ID NO:2513	R0264:C03_1	frame -2	from 21 to 77
SEQ ID NO:2514	R0264:C04_1	frame -3	from 48 to 122
SEQ ID NO:2515	R0244:C02_1	frame 1	from 1 to 64
SEQ ID NO:2516	R0244:C02_2	frame -1	from 8 to 107
SEQ ID NO:2517	R0244:C02_3	frame -2	from 19 to 70
SEQ ID NO:2518	R0245:A02_1	frame 2	from 12 to 61
SEQ ID NO:2519	R0245:A02_2	frame -3	from 42 to 92
SEQ ID NO:2520	'51734.1_gaiger.ABI'_1	frame 1	from 12 to 98
SEQ ID NO:2521	'51734.1_gaiger.ABI'_2	frame 3	from 22 to 76
SEQ ID NO:2522	'51734.1_gaiger.ABI'_3	frame -2	from 18 to 137
SEQ ID NO:2523	'51870.1_gaiger.ABI'_1	frame 3	from 33 to 107
SEQ ID NO:2524	'51870.1_gaiger.ABI'_2	frame -2	from 27 to 85
SEQ ID NO:2525	'51870.1_gaiger.ABI'_3	frame -3	from 65 to 115
SEQ ID NO:2526	'51975.1_gaiger.ABI'_1	frame 1	from 17 to 88
SEQ ID NO:2527	'51975.1_gaiger.ABI'_2	frame 1	from 90 to 141

Sequence Identifier Number	ORF Identifier	Translation Frame	Beginning and Ending
SEQ ID NO:2528	'51975.1_gaiger.ABI'_3	frame -1	from 73 to 147
SEQ ID NO:2529	'51975.1_gaiger.ABI'_4	frame -3	from 1 to 93
SEQ ID NO:2530	'52260.1_gaiger.ABI'_1	frame 1	from 23 to 75
SEQ ID NO:2531	'52260.1_gaiger.ABI'_2	frame -1	from 48 to 105
SEQ ID NO:2532	'52260.1_gaiger.ABI'_3	frame -3	from 13 to 79

6. REFERENCES

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All of the compositions and methods disclosed and claimed herein can be made and executed without undue experimentation in light of the present disclosure. While the compositions and methods of this invention have been described in terms of preferred embodiments, it will be apparent to those of skill in the art that variations may be applied to the composition, methods and in the steps or in the sequence of steps of the method described herein without departing from the concept, spirit and scope of the invention. More specifically, it will be apparent that certain agents which are both chemically and physiologically related may be substituted for the agents described herein while the same or similar results would be achieved. All such similar substitutes and modifications apparent to those skilled in the art are deemed to be within the spirit, scope and concept of the invention as defined by the appended claims. Accordingly, the exclusive rights sought to be patented are as described in the claims below:

CLAIMS:

1. A composition comprising at least a first isolated peptide or polypeptide comprising at least a first isolated coding region that comprises an amino acid sequence that is at least about 90% identical to the amino acid sequence of any one of SEQ ID NO:669 to SEQ ID NO:2532.
2. The composition according to claim 1, wherein said at least a first isolated coding region comprises an amino acid sequence that is at least about 92% identical to the amino acid sequence of any one of SEQ ID NO:669 to SEQ ID NO:2532.
3. The composition according to claim 1 or claim 2, wherein said at least a first isolated coding region comprises an amino acid sequence that is at least about 94% identical to the amino acid sequence of any one of SEQ ID NO:669 to SEQ ID NO:2532.
4. The composition according to any preceding claim, wherein said at least a first isolated coding region comprises an amino acid sequence that is at least about 96% identical to the amino acid sequence of any one of SEQ ID NO:669 to SEQ ID NO:2532.
5. The composition according to any preceding claim, wherein said at least a first isolated coding region comprises an amino acid sequence that is at least about 98% identical to the amino acid sequence of any one of SEQ ID NO:669 to SEQ ID NO:2532.

6. The composition according to any preceding claim, wherein said at least a first isolated coding region comprises a sequence of at least about 30 contiguous amino acids from any one of SEQ ID NO:669 to SEQ ID NO:2532.
7. The composition according to any preceding claim, wherein said at least a first isolated coding region comprises a sequence of at least about 40 contiguous amino acids from any one of SEQ ID NO:669 to SEQ ID NO:2532.
8. The composition according to any preceding claim, wherein said at least a first isolated coding region comprises a sequence of at least about 50 contiguous amino acids from any one of SEQ ID NO:669 to SEQ ID NO:2532.
9. The composition according to any preceding claim, wherein said at least a first isolated coding region comprises a sequence of at least about 60 contiguous amino acids from any one of SEQ ID NO:669 to SEQ ID NO:2532.
10. The composition according to any preceding claim, wherein said at least a first isolated coding region comprises a sequence of at least about 70 contiguous amino acids from any one of SEQ ID NO:669 to SEQ ID NO:2532.
11. The composition according to any preceding claim, wherein said at least a first isolated coding region comprises a sequence of at least about 80 contiguous amino acids from any one of SEQ ID NO:669 to SEQ ID NO:2532.

12. The composition according to any preceding claim, wherein said at least a first isolated coding region comprises a sequence of at least about 90 contiguous amino acids from any one of SEQ ID NO:669 to SEQ ID NO:2532.
13. The composition according to any preceding claim, wherein said at least a first isolated coding region comprises a sequence of at least about 100 contiguous amino acids from any one of SEQ ID NO:669 to SEQ ID NO:2532.
14. The composition according to any preceding claim, wherein said at least a first isolated coding region comprises a sequence of at least about 200 contiguous amino acids from any one of SEQ ID NO:669 to SEQ ID NO:2532.
15. The composition according to any preceding claim, wherein said at least a first isolated coding region comprises the amino acid sequence of any one of SEQ ID NO:669 to SEQ ID NO:2532.
16. The composition according to any preceding claim, wherein said at least a first isolated coding region comprises the amino acid sequence of any one of SEQ ID NO:669 to SEQ ID NO:1380.
17. The composition according to any one of claims 1 to 15, wherein said at least a first isolated coding region comprises the amino acid sequence of any one of SEQ ID NO:1381 to SEQ ID NO:1859.

18. The composition according to any one of claims 1 to 15, wherein said at least a first isolated coding region comprises the amino acid sequence of any one of SEQ ID NO:1860 to SEQ ID NO:2105.
19. The composition according to any one of claims 1 to 15, wherein said at least a first isolated coding region comprises the amino acid sequence of any one of SEQ ID NO:2106 to SEQ ID NO:2375.
20. The composition according to any one of claims 1 to 15, wherein said at least a first isolated coding region comprises the amino acid sequence of any one of SEQ ID NO:2376 to SEQ ID NO:2532.
21. The composition according to any preceding claim, wherein said at least a first isolated coding region comprises the amino acid sequence of any one of SEQ ID NO:669, SEQ ID NO:670, SEQ ID NO:671, SEQ ID NO:672, SEQ ID NO:673, SEQ ID NO:674, SEQ ID NO:675, SEQ ID NO:676, SEQ ID NO:677, SEQ ID NO:678, SEQ ID NO:679, SEQ ID NO:680, SEQ ID NO:681, SEQ ID NO:682, SEQ ID NO:683, SEQ ID NO:684, SEQ ID NO:685, SEQ ID NO:686, SEQ ID NO:687, SEQ ID NO:688, SEQ ID NO:689, SEQ ID NO:690, SEQ ID NO:691, SEQ ID NO:692, SEQ ID NO:693, SEQ ID NO:694, SEQ ID NO:695, SEQ ID NO:696, SEQ ID NO:697, SEQ ID NO:698, SEQ ID NO:699, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703, SEQ ID NO:704, SEQ ID NO:705, SEQ ID NO:706, SEQ ID NO:707, SEQ ID NO:708, SEQ ID NO:709, SEQ ID NO:710, SEQ ID NO:711, SEQ ID NO:712, SEQ ID NO:713, SEQ ID NO:714, SEQ ID NO:715, SEQ ID NO:716, SEQ ID NO:717, SEQ ID NO:718, SEQ ID NO:719, SEQ ID NO:720, SEQ ID NO:721, SEQ ID NO:722, SEQ ID NO:723, SEQ ID NO:724, SEQ ID NO:725, SEQ ID NO:726, SEQ ID NO:727, SEQ ID NO:728, SEQ ID NO:729, SEQ ID NO:730, SEQ ID NO:731, SEQ ID NO:732, SEQ ID NO:733, SEQ ID NO:734, SEQ ID NO:735, SEQ ID NO:736,

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22. The composition according to any one of claims 1 to 20, wherein said at least a first isolated coding region comprises the amino acid sequence of any one of SEQ ID NO:901, SEQ ID NO:902, SEQ ID NO:903, SEQ ID NO:904, SEQ ID NO:905, SEQ ID NO:906, SEQ ID NO:907, SEQ ID NO:908, SEQ ID NO:909, SEQ ID NO:910, SEQ ID NO:911, SEQ ID NO:912, SEQ ID NO:913, SEQ ID NO:914, SEQ ID NO:915, SEQ ID NO:916, SEQ ID NO:917, SEQ ID NO:918, SEQ ID NO:919, SEQ ID NO:920, SEQ ID NO:921, SEQ ID NO:922, SEQ ID NO:923, SEQ ID NO:924, SEQ ID NO:925, SEQ ID NO:926, SEQ ID NO:927, SEQ ID NO:928, SEQ ID NO:929, SEQ ID NO:930, SEQ ID NO:931, SEQ ID NO:932, SEQ ID NO:933, SEQ ID NO:934, SEQ ID NO:935, SEQ ID NO:936, SEQ ID NO:937, SEQ ID NO:938, SEQ ID NO:939, SEQ ID NO:940, SEQ ID NO:941, SEQ ID NO:942, SEQ ID NO:943, SEQ ID NO:944, SEQ ID NO:945, SEQ ID NO:946, SEQ ID NO:947, SEQ ID NO:948, SEQ ID NO:949, SEQ ID NO:950, SEQ ID NO:951, SEQ ID NO:952, SEQ ID NO:953, SEQ ID NO:954, SEQ ID NO:955, SEQ ID NO:956, SEQ ID NO:957, SEQ ID NO:958, SEQ ID NO:959, SEQ ID NO:960, SEQ ID NO:961, SEQ ID NO:962, SEQ ID NO:963, SEQ ID NO:964, SEQ ID NO:965, SEQ ID NO:966, SEQ ID NO:967, SEQ ID NO:968, SEQ ID NO:969, SEQ ID NO:970, SEQ ID NO:971, SEQ ID NO:972, SEQ ID NO:973, SEQ ID NO:974, SEQ ID NO:975, SEQ ID NO:976, SEQ ID NO:977, SEQ ID NO:978, SEQ ID NO:979, SEQ ID NO:980, SEQ ID NO:981, SEQ ID NO:982, SEQ ID NO:983, SEQ ID NO:984, SEQ ID NO:985, SEQ ID NO:986, SEQ ID NO:987, SEQ ID NO:988, SEQ ID NO:989, SEQ ID NO:990, SEQ ID NO:991, SEQ ID NO:992, SEQ ID NO:993, SEQ ID NO:994, SEQ ID NO:995, SEQ ID NO:996, SEQ ID NO:997, SEQ ID NO:998, SEQ ID NO:999, SEQ ID NO:1000, SEQ ID NO:1001, SEQ ID NO:1002, SEQ ID NO:1003, SEQ ID

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23. The composition according to any one of claims 1 to 20, wherein said at least a first isolated coding region comprises the amino acid sequence of any one of SEQ ID NO:1201, SEQ ID NO:1202, SEQ ID NO:1203, SEQ ID NO:1204, SEQ ID NO:1205, SEQ ID NO:1206, SEQ ID NO:1207, SEQ ID NO:1208, SEQ ID NO:1209, SEQ ID NO:1210, SEQ ID NO:1211, SEQ ID NO:1212, SEQ ID NO:1213, SEQ ID NO:1214, SEQ ID NO:1215, SEQ ID NO:1216, SEQ ID NO:1217, SEQ ID NO:1218, SEQ ID NO:1219, SEQ ID NO:1220, SEQ ID NO:1221, SEQ ID NO:1222, SEQ ID NO:1223, SEQ ID NO:1224, SEQ ID NO:1225, SEQ ID NO:1226, SEQ ID NO:1227, SEQ ID NO:1228, SEQ ID NO:1229, SEQ ID NO:1230, SEQ ID NO:1231, SEQ ID NO:1232, SEQ ID NO:1233, SEQ ID NO:1234, SEQ ID NO:1235, SEQ ID NO:1236, SEQ ID NO:1237, SEQ ID NO:1238, SEQ ID NO:1239, SEQ ID NO:1240, SEQ ID

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24. The composition according to any one of claims 1 to 20, wherein said at least a first isolated coding region comprises the amino acid sequence of any one of SEQ ID NO:1381, SEQ ID NO:1382, SEQ ID NO:1383, SEQ ID NO:1384, SEQ ID NO:1385, SEQ ID NO:1386, SEQ ID NO:1387, SEQ ID NO:1388, SEQ ID NO:1389, SEQ ID NO:1390, SEQ ID NO:1391, SEQ ID NO:1392, SEQ ID NO:1393, SEQ ID NO:1394, SEQ ID NO:1395, SEQ ID NO:1396, SEQ ID NO:1397, SEQ ID NO:1398, SEQ ID NO:1399, SEQ ID NO:1400, SEQ ID NO:1401, SEQ ID NO:1402, SEQ ID NO:1403, SEQ ID NO:1404, SEQ ID NO:1405, SEQ ID NO:1406, SEQ ID NO:1407, SEQ ID NO:1408, SEQ ID NO:1409, SEQ ID NO:1410, SEQ ID NO:1411, SEQ ID NO:1412, SEQ ID NO:1413, SEQ ID NO:1414, SEQ ID NO:1415, SEQ ID NO:1416, SEQ ID NO:1417, SEQ ID NO:1418, SEQ ID NO:1419, SEQ ID NO:1420, SEQ ID NO:1421, SEQ ID NO:1422, SEQ ID NO:1423, SEQ ID NO:1424, SEQ ID NO:1425, SEQ ID NO:1426, SEQ ID NO:1427, SEQ ID NO:1428, SEQ ID NO:1429, SEQ ID NO:1430, SEQ ID NO:1431, SEQ ID NO:1432, SEQ ID NO:1433, SEQ ID NO:1434, SEQ ID NO:1435, SEQ ID NO:1436, SEQ ID NO:1437, SEQ ID NO:1438, SEQ ID NO:1439, SEQ ID NO:1440, SEQ ID NO:1441, SEQ ID NO:1442, SEQ ID NO:1443, SEQ ID NO:1444, SEQ ID NO:1445, SEQ ID NO:1446, SEQ ID NO:1447, SEQ ID NO:1448, SEQ ID NO:1449, SEQ ID NO:1450, SEQ ID NO:1451, SEQ ID NO:1452, SEQ ID NO:1453, SEQ ID NO:1454, SEQ ID NO:1455, SEQ ID NO:1456, SEQ ID NO:1457, SEQ ID NO:1458, SEQ ID NO:1459, SEQ ID NO:1460, SEQ ID NO:1461, SEQ ID NO:1462, SEQ ID NO:1463, SEQ ID NO:1464, SEQ ID NO:1465, SEQ ID NO:1466, SEQ ID NO:1467, SEQ ID NO:1468, SEQ ID NO:1469, SEQ ID NO:1470, SEQ ID NO:1471, SEQ ID NO:1472, SEQ ID NO:1473, SEQ ID NO:1474, SEQ ID NO:1475, SEQ ID NO:1476, SEQ ID NO:1477, SEQ ID NO:1478, SEQ ID NO:1479, SEQ ID NO:1480, SEQ ID

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25. The composition according to any one of claims 1 to 20, wherein said at least a first isolated coding region comprises the amino acid sequence of any one of SEQ ID NO:1700, SEQ ID NO:1701, SEQ ID NO:1702, SEQ ID NO:1703, SEQ ID NO:1704, SEQ ID NO:1705, SEQ ID NO:1706, SEQ ID NO:1707, SEQ ID NO:1708, SEQ ID NO:1709, SEQ ID NO:1710, SEQ ID NO:1711, SEQ ID NO:1712, SEQ ID NO:1713, SEQ ID NO:1714, SEQ ID NO:1715, SEQ ID NO:1716, SEQ ID NO:1717, SEQ ID NO:1718, SEQ ID NO:1719, SEQ ID

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26. The composition according to any one of claims 1 to 20, wherein said at least a first isolated coding region comprises the amino acid sequence of any one of SEQ ID NO:1860, SEQ ID NO:1861, SEQ ID NO:1862, SEQ ID NO:1863, SEQ ID NO:1864, SEQ ID NO:1865, SEQ ID NO:1866, SEQ ID NO:1867, SEQ ID NO:1868, SEQ ID NO:1869, SEQ ID NO:1870, SEQ ID NO:1871, SEQ ID NO:1872, SEQ ID NO:1873, SEQ ID NO:1874, SEQ ID NO:1875, SEQ ID NO:1876, SEQ ID NO:1877, SEQ ID NO:1878, SEQ ID NO:1879, SEQ ID NO:1880, SEQ ID NO:1881, SEQ ID NO:1882, SEQ ID NO:1883, SEQ ID NO:1884, SEQ ID NO:1885, SEQ ID NO:1886, SEQ ID NO:1887, SEQ ID NO:1888, SEQ ID NO:1889, SEQ ID NO:1890, SEQ ID NO:1891, SEQ ID NO:1892, SEQ ID NO:1893, SEQ ID NO:1894, SEQ ID NO:1895, SEQ ID NO:1896, SEQ ID NO:1897, SEQ ID NO:1898, SEQ ID NO:1899, SEQ ID NO:1900, SEQ ID NO:1901, SEQ ID NO:1902, SEQ ID NO:1903, SEQ ID NO:1904, SEQ ID NO:1905, SEQ ID NO:1906, SEQ ID NO:1907, SEQ ID NO:1908, SEQ ID NO:1909, SEQ ID NO:1910, SEQ ID NO:1911, SEQ ID NO:1912, SEQ ID NO:1913, SEQ ID NO:1914, SEQ ID NO:1915, SEQ ID NO:1916, SEQ ID NO:1917, SEQ ID NO:1918, SEQ ID NO:1919, SEQ ID NO:1920, SEQ ID NO:1921, SEQ ID NO:1922, SEQ ID NO:1923, SEQ ID NO:1924, SEQ ID NO:1925, SEQ ID NO:1926, SEQ ID NO:1927, SEQ ID NO:1928, SEQ ID NO:1929, SEQ ID NO:1930, SEQ ID NO:1931, SEQ ID NO:1932, SEQ ID NO:1933, SEQ ID NO:1934, SEQ ID NO:1935, SEQ ID NO:1936, SEQ ID NO:1937, SEQ ID NO:1938, SEQ ID NO:1939, SEQ ID NO:1940, SEQ ID NO:1941, SEQ ID NO:1942, SEQ ID NO:1943, SEQ ID NO:1944, SEQ ID NO:1945, SEQ ID NO:1946, SEQ ID NO:1947, SEQ ID NO:1948, SEQ ID NO:1949, SEQ ID NO:1950, SEQ ID NO:1951, SEQ ID NO:1952, SEQ ID NO:1953, SEQ ID NO:1954, SEQ ID NO:1955, SEQ ID NO:1956, SEQ ID NO:1957, SEQ ID NO:1958, SEQ ID NO:1959, SEQ ID

NO:1960, SEQ ID NO:1961, SEQ ID NO:1962, SEQ ID NO:1963, SEQ ID NO:1964, SEQ ID NO:1965, SEQ ID NO:1966, SEQ ID NO:1967, SEQ ID NO:1968, SEQ ID NO:1969, SEQ ID NO:1970, SEQ ID NO:1971, SEQ ID NO:1972, SEQ ID NO:1973, SEQ ID NO:1974, SEQ ID NO:1975, SEQ ID NO:1976, SEQ ID NO:1977, SEQ ID NO:1978, SEQ ID NO:1979, SEQ ID NO:1980, SEQ ID NO:1981, SEQ ID NO:1982, SEQ ID NO:1983, SEQ ID NO:1984, SEQ ID NO:1985, SEQ ID NO:1986, SEQ ID NO:1987, SEQ ID NO:1988, SEQ ID NO:1989, SEQ ID NO:1990, SEQ ID NO:1991, SEQ ID NO:1992, SEQ ID NO:1993, SEQ ID NO:1994, SEQ ID NO:1995, SEQ ID NO:1996, SEQ ID NO:1997, SEQ ID NO:1998, and SEQ ID NO:1999.

27. The composition according to any one of claims 1 to 20, wherein said at least a first isolated coding region comprises the amino acid sequence of any one of SEQ ID NO:2000, SEQ ID NO:2001, SEQ ID NO:2002, SEQ ID NO:2003, SEQ ID NO:2004, SEQ ID NO:2005, SEQ ID NO:2006, SEQ ID NO:2007, SEQ ID NO:2008, SEQ ID NO:2009, SEQ ID NO:2010, SEQ ID NO:2011, SEQ ID NO:2012, SEQ ID NO:2013, SEQ ID NO:2014, SEQ ID NO:2015, SEQ ID NO:2016, SEQ ID NO:2017, SEQ ID NO:2018, SEQ ID NO:2019, SEQ ID NO:2020, SEQ ID NO:2021, SEQ ID NO:2022, SEQ ID NO:2023, SEQ ID NO:2024, SEQ ID NO:2025, SEQ ID NO:2026, SEQ ID NO:2027, SEQ ID NO:2028, SEQ ID NO:2029, SEQ ID NO:2030, SEQ ID NO:2031, SEQ ID NO:2032, SEQ ID NO:2033, SEQ ID NO:2034, SEQ ID NO:2035, SEQ ID NO:2036, SEQ ID NO:2037, SEQ ID NO:2038, SEQ ID NO:2039, SEQ ID NO:2040, SEQ ID NO:2041, SEQ ID NO:2042, SEQ ID NO:2043, SEQ ID NO:2044, SEQ ID NO:2045, SEQ ID NO:2046, SEQ ID NO:2047, SEQ ID NO:2048, SEQ ID NO:2049, SEQ ID NO:2050, SEQ ID NO:2051, SEQ ID NO:2052, SEQ ID NO:2053, SEQ ID NO:2054, SEQ ID NO:2055, SEQ ID NO:2056, SEQ ID NO:2057, SEQ ID NO:2058, SEQ ID NO:2059, SEQ ID NO:2060, SEQ ID NO:2061, SEQ ID NO:2062, SEQ ID NO:2063, SEQ ID NO:2064, SEQ ID NO:2065, SEQ ID NO:2066, SEQ ID NO:2067, SEQ ID NO:2068, SEQ ID NO:2069, SEQ ID NO:2070, SEQ ID NO:2071, SEQ ID

NO:2072, SEQ ID NO:2073, SEQ ID NO:2074, SEQ ID NO:2075, SEQ ID NO:2076, SEQ ID NO:2077, SEQ ID NO:2078, SEQ ID NO:2079, SEQ ID NO:2080, SEQ ID NO:2081, SEQ ID NO:2082, SEQ ID NO:2083, SEQ ID NO:2084, SEQ ID NO:2085, SEQ ID NO:2086, SEQ ID NO:2087, SEQ ID NO:2088, SEQ ID NO:2089, SEQ ID NO:2090, SEQ ID NO:2091, SEQ ID NO:2092, SEQ ID NO:2093, SEQ ID NO:2094, SEQ ID NO:2095, SEQ ID NO:2096, SEQ ID NO:2097, SEQ ID NO:2098, SEQ ID NO:2099, SEQ ID NO:2100, SEQ ID NO:2101, SEQ ID NO:2102, SEQ ID NO:2103, SEQ ID NO:2104, and SEQ ID NO:2105.

28. The composition according to any one of claims 1 to 20, wherein said at least a first isolated coding region comprises the amino acid sequence of any one of SEQ ID NO:2106, SEQ ID NO:2107, SEQ ID NO:2108, SEQ ID NO:2109, SEQ ID NO:2110, SEQ ID NO:2111, SEQ ID NO:2112, SEQ ID NO:2113, SEQ ID NO:2114, SEQ ID NO:2115, SEQ ID NO:2116, SEQ ID NO:2117, SEQ ID NO:2118, SEQ ID NO:2119, SEQ ID NO:2120, SEQ ID NO:2121, SEQ ID NO:2122, SEQ ID NO:2123, SEQ ID NO:2124, SEQ ID NO:2125, SEQ ID NO:2126, SEQ ID NO:2127, SEQ ID NO:2128, SEQ ID NO:2129, SEQ ID NO:2130, SEQ ID NO:2131, SEQ ID NO:2132, SEQ ID NO:2133, SEQ ID NO:2134, SEQ ID NO:2135, SEQ ID NO:2136, SEQ ID NO:2137, SEQ ID NO:2138, SEQ ID NO:2139, SEQ ID NO:2140, SEQ ID NO:2141, SEQ ID NO:2142, SEQ ID NO:2143, SEQ ID NO:2144, SEQ ID NO:2145, SEQ ID NO:2146, SEQ ID NO:2147, SEQ ID NO:2148, SEQ ID NO:2149, SEQ ID NO:2150, SEQ ID NO:2151, SEQ ID NO:2152, SEQ ID NO:2153, SEQ ID NO:2154, SEQ ID NO:2155, SEQ ID NO:2156, SEQ ID NO:2157, SEQ ID NO:2158, SEQ ID NO:2159, SEQ ID NO:2160, SEQ ID NO:2161, SEQ ID NO:2162, SEQ ID NO:2163, SEQ ID NO:2164, SEQ ID NO:2165, SEQ ID NO:2166, SEQ ID NO:2167, SEQ ID NO:2168, SEQ ID NO:2169, SEQ ID NO:2170, SEQ ID NO:2171, SEQ ID NO:2172, SEQ ID NO:2173, SEQ ID NO:2174, SEQ ID NO:2175, SEQ ID NO:2176, SEQ ID NO:2177, SEQ ID NO:2178, SEQ ID NO:2179, SEQ ID NO:2180, SEQ ID NO:2181, SEQ ID

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29. The composition according to any one of claims 1 to 20, wherein said at least a first isolated coding region comprises the amino acid sequence of any one of SEQ ID NO:2300, SEQ ID NO:2301, SEQ ID NO:2302, SEQ ID NO:2303, SEQ ID NO:2304, SEQ ID NO:2305, SEQ ID NO:2306, SEQ ID NO:2307, SEQ ID NO:2308, SEQ ID NO:2309, SEQ ID NO:2310, SEQ ID NO:2311, SEQ ID NO:2312, SEQ ID NO:2313, SEQ ID NO:2314, SEQ ID NO:2315, SEQ ID NO:2316, SEQ ID NO:2317, SEQ ID NO:2318, SEQ ID NO:2319, SEQ ID NO:2320, SEQ ID NO:2321, SEQ ID NO:2322, SEQ ID NO:2323, SEQ ID NO:2324, SEQ ID NO:2325, SEQ ID NO:2326, SEQ ID NO:2327, SEQ ID NO:2328, SEQ ID NO:2329, SEQ ID NO:2330, SEQ ID NO:2331, SEQ ID NO:2332, SEQ ID NO:2333, SEQ ID NO:2334, SEQ ID NO:2335, SEQ ID NO:2336, SEQ ID NO:2337, SEQ ID NO:2338, SEQ ID NO:2339, SEQ ID NO:2340, SEQ ID NO:2341, SEQ ID NO:2342, SEQ ID NO:2343, SEQ ID NO:2344, SEQ ID NO:2345, SEQ ID NO:2346, SEQ ID NO:2347, SEQ ID NO:2348, SEQ ID NO:2349, SEQ ID NO:2350, SEQ ID NO:2351, SEQ ID NO:2352, SEQ ID NO:2353, SEQ ID NO:2354, SEQ ID NO:2355, SEQ ID NO:2356, SEQ ID NO:2357, SEQ ID NO:2358, SEQ ID NO:2359, SEQ ID NO:2360, SEQ ID NO:2361, SEQ ID NO:2362, SEQ ID NO:2363, SEQ ID NO:2364, SEQ ID NO:2365, SEQ ID NO:2366, SEQ ID NO:2367, SEQ ID NO:2368, SEQ ID NO:2369, SEQ ID NO:2370, SEQ ID NO:2371, SEQ ID NO:2372, SEQ ID NO:2373, SEQ ID NO:2374, and SEQ ID NO:2375.
30. The composition according to any one of claims 1 to 20, wherein said at least a first isolated coding region comprises the amino acid sequence of any one of SEQ ID NO:2376, SEQ ID NO:2377, SEQ ID NO:2378, SEQ ID NO:2379, SEQ ID NO:2380, SEQ ID NO:2381, SEQ ID NO:2382, SEQ ID NO:2383, SEQ ID NO:2384, SEQ ID NO:2385, SEQ ID NO:2386, SEQ ID NO:2387, SEQ ID NO:2388, SEQ ID NO:2389, SEQ ID NO:2390, SEQ ID NO:2391, SEQ ID NO:2392, SEQ ID NO:2393, SEQ ID NO:2394, SEQ ID NO:2395, SEQ ID NO:2396, SEQ ID NO:2397, SEQ ID NO:2398, SEQ ID NO:2399, SEQ ID NO:2400, SEQ ID NO:2401, SEQ ID NO:2402, SEQ ID NO:2403, SEQ ID

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NO:2520, SEQ ID NO:2521, SEQ ID NO:2522, SEQ ID NO:2523, SEQ ID
NO:2524, SEQ ID NO:2525, SEQ ID NO:2526, SEQ ID NO:2527, SEQ ID

NO:2528, SEQ ID NO:2529, SEQ ID NO:2530, SEQ ID NO:2531, and SEQ ID NO:2532.

31. The composition according to any preceding claim, wherein said at least a first isolated coding region comprises an amino acid sequence that is encoded by at least a first nucleic acid segment that comprises an at least 21 contiguous nucleotide sequence of any one of SEQ ID NO:1 to SEQ ID NO:668.
32. The composition according to any preceding claim, wherein said at least a first isolated coding region comprises an amino acid sequence that is encoded by at least a first nucleic acid segment that comprises an at least about 30 contiguous nucleotide sequence of any one of SEQ ID NO:1 to SEQ ID NO:668.
33. The composition according to any preceding claim, wherein said at least a first isolated coding region comprises an amino acid sequence that is encoded by at least a first nucleic acid segment that comprises an at least about 45 contiguous nucleotide sequence of any one of SEQ ID NO:1 to SEQ ID NO:668.
34. The composition according to any preceding claim, wherein said at least a first isolated coding region comprises an amino acid sequence that is encoded by at least a first nucleic acid segment that comprises an at least about 60 contiguous nucleotide sequence of any one of SEQ ID NO:1 to SEQ ID NO:668.
35. The composition according to any preceding claim, wherein said at least a first isolated coding region comprises an amino acid sequence that is encoded by at least a first nucleic acid segment that comprises an at least about 75 contiguous nucleotide sequence of any one of SEQ ID NO:1 to SEQ ID NO:668.

36. The composition according to any preceding claim, wherein said at least a first isolated coding region comprises an amino acid sequence that is encoded by at least a first nucleic acid segment that comprises an at least about 90 contiguous nucleotide sequence of any one of SEQ ID NO:1 to SEQ ID NO:668.
37. The composition according to any preceding claim, wherein said at least a first isolated coding region comprises an amino acid sequence that is encoded by at least a first nucleic acid segment that comprises an at least about 120 contiguous nucleotide sequence of any one of SEQ ID NO:1 to SEQ ID NO:278.
38. The composition according to any one of claims 1 to 36, wherein said at least a first isolated coding region comprises an amino acid sequence that is encoded by at least a first nucleic acid segment that comprises an at least about 120 contiguous nucleotide sequence of any one of SEQ ID NO:279 to SEQ ID NO:436.
39. The composition according to any one of claims 1 to 36, wherein said at least a first isolated coding region comprises an amino acid sequence that is encoded by at least a first nucleic acid segment that comprises an at least about 120 contiguous nucleotide sequence of any one of SEQ ID NO:437 to SEQ ID NO:528.
40. The composition according to any one of claims 1 to 36, wherein said at least a first isolated coding region comprises an amino acid sequence that is encoded by at least a first nucleic acid segment that comprises an at least about 120 contiguous nucleotide sequence of any one of SEQ ID NO:529 to SEQ ID NO:610.

41. The composition according to any one of claims 1 to 36, wherein said at least a first isolated coding region comprises an amino acid sequence that is encoded by at least a first nucleic acid segment that comprises an at least about 120 contiguous nucleotide sequence of any one of SEQ ID NO:611 to SEQ ID NO:664.
42. The composition according to any one of claims 1 to 36, wherein said at least a first isolated coding region comprises an amino acid sequence that is encoded by at least a first nucleic acid segment that comprises an at least about 120 contiguous nucleotide sequence of SEQ ID NO:665 or SEQ ID NO:666.
43. The composition according to any one of claims 1 to 36, wherein said at least a first isolated coding region comprises an amino acid sequence that is encoded by at least a first nucleic acid segment that comprises an at least about 120 contiguous nucleotide sequence of SEQ ID NO:667 or SEQ ID NO:668.
44. The composition according to any preceding claim, wherein said first at least a first isolated coding region comprises an amino acid sequence that is encoded by at least a first nucleic acid segment that comprises a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54,

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NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,
SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID

NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, SEQ ID NO:242, SEQ ID NO:243, SEQ ID NO:244, SEQ ID NO:245, SEQ ID NO:246, SEQ ID NO:247, SEQ ID NO:248, SEQ ID NO:249, SEQ ID NO:250, SEQ ID NO:251, SEQ ID NO:252, SEQ ID NO:253, SEQ ID NO:254, SEQ ID NO:255, SEQ ID NO:256, SEQ ID NO:257, SEQ ID NO:258, SEQ ID NO:259, SEQ ID NO:260, SEQ ID NO:261, SEQ ID NO:262, SEQ ID NO:263, SEQ ID NO:264, SEQ ID NO:265, SEQ ID NO:266, SEQ ID NO:267, SEQ ID NO:268, SEQ ID NO:269, SEQ ID NO:270, SEQ ID NO:271, SEQ ID NO:272, SEQ ID NO:273, SEQ ID NO:274, SEQ ID NO:275, SEQ ID NO:276, SEQ ID NO:277, and SEQ ID NO:278.

45. The composition according to any preceding claim, wherein said first at least a first isolated coding region comprises an amino acid sequence that is encoded by at least a first nucleic acid segment that comprises a nucleotide sequence selected from the group consisting of SEQ ID NO:279, SEQ ID NO:280, SEQ ID NO:281, SEQ ID NO:282, SEQ ID NO:283, SEQ ID NO:284, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:287, SEQ ID NO:288, SEQ ID NO:289, SEQ ID NO:290, SEQ ID NO:291, SEQ ID NO:292, SEQ ID NO:293, SEQ ID NO:294, SEQ ID NO:295, SEQ ID NO:296, SEQ ID NO:297, SEQ ID NO:298, SEQ ID NO:299, SEQ ID NO:300, SEQ ID NO:301, SEQ ID NO:302, SEQ ID NO:303, SEQ ID NO:304, SEQ ID NO:305, SEQ ID NO:306, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:309, SEQ ID NO:310, SEQ ID NO:311, SEQ ID NO:312, SEQ ID NO:313, SEQ ID NO:314, SEQ ID NO:315, SEQ ID NO:316, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:319, SEQ ID NO:320, SEQ ID NO:321, SEQ ID

NO:322, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:325, SEQ ID NO:326, SEQ ID NO:327, SEQ ID NO:328, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:331, SEQ ID NO:332, SEQ ID NO:333, SEQ ID NO:334, SEQ ID NO:335, SEQ ID NO:336, SEQ ID NO:337, SEQ ID NO:338, SEQ ID NO:339, SEQ ID NO:340, SEQ ID NO:341, SEQ ID NO:342, SEQ ID NO:343, SEQ ID NO:344, SEQ ID NO:345, SEQ ID NO:346, SEQ ID NO:347, SEQ ID NO:348, SEQ ID NO:349, SEQ ID NO:350, SEQ ID NO:351, SEQ ID NO:352, SEQ ID NO:353, SEQ ID NO:354, SEQ ID NO:355, SEQ ID NO:356, SEQ ID NO:357, SEQ ID NO:358, SEQ ID NO:359, SEQ ID NO:360, SEQ ID NO:361, SEQ ID NO:362, SEQ ID NO:363, SEQ ID NO:364, SEQ ID NO:365, SEQ ID NO:366, SEQ ID NO:367, SEQ ID NO:368, SEQ ID NO:369, SEQ ID NO:370, SEQ ID NO:371, SEQ ID NO:372, SEQ ID NO:373, SEQ ID NO:374, SEQ ID NO:375, SEQ ID NO:376, SEQ ID NO:377, SEQ ID NO:378, SEQ ID NO:379, SEQ ID NO:380, SEQ ID NO:381, SEQ ID NO:382, SEQ ID NO:383, SEQ ID NO:384, SEQ ID NO:385, SEQ ID NO:386, SEQ ID NO:387, SEQ ID NO:388, SEQ ID NO:389, SEQ ID NO:390, SEQ ID NO:391, SEQ ID NO:392, SEQ ID NO:393, SEQ ID NO:394, SEQ ID NO:395, SEQ ID NO:396, SEQ ID NO:397, SEQ ID NO:398, SEQ ID NO:399, SEQ ID NO:400, SEQ ID NO:401, SEQ ID NO:402, SEQ ID NO:403, SEQ ID NO:404, SEQ ID NO:405, SEQ ID NO:406, SEQ ID NO:407, SEQ ID NO:408, SEQ ID NO:409, SEQ ID NO:410, SEQ ID NO:411, SEQ ID NO:412, SEQ ID NO:413, SEQ ID NO:414, SEQ ID NO:415, SEQ ID NO:416, SEQ ID NO:417, SEQ ID NO:418, SEQ ID NO:419, SEQ ID NO:420, SEQ ID NO:421, SEQ ID NO:422, SEQ ID NO:423, SEQ ID NO:424, SEQ ID NO:425, SEQ ID NO:426, SEQ ID NO:427, SEQ ID NO:428, SEQ ID NO:429, SEQ ID NO:430, SEQ ID NO:431, SEQ ID NO:432, SEQ ID NO:433, SEQ ID NO:434, SEQ ID NO:435, and SEQ ID NO:436.

46. The composition according to any preceding claim, wherein said first at least a first isolated coding region comprises an amino acid sequence that is encoded by at least a first nucleic acid segment that comprises a nucleotide sequence selected from the group consisting of SEQ ID NO:437, SEQ ID NO:438, SEQ ID NO:439,

SEQ ID NO:440, SEQ ID NO:441, SEQ ID NO:442, SEQ ID NO:443, SEQ ID NO:444, SEQ ID NO:445, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:449, SEQ ID NO:450, SEQ ID NO:451, SEQ ID NO:452, SEQ ID NO:453, SEQ ID NO:454, SEQ ID NO:455, SEQ ID NO:456, SEQ ID NO:457, SEQ ID NO:458, SEQ ID NO:459, SEQ ID NO:460, SEQ ID NO:461, SEQ ID NO:462, SEQ ID NO:463, SEQ ID NO:464, SEQ ID NO:465, SEQ ID NO:466, SEQ ID NO:467, SEQ ID NO:468, SEQ ID NO:469, SEQ ID NO:470, SEQ ID NO:471, SEQ ID NO:472, SEQ ID NO:473, SEQ ID NO:474, SEQ ID NO:475, SEQ ID NO:476, SEQ ID NO:477, SEQ ID NO:478, SEQ ID NO:479, SEQ ID NO:480, SEQ ID NO:481, SEQ ID NO:482, SEQ ID NO:483, SEQ ID NO:484, SEQ ID NO:485, SEQ ID NO:486, SEQ ID NO:487, SEQ ID NO:488, SEQ ID NO:489, SEQ ID NO:490, SEQ ID NO:491, SEQ ID NO:492, SEQ ID NO:493, SEQ ID NO:494, SEQ ID NO:495, SEQ ID NO:496, SEQ ID NO:497, SEQ ID NO:498, SEQ ID NO:499, SEQ ID NO:500, SEQ ID NO:501, SEQ ID NO:502, SEQ ID NO:503, SEQ ID NO:504, SEQ ID NO:505, SEQ ID NO:506, SEQ ID NO:507, SEQ ID NO:508, SEQ ID NO:509, SEQ ID NO:510, SEQ ID NO:511, SEQ ID NO:512, SEQ ID NO:513, SEQ ID NO:514, SEQ ID NO:515, SEQ ID NO:516, SEQ ID NO:517, SEQ ID NO:518, SEQ ID NO:519, SEQ ID NO:520, SEQ ID NO:521, SEQ ID NO:522, SEQ ID NO:523, SEQ ID NO:524, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, and SEQ ID NO:528.

47. The composition according to any preceding claim, wherein said first at least a first isolated coding region comprises an amino acid sequence that is encoded by at least a first nucleic acid segment that comprises a nucleotide sequence selected from the group consisting of SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:540, SEQ ID NO:541, SEQ ID NO:542, SEQ ID NO:543, SEQ ID NO:544, SEQ ID NO:545, SEQ ID NO:546, SEQ ID NO:547, SEQ ID NO:548, SEQ ID NO:549, SEQ ID NO:550, SEQ ID NO:551, SEQ ID NO:552, SEQ ID NO:553, SEQ ID NO:554, SEQ ID NO:555, SEQ ID NO:556, SEQ ID NO:557, SEQ ID NO:558,

SEQ ID NO:559, SEQ ID NO:560, SEQ ID NO:561, SEQ ID NO:562, SEQ ID NO:563, SEQ ID NO:564, SEQ ID NO:565, SEQ ID NO:566, SEQ ID NO:567, SEQ ID NO:568, SEQ ID NO:569, SEQ ID NO:570, SEQ ID NO:571, SEQ ID NO:572, SEQ ID NO:573, SEQ ID NO:574, SEQ ID NO:575, SEQ ID NO:576, SEQ ID NO:577, SEQ ID NO:578, SEQ ID NO:579, SEQ ID NO:580, SEQ ID NO:581, SEQ ID NO:582, SEQ ID NO:583, SEQ ID NO:584, SEQ ID NO:585, SEQ ID NO:586, SEQ ID NO:587, SEQ ID NO:588, SEQ ID NO:589, SEQ ID NO:590, SEQ ID NO:591, SEQ ID NO:592, SEQ ID NO:593, SEQ ID NO:594, SEQ ID NO:595, SEQ ID NO:596, SEQ ID NO:597, SEQ ID NO:598, SEQ ID NO:599, SEQ ID NO:600, SEQ ID NO:601, SEQ ID NO:602, SEQ ID NO:603, SEQ ID NO:604, SEQ ID NO:605, SEQ ID NO:606, SEQ ID NO:607, SEQ ID NO:608, SEQ ID NO:609, and SEQ ID NO:610.

48. The composition according to any preceding claim, wherein said first at least a first isolated coding region comprises an amino acid sequence that is encoded by at least a first nucleic acid segment that comprises a nucleotide sequence selected from the group consisting of SEQ ID NO:611, SEQ ID NO:612, SEQ ID NO:613, SEQ ID NO:614, SEQ ID NO:615, SEQ ID NO:616, SEQ ID NO:617, SEQ ID NO:618, SEQ ID NO:619, SEQ ID NO:620, SEQ ID NO:621, SEQ ID NO:622, SEQ ID NO:623, SEQ ID NO:624, SEQ ID NO:625, SEQ ID NO:626, SEQ ID NO:627, SEQ ID NO:628, SEQ ID NO:629, SEQ ID NO:630, SEQ ID NO:631, SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:634, SEQ ID NO:635, SEQ ID NO:636, SEQ ID NO:637, SEQ ID NO:638, SEQ ID NO:639, SEQ ID NO:640, SEQ ID NO:641, SEQ ID NO:642, SEQ ID NO:643, SEQ ID NO:644, SEQ ID NO:645, SEQ ID NO:646, SEQ ID NO:647, SEQ ID NO:648, SEQ ID NO:649, SEQ ID NO:650, SEQ ID NO:651, SEQ ID NO:652, SEQ ID NO:653, SEQ ID NO:654, SEQ ID NO:655, SEQ ID NO:656, SEQ ID NO:657, SEQ ID NO:658, SEQ ID NO:659, SEQ ID NO:660, SEQ ID NO:661, SEQ ID NO:662, SEQ ID NO:663, and SEQ ID NO:664.

49. The composition according to any preceding claim, wherein said first at least a first isolated coding region comprises an amino acid sequence that is encoded by at least a first nucleic acid segment that comprises a nucleotide sequence selected from the group consisting of SEQ ID NO:665 and SEQ ID NO:666.
50. The composition according to any preceding claim, wherein said first at least a first isolated coding region comprises an amino acid sequence that is encoded by at least a first nucleic acid segment that comprises a nucleotide sequence selected from the group consisting of SEQ ID NO:667 and SEQ ID NO:668.
51. The composition according to any preceding claim, further comprising at least a second isolated peptide or polypeptide comprising at least a second isolated coding region that comprises an amino acid sequence that is at least about 91% identical to the amino acid sequence of any one of SEQ ID NO:669 to SEQ ID NO:2532.
52. The composition according to any preceding claim, further comprising at least a second isolated peptide or polypeptide comprising at least a second isolated coding region that comprises an amino acid sequence that is at least about 93% identical to the amino acid sequence of any one of SEQ ID NO:669 to SEQ ID NO:2532.
53. The composition according to any preceding claim, further comprising at least a second isolated peptide or polypeptide comprising at least a second isolated coding region that comprises an amino acid sequence that is at least about 95% identical to the amino acid sequence of any one of SEQ ID NO:669 to SEQ ID NO:2532.
54. The composition according to any preceding claim, further comprising at least a second isolated peptide or polypeptide comprising at least a second isolated coding

region that comprises an amino acid sequence that is at least about 97% identical to the amino acid sequence of any one of SEQ ID NO:669 to SEQ ID NO:2532.

55. The composition according to any preceding claim, further comprising at least a second isolated peptide or polypeptide comprising at least a second isolated coding region that comprises an amino acid sequence that is at least about 99% identical to the amino acid sequence of any one of SEQ ID NO:669 to SEQ ID NO:2532.
56. A composition comprising at least a first hybridoma cell line that produces a monoclonal antibody having immunospecificity for a peptide or polypeptide as defined in any one of claims 1 to 55.
57. A composition comprising at least a first monoclonal antibody, or an antigen-binding fragment thereof, that has immunospecificity for a peptide or polypeptide as defined in any one of claims 1 to 55.
58. The composition according to claim 57, comprising a light chain variable region, a heavy-chain variable region, a Fab fragment, a F(ab)₂ fragment, an Fv fragment, an scFv fragment, or an antigen-binding fragment of said antibody.
59. A composition comprising at least a first isolated antigen-presenting cell that expresses a peptide or polypeptide as defined in any one of claims 1 to 55.
60. A composition comprising a plurality of isolated T cells that specifically react with a peptide or polypeptide as defined in any one of claims 1 to 55.

61. The composition according to claim 60, wherein said plurality of isolated T cells is stimulated or expanded by contacting said T cells with a peptide or polypeptide as defined in any one of claims 1 to 55.
62. The composition according to claim 60 or claim 61, wherein said plurality of isolated T cells is cloned prior to expansion.
63. The composition according to any one of claims 60 to 62, wherein said plurality of isolated T cells is obtained from bone marrow, a bone marrow fraction, peripheral blood, or a peripheral blood fraction.
64. The composition according to any one of claims 60 to 63, wherein said bone marrow, bone marrow fraction, peripheral blood, or peripheral blood fraction is obtained from a mammal that is afflicted with at least a first hematological malignancy.
65. The composition according to any one of claims 60 to 64, wherein said bone marrow, bone marrow fraction, peripheral blood, or peripheral blood fraction is obtained from a mammal that is not afflicted with a hematological malignancy.
66. A composition comprising: (a) at least a first isolated polynucleotide that comprises at least a first isolated nucleic acid segment that encodes (i) at least a first peptide or polypeptide as defined in any one of claims 1 to 48, or (ii) an antibody or antigen binding fragment as defined in claim 50 or claim 51; or (b) at least a first isolated polynucleotide that comprises at least a first nucleic acid segment that comprises an at least 21 contiguous nucleotide sequence according to any one of SEQ ID NO:1 to SEQ ID NO:668.

67. The composition according to claim 66, comprising at least a first isolated polynucleotide that comprises at least a first nucleic acid segment that encodes (a) a peptide or polypeptide as defined in any one of claims 1 to 55, or (b) an antibody or antigen binding fragment as defined in claim 57 or claim 58.
68. The composition according to claim 66, comprising at least a first isolated polynucleotide comprising at least a first isolated nucleic acid segment that comprises at least 30 contiguous nucleotides from any one of SEQ ID NO:1 to SEQ ID NO:668.
69. The composition according to claim 68, comprising at least a first isolated polynucleotide comprising at least a first isolated nucleic acid segment that comprises at least 45 contiguous nucleotides from any one of SEQ ID NO:1 to SEQ ID NO:668.
70. The composition according to claim 68 or claim 69, comprising at least a first isolated polynucleotide comprising at least a first isolated nucleic acid segment that comprises at least 60 contiguous nucleotides from any one of SEQ ID NO:1 to SEQ ID NO:668.
71. The composition according to any one of claims 68 to 70, comprising at least a first isolated polynucleotide comprising at least a first isolated nucleic acid segment that comprises at least 75 contiguous nucleotides from any one of SEQ ID NO:1 to SEQ ID NO:668.

72. The composition according to any one of claims 68 to 71, comprising at least a first isolated polynucleotide comprising at least a first isolated nucleic acid segment that comprises at least 90 contiguous nucleotides from any one of SEQ ID NO:1 to SEQ ID NO:668.
73. The composition according to any one of claims 68 to 72, comprising at least a first isolated polynucleotide comprising at least a first isolated nucleic acid segment that comprises at least 120 contiguous nucleotides from any one of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID

NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, SEQ ID NO:242, SEQ ID NO:243, SEQ ID NO:244, SEQ ID NO:245, SEQ ID NO:246, SEQ ID NO:247, SEQ ID NO:248, SEQ ID NO:249, SEQ ID NO:250, SEQ ID NO:251, SEQ ID NO:252, SEQ ID NO:253, SEQ ID NO:254, SEQ ID NO:255, SEQ ID NO:256, SEQ ID NO:257, SEQ ID NO:258, SEQ ID

NO:259, SEQ ID NO:260, SEQ ID NO:261, SEQ ID NO:262, SEQ ID NO:263, SEQ ID NO:264, SEQ ID NO:265, SEQ ID NO:266, SEQ ID NO:267, SEQ ID NO:268, SEQ ID NO:269, SEQ ID NO:270, SEQ ID NO:271, SEQ ID NO:272, SEQ ID NO:273, SEQ ID NO:274, SEQ ID NO:275, SEQ ID NO:276, SEQ ID NO:277, and SEQ ID NO:278.

74. The composition according to any one of claims 68 to 72, comprising at least a first isolated polynucleotide comprising at least a first isolated nucleic acid segment that comprises at least 120 contiguous nucleotides from any one of SEQ ID NO:279, SEQ ID NO:280, SEQ ID NO:281, SEQ ID NO:282, SEQ ID NO:283, SEQ ID NO:284, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:287, SEQ ID NO:288, SEQ ID NO:289, SEQ ID NO:290, SEQ ID NO:291, SEQ ID NO:292, SEQ ID NO:293, SEQ ID NO:294, SEQ ID NO:295, SEQ ID NO:296, SEQ ID NO:297, SEQ ID NO:298, SEQ ID NO:299, SEQ ID NO:300, SEQ ID NO:301, SEQ ID NO:302, SEQ ID NO:303, SEQ ID NO:304, SEQ ID NO:305, SEQ ID NO:306, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:309, SEQ ID NO:310, SEQ ID NO:311, SEQ ID NO:312, SEQ ID NO:313, SEQ ID NO:314, SEQ ID NO:315, SEQ ID NO:316, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:319, SEQ ID NO:320, SEQ ID NO:321, SEQ ID NO:322, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:325, SEQ ID NO:326, SEQ ID NO:327, SEQ ID NO:328, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:331, SEQ ID NO:332, SEQ ID NO:333, SEQ ID NO:334, SEQ ID NO:335, SEQ ID NO:336, SEQ ID NO:337, SEQ ID NO:338, SEQ ID NO:339, SEQ ID NO:340, SEQ ID NO:341, SEQ ID NO:342, SEQ ID NO:343, SEQ ID NO:344, SEQ ID NO:345, SEQ ID NO:346, SEQ ID NO:347, SEQ ID NO:348, SEQ ID NO:349, SEQ ID NO:350, SEQ ID NO:351, SEQ ID NO:352, SEQ ID NO:353, SEQ ID NO:354, SEQ ID NO:355, SEQ ID NO:356, SEQ ID NO:357, SEQ ID NO:358, SEQ ID NO:359, SEQ ID NO:360, SEQ ID NO:361, SEQ ID NO:362, SEQ ID NO:363, SEQ ID NO:364, SEQ ID NO:365, SEQ ID NO:366, SEQ ID NO:367, SEQ ID NO:368, SEQ ID NO:369, SEQ ID NO:370, SEQ ID NO:371, SEQ ID NO:372, SEQ ID NO:373, SEQ ID NO:374, SEQ ID NO:375, SEQ ID NO:376, SEQ ID NO:377, SEQ ID

NO:378, SEQ ID NO:379, SEQ ID NO:380, SEQ ID NO:381, SEQ ID NO:382, SEQ ID NO:383, SEQ ID NO:384, SEQ ID NO:385, SEQ ID NO:386, SEQ ID NO:387, SEQ ID NO:388, SEQ ID NO:389, SEQ ID NO:390, SEQ ID NO:391, SEQ ID NO:392, SEQ ID NO:393, SEQ ID NO:394, SEQ ID NO:395, SEQ ID NO:396, SEQ ID NO:397, SEQ ID NO:398, SEQ ID NO:399, SEQ ID NO:400, SEQ ID NO:401, SEQ ID NO:402, SEQ ID NO:403, SEQ ID NO:404, SEQ ID NO:405, SEQ ID NO:406, SEQ ID NO:407, SEQ ID NO:408, SEQ ID NO:409, SEQ ID NO:410, SEQ ID NO:411, SEQ ID NO:412, SEQ ID NO:413, SEQ ID NO:414, SEQ ID NO:415, SEQ ID NO:416, SEQ ID NO:417, SEQ ID NO:418, SEQ ID NO:419, SEQ ID NO:420, SEQ ID NO:421, SEQ ID NO:422, SEQ ID NO:423, SEQ ID NO:424, SEQ ID NO:425, SEQ ID NO:426, SEQ ID NO:427, SEQ ID NO:428, SEQ ID NO:429, SEQ ID NO:430, SEQ ID NO:431, SEQ ID NO:432, SEQ ID NO:433, SEQ ID NO:434, SEQ ID NO:435, and SEQ ID NO:436.

75. The composition according to any one of claims 68 to 72, comprising at least a first isolated polynucleotide comprising at least a first isolated nucleic acid segment that comprises at least 120 contiguous nucleotides from any one of SEQ ID NO:437, SEQ ID NO:438, SEQ ID NO:439, SEQ ID NO:440, SEQ ID NO:441, SEQ ID NO:442, SEQ ID NO:443, SEQ ID NO:444, SEQ ID NO:445, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:449, SEQ ID NO:450, SEQ ID NO:451, SEQ ID NO:452, SEQ ID NO:453, SEQ ID NO:454, SEQ ID NO:455, SEQ ID NO:456, SEQ ID NO:457, SEQ ID NO:458, SEQ ID NO:459, SEQ ID NO:460, SEQ ID NO:461, SEQ ID NO:462, SEQ ID NO:463, SEQ ID NO:464, SEQ ID NO:465, SEQ ID NO:466, SEQ ID NO:467, SEQ ID NO:468, SEQ ID NO:469, SEQ ID NO:470, SEQ ID NO:471, SEQ ID NO:472, SEQ ID NO:473, SEQ ID NO:474, SEQ ID NO:475, SEQ ID NO:476, SEQ ID NO:477, SEQ ID NO:478, SEQ ID NO:479, SEQ ID NO:480, SEQ ID NO:481, SEQ ID NO:482, SEQ ID NO:483, SEQ ID NO:484, SEQ ID NO:485, SEQ ID NO:486, SEQ ID NO:487, SEQ ID NO:488, SEQ ID NO:489, SEQ ID NO:490, SEQ ID NO:491, SEQ ID NO:492, SEQ ID NO:493, SEQ ID NO:494, SEQ ID NO:495,

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76. The composition according to any one of claims 68 to 72, comprising at least a first isolated polynucleotide comprising at least a first isolated nucleic acid segment that comprises at least 120 contiguous nucleotides from any one of SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:540, SEQ ID NO:541, SEQ ID NO:542, SEQ ID NO:543, SEQ ID NO:544, SEQ ID NO:545, SEQ ID NO:546, SEQ ID NO:547, SEQ ID NO:548, SEQ ID NO:549, SEQ ID NO:550, SEQ ID NO:551, SEQ ID NO:552, SEQ ID NO:553, SEQ ID NO:554, SEQ ID NO:555, SEQ ID NO:556, SEQ ID NO:557, SEQ ID NO:558, SEQ ID NO:559, SEQ ID NO:560, SEQ ID NO:561, SEQ ID NO:562, SEQ ID NO:563, SEQ ID NO:564, SEQ ID NO:565, SEQ ID NO:566, SEQ ID NO:567, SEQ ID NO:568, SEQ ID NO:569, SEQ ID NO:570, SEQ ID NO:571, SEQ ID NO:572, SEQ ID NO:573, SEQ ID NO:574, SEQ ID NO:575, SEQ ID NO:576, SEQ ID NO:577, SEQ ID NO:578, SEQ ID NO:579, SEQ ID NO:580, SEQ ID NO:581, SEQ ID NO:582, SEQ ID NO:583, SEQ ID NO:584, SEQ ID NO:585, SEQ ID NO:586, SEQ ID NO:587, SEQ ID NO:588, SEQ ID NO:589, SEQ ID NO:590, SEQ ID NO:591, SEQ ID NO:592, SEQ ID NO:593, SEQ ID NO:594, SEQ ID NO:595, SEQ ID NO:596, SEQ ID NO:597, SEQ ID NO:598, SEQ ID NO:599, SEQ ID NO:600, SEQ ID NO:601, SEQ ID NO:602, SEQ ID NO:603, SEQ ID NO:604, SEQ ID NO:605, SEQ ID NO:606, SEQ ID NO:607, SEQ ID NO:608, SEQ ID NO:609, and SEQ ID NO:610.

77. The composition according to any one of claims 68 to 72, comprising at least a first isolated polynucleotide comprising at least a first isolated nucleic acid segment that comprises at least 120 contiguous nucleotides from any one of SEQ ID NO:611, SEQ ID NO:612, SEQ ID NO:613, SEQ ID NO:614, SEQ ID NO:615, SEQ ID NO:616, SEQ ID NO:617, SEQ ID NO:618, SEQ ID NO:619, SEQ ID NO:620, SEQ ID NO:621, SEQ ID NO:622, SEQ ID NO:623, SEQ ID NO:624, SEQ ID NO:625, SEQ ID NO:626, SEQ ID NO:627, SEQ ID NO:628, SEQ ID NO:629, SEQ ID NO:630, SEQ ID NO:631, SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:634, SEQ ID NO:635, SEQ ID NO:636, SEQ ID NO:637, SEQ ID NO:638, SEQ ID NO:639, SEQ ID NO:640, SEQ ID NO:641, SEQ ID NO:642, SEQ ID NO:643, SEQ ID NO:644, SEQ ID NO:645, SEQ ID NO:646, SEQ ID NO:647, SEQ ID NO:648, SEQ ID NO:649, SEQ ID NO:650, SEQ ID NO:651, SEQ ID NO:652, SEQ ID NO:653, SEQ ID NO:654, SEQ ID NO:655, SEQ ID NO:656, SEQ ID NO:657, SEQ ID NO:658, SEQ ID NO:659, SEQ ID NO:660, SEQ ID NO:661, SEQ ID NO:662, SEQ ID NO:663, and SEQ ID NO:664.
78. The composition according to any one of claims 68 to 72, comprising at least a first isolated polynucleotide comprising at least a first isolated nucleic acid segment that comprises at least 120 contiguous nucleotides from SEQ ID NO:665 or SEQ ID NO:666.
79. The composition according to any one of claims 68 to 72, comprising at least a first isolated polynucleotide comprising at least a first isolated nucleic acid segment that comprises at least 120 contiguous nucleotides from SEQ ID NO:667 or SEQ ID NO:668.

80. The composition according to any preceding claim, wherein said isolated coding region is from 25 to about 1000 amino acids in length, or said nucleic acid segment is from 50 to about 10,000 nucleotides in length.
81. The composition according to any preceding claim, wherein said isolated coding region is from 50 to about 900 amino acids in length, or said nucleic acid segment is from 150 to about 8000 nucleotides in length.
82. The composition according to any preceding claim, wherein said isolated coding region is from 75 to about 800 amino acids in length, or said nucleic acid segment is from 250 to about 6000 nucleotides in length.
83. The composition according to any preceding claim, wherein said isolated coding region is from 100 to about 700 amino acids in length, or said nucleic acid segment is from 350 to about 4000 nucleotides in length.
84. The composition according to any preceding claim, wherein said isolated coding region is from 125 to about 600 amino acids in length, or said nucleic acid segment is from 450 to about 2000 nucleotides in length.
85. The composition according to any preceding claim, wherein said nucleic acid segment is operably positioned under the control of at least a first heterologous promoter.
86. The composition according to any preceding claim, wherein said nucleic acid segment is comprised within a vector.

87. The composition according to any preceding claim, wherein said nucleic acid segment is comprised within a plasmid or viral vector.
88. The composition according to any preceding claim, wherein said polypeptide or said polynucleotide is comprised within a host cell.
89. The composition according to any preceding claim, wherein said polypeptide or said polynucleotide is comprised within a human blood or bone marrow cell.
90. The composition according to any preceding claim, wherein said first isolated polynucleotide further comprises at least a second isolated nucleic acid segment that encodes a second peptide or polypeptide.
91. The composition according to claim 90, wherein said at least a first isolated polynucleotide comprises at least a first isolated nucleic acid segment is operably attached, in frame, to said at least a second isolated nucleic acid segment, and wherein said first isolated polynucleotide encodes a fusion protein in which said first peptide or polypeptide is linked to said peptide or polypeptide.
92. The composition according to claim 90, wherein said at least a second isolated nucleic acid segment encodes a second distinct peptide or polypeptide.
93. The composition according to claim 92, wherein said at least a second isolated nucleic acid segment encodes an adjuvant peptide or polypeptide.

94. The composition according to any preceding claim, further comprising at least a second isolated peptide or polypeptide, or at least a second isolated polynucleotide that encodes said second isolated peptide or polypeptide.
95. The composition according to claim 94, wherein said at least a second isolated peptide or polypeptide, comprises a first adjuvant polypeptide, a first fusion protein, a first detectable protein, or at least a second distinct peptide or polypeptide as defined in any one of claims 1 to 55, or wherein said second isolated polynucleotide encodes said first adjuvant polypeptide, said first fusion protein, said first detectable protein, or said second distinct peptide or polypeptide.
96. The composition according to any preceding claim, further comprising at least a third isolated peptide or polypeptide, or at least a third isolated polynucleotide that encodes said third isolated peptide or polypeptide.
97. The composition according to any preceding claim, further comprising a pharmaceutically acceptable excipient.
98. The composition according to any preceding claim, wherein said composition is formulated for parenteral, intravenous, intraarterial, intraosseus, intrathecal, intraperitoneal, subcutaneous, intranasal, transdermal, sublingual, or oral administration.
99. The composition according to any preceding claim, further comprising at least a first immunostimulant or at least a first adjuvant.

100. The composition according to any preceding claim, further comprising at least a first immunostimulant or at least a first adjuvant that preferentially enhances a T-cell response in a human.
101. The composition according to any preceding claim, further comprising at least a first immunostimulant or at least a first adjuvant selected from the group consisting of Montanide ISA50, Seppic Montanide ISA720, a cytokine, a microsphere, a dimethyl dioctadecyl ammonium bromide adjuvant, AS-1, AS-2, Ribi Adjuvant, QS21, saponin, microfluidized Syntex adjuvant, MV, ddMV, an immune stimulating complex and an inactivated toxin.
102. The composition according to any preceding claim, further comprising at least a first detection reagent.
103. The composition according to any preceding claim, for use in detecting a hematological malignancy in a blood or bone marrow cell.
104. The composition according to any preceding claim, for use in detecting cancer in a human.
105. The composition according to any preceding claim, for use in detecting cancer in a human having, suspected of having, or at risk for developing at least a first hematological malignancy in a blood or bone marrow cell.
106. The composition according to any preceding claim for use in diagnosis or prognosis.

107. The composition according to any preceding claim for use in diagnosis or prognosis of a hematological malignancy in an animal.
108. The composition according to any preceding claim for use in diagnosis or prognosis of a hematological malignancy selected from the group consisting of chronic lymphocytic leukemia, lymphoma, follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma, T cell non-Hodgkin's lymphoma, and B cell non-Hodgkin's lymphoma.
109. The composition according to any preceding claim, for use in the diagnosis or prognosis of a hematological malignancy selected from the group consisting of Hodgkin's lymphoma, follicular lymphoma, B cell non-Hodgkin's lymphoma, T cell non-Hodgkin's lymphoma, lymphoma and chronic lymphocytic leukemia in a human having, suspected of having, or at risk for developing said hematological malignancy.
110. The composition according to any preceding claim, for use in generating an immune response in an animal.
111. The composition according to any preceding claim, for use in generating a T-cell response in an animal.
112. The composition according to any preceding claim for use in therapy.

113. The composition according to any preceding claim for use in therapy of a hematological malignancy in an animal.
114. The composition according to any preceding claim for use in therapy of a hematological malignancy selected from the group consisting of Hodgkin's lymphoma, follicular lymphoma, B cell non-Hodgkin's lymphoma, T cell non-Hodgkin's lymphoma, lymphoma and chronic lymphocytic leukemia in a human having, suspected of having, or at risk for developing said hematological malignancy.
115. The composition according to any preceding claim, further comprising at least a second therapeutic, diagnostic, prognostic, or detection agent.
116. The composition according to any one of claims 16, 21, 22, 23, 37, 43, 44, 50, 73, or 79, for use in detection, diagnosis, prognosis, or therapy of Hodgkin's lymphoma.
117. The composition according to any one of claims 17, 24, 25, 38, 45, or 74 for use in detection, diagnosis, prognosis, or therapy of follicular lymphoma.
118. The composition according to any one of claims 18, 26, 27, 39, 42, 43, 46, 49, 50, 75, 78, or 79, for use in detection, diagnosis, prognosis, or therapy of B cell non-Hodgkin's lymphoma.
119. The composition according to any one of claims 19, 28, 29, 40, 42, 47, 49, 76, or 78, for use in detection, diagnosis, prognosis, or therapy of T cell non-Hodgkin's lymphoma.

120. The composition according to any one of claims 20, 30, 41, 48, or 77, for use in detection, diagnosis, prognosis, or therapy of lymphoma.
121. The composition according to any one of claims 42, 49, or 78, for use in detection, diagnosis, prognosis, or therapy of chronic lymphocytic leukemia.
122. Use of a composition in accordance with any preceding claim, in the manufacture of a medicament for treating or preventing a hematological malignancy in an animal.
123. Use according to claim 121, in the manufacture of a medicament for treating or preventing a hematological malignancy selected from the group consisting of Hodgkin's lymphoma, follicular lymphoma, B cell non-Hodgkin's lymphoma, T cell non-Hodgkin's lymphoma, lymphoma, and chronic lymphocytic leukemia in an animal.
124. Use according to any one of claims 121 to 123, in the manufacture of a medicament intended for administration to a human patient having, suspected of having, or at risk for developing a hematological malignancy selected from the group consisting of Hodgkin's lymphoma, follicular lymphoma, B cell non-Hodgkin's lymphoma, T cell non-Hodgkin's lymphoma, lymphoma, and chronic lymphocytic leukemia.
125. Use according to any one of claims 121 to 124, wherein said medicament is intended for generating a T-cell response or an immune response in an animal.

126. Use according to any one of claims 121 to 125, wherein said medicament is formulated for parenteral, intravenous, intraarterial, intraosseus, intrathecal, intraperitoneal, subcutaneous, intranasal, transdermal, sublingual, or oral administration.
127. A kit comprising a composition in accordance with any one of claims 1 to 120, and instructions for using said kit.
128. The kit according to claim 127, comprising a therapeutically-effective amount of a composition in accordance with any one of claims 1 to 120.
129. The kit according to claim 127 or claim 128, wherein said kit further comprises at least a first diagnostic reagent.
130. The kit according to any one of claims 127 to 129, wherein said kit further comprises a therapeutically effective amount of at least a second therapeutic agent.
131. The kit according to claim 130, wherein said second therapeutic agent comprises at least a first anti-cancer agent.
132. The kit according to any one of claims 127 to 131, wherein said kit further comprises an effective amount of at least a first diagnostic reagent that detects (a) a peptide or polypeptide as defined in any one of claims 1 to 48, or (b) a polynucleotide as defined in any one of claims 59 to 101, or (c) an antibody having immunospecificity for said peptide or polypeptide, or an antigen binding fragment thereof.

133. A method of generating an immune response in an animal, comprising providing to said animal an effective amount of a composition in accordance with any one of claims 1 to 120.
134. A method of generating a T-cell response in an animal, comprising providing to said animal an effective amount of a composition in accordance with any one of claims 1 to 120.
135. The method according to claim 133 or claim 134, wherein said animal is a human.
136. The method according to any one of claims 133 to 135, wherein said human has, is suspected of having, or is at risk for developing a hematological malignancy selected from the group consisting of Hodgkin's lymphoma, follicular lymphoma, B cell non-Hodgkin's lymphoma, T cell non-Hodgkin's lymphoma, lymphoma, and chronic lymphocytic leukemia.
137. The method according to any one of claims 133 to 136, wherein an effective amount of at least a second diagnostic or therapeutic agent is administered to said human.
138. The method according to claim 137, wherein said second diagnostic or therapeutic agent comprises a composition in accordance with any one of claims 1 to 120.
139. The method according to any one of claims 133 to 138, wherein an effective amount of at least a third diagnostic or therapeutic agent is administered to said human.

140. A method of assessing the risk of a human patient in developing a hematological malignancy selected from the group consisting of Hodgkin's lymphoma, follicular lymphoma, B cell non-Hodgkin's lymphoma, T cell non-Hodgkin's lymphoma, lymphoma; and chronic lymphocytic leukemia, said method comprising detecting the presence of a peptide or polypeptide as defined in any one of claims 1 to 48, or a polynucleotide as defined in any one of claims 59 to 101 in a clinical sample obtained from said patient, wherein an increased level of said peptide or said polypeptide, relative to an unaffected human is indicative of an increased risk for developing said hematological malignancy.
141. A method of detecting a Hodgkin's lymphoma hematological malignancy-related polypeptide, polynucleotide, antibody, or an antigen binding fragment thereof, or in a biological sample or an animal cell said method comprising, contacting a sample or a cell suspected of containing a Hodgkin's lymphoma hematological malignancy with a labeled composition according to any one of claims 16, 21, 22, 23, 37, 43, 44, 50, 73, or 79, under conditions effective and for a time sufficient to allow immunocomplexes or specific hybridization complexes to form, wherein the presence of labeled immunocomplexes or labeled hybridization complexes is indicative of the presence of said Hodgkin's lymphoma hematological malignancy-related polypeptide, polynucleotide, antibody, or antigen binding fragment in said sample or said cell.
142. A method of detecting a follicular lymphoma hematological malignancy-related polypeptide, polynucleotide, antibody, or an antigen binding fragment thereof, or in a biological sample or an animal cell said method comprising, contacting a sample or a cell suspected of containing a follicular lymphoma hematological malignancy with a labeled composition according to any one of claims 17, 24, 25, 38, 45, or 74, under conditions effective and for a time sufficient to allow immunocomplexes or specific hybridization complexes to form, wherein the presence of labeled immunocomplexes

or labeled hybridization complexes is indicative of the presence of said follicular lymphoma hematological malignancy-related polypeptide, polynucleotide, antibody, or antigen binding fragment in said sample or said cell.

143. A method of detecting a B cell non-Hodgkin's lymphoma hematological malignancy-related polypeptide, polynucleotide, antibody, or an antigen binding fragment thereof, or in a biological sample or an animal cell said method comprising, contacting a sample or a cell suspected of containing a B cell non-Hodgkin's lymphoma hematological malignancy with a labeled composition according to any one of claims 18, 26, 27, 39, 42, 43, 46, 49, 50, 75, 78, or 79, under conditions effective and for a time sufficient to allow immunocomplexes or specific hybridization complexes to form, wherein the presence of labeled immunocomplexes or labeled hybridization complexes is indicative of the presence of said B cell non-Hodgkin's lymphoma hematological malignancy-related polypeptide, polynucleotide, antibody, or antigen binding fragment in said sample or said cell.
144. A method of detecting a T cell non-Hodgkin's lymphoma hematological malignancy-related polypeptide, polynucleotide, antibody, or an antigen binding fragment thereof, or in a biological sample or an animal cell said method comprising, contacting a sample or a cell suspected of containing a T cell non-Hodgkin's lymphoma hematological malignancy with: a labeled composition according to any one of claims 19, 28, 29, 40, 42, 47, 49, 76, or 78, under conditions effective and for a time sufficient to allow immunocomplexes or specific hybridization complexes to form, wherein the presence of labeled immunocomplexes or labeled hybridization complexes is indicative of the presence of said T cell non-Hodgkin's lymphoma hematological malignancy-related polypeptide, polynucleotide, antibody, or antigen binding fragment in said sample or said cell.

145. A method of detecting a lymphoma-related malignancy polypeptide, polynucleotide, antibody, or an antigen binding fragment thereof, or in a biological sample or an animal cell said method comprising, contacting a sample or a cell suspected of containing a lymphoma-related malignancy with a labeled composition according to any one of claims 20, 30, 41, 48, or 77, under conditions effective and for a time sufficient to allow immunocomplexes or specific hybridization complexes to form, wherein the presence of labeled immunocomplexes or labeled hybridization complexes is indicative of the presence of said lymphoma-related malignancy-related polypeptide, polynucleotide, antibody, or antigen binding fragment in said sample or said cell.

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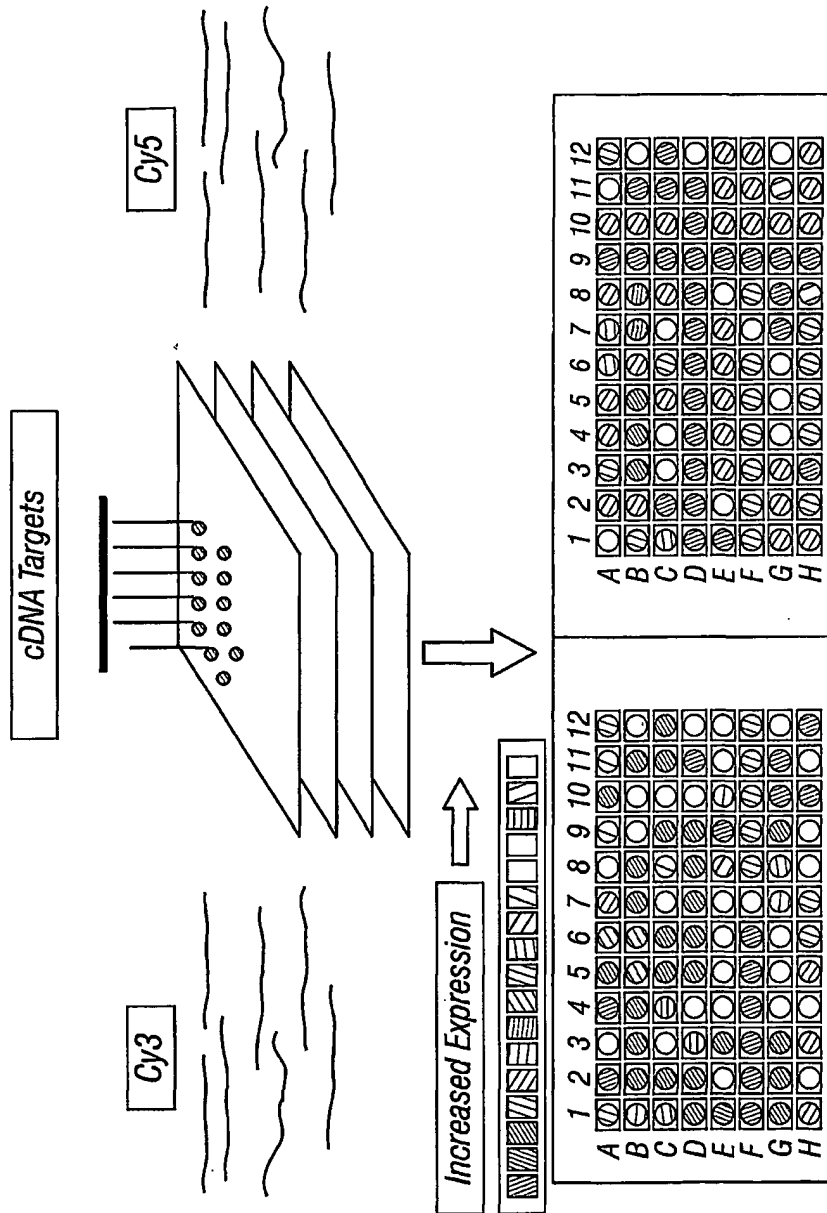


FIG. 1

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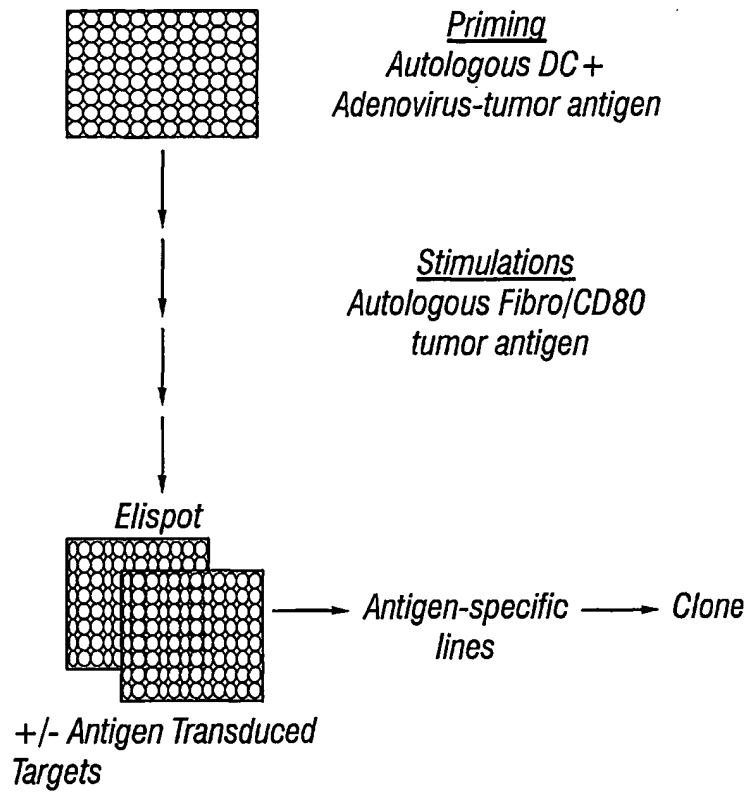


FIG. 2

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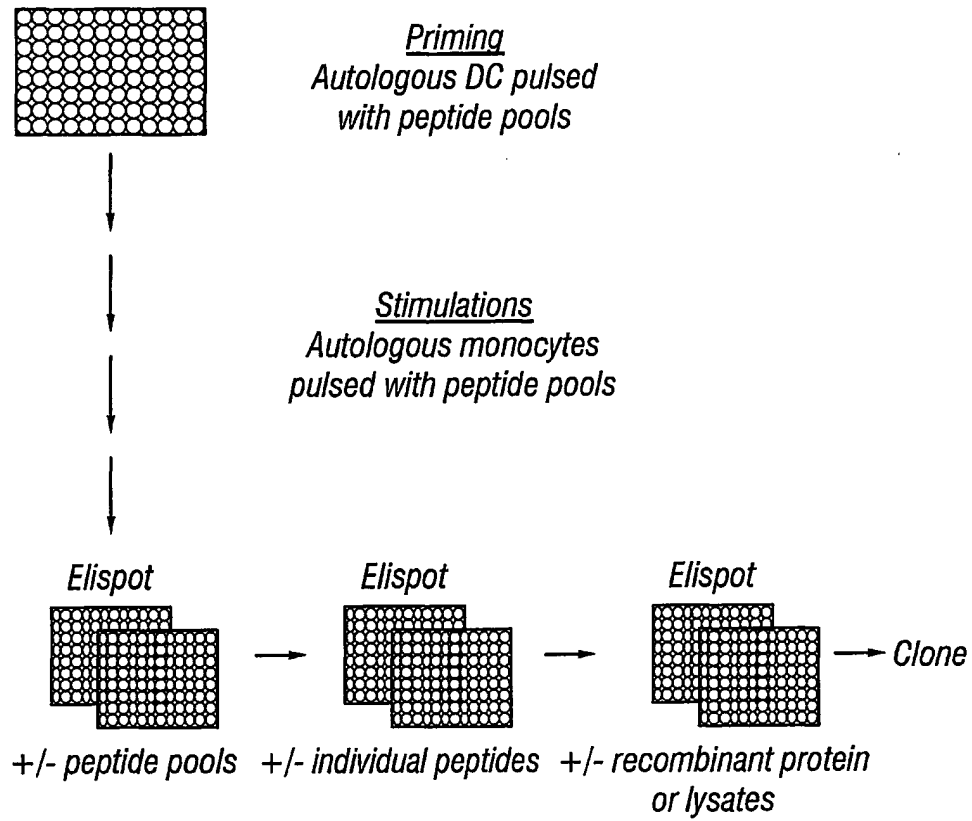
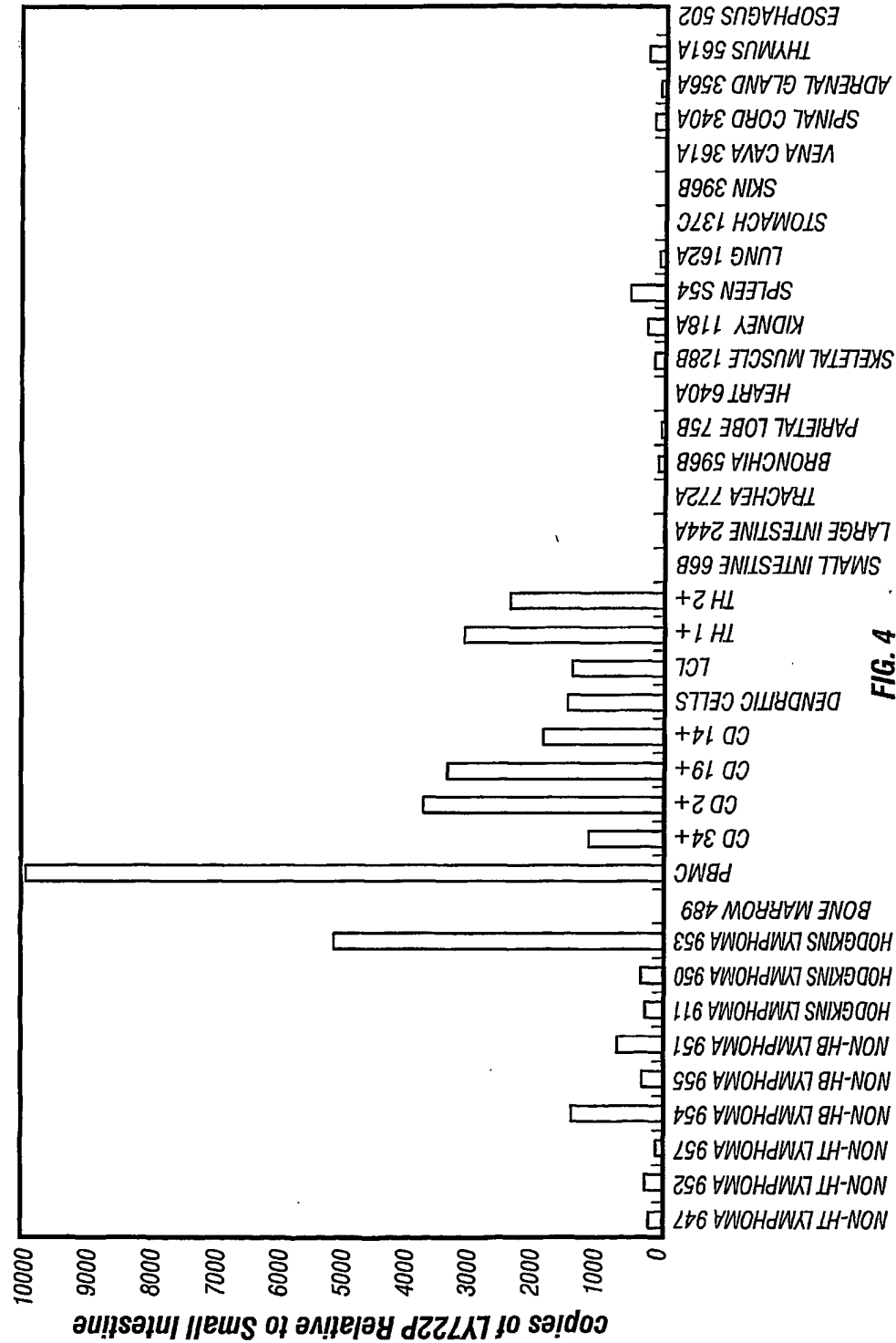
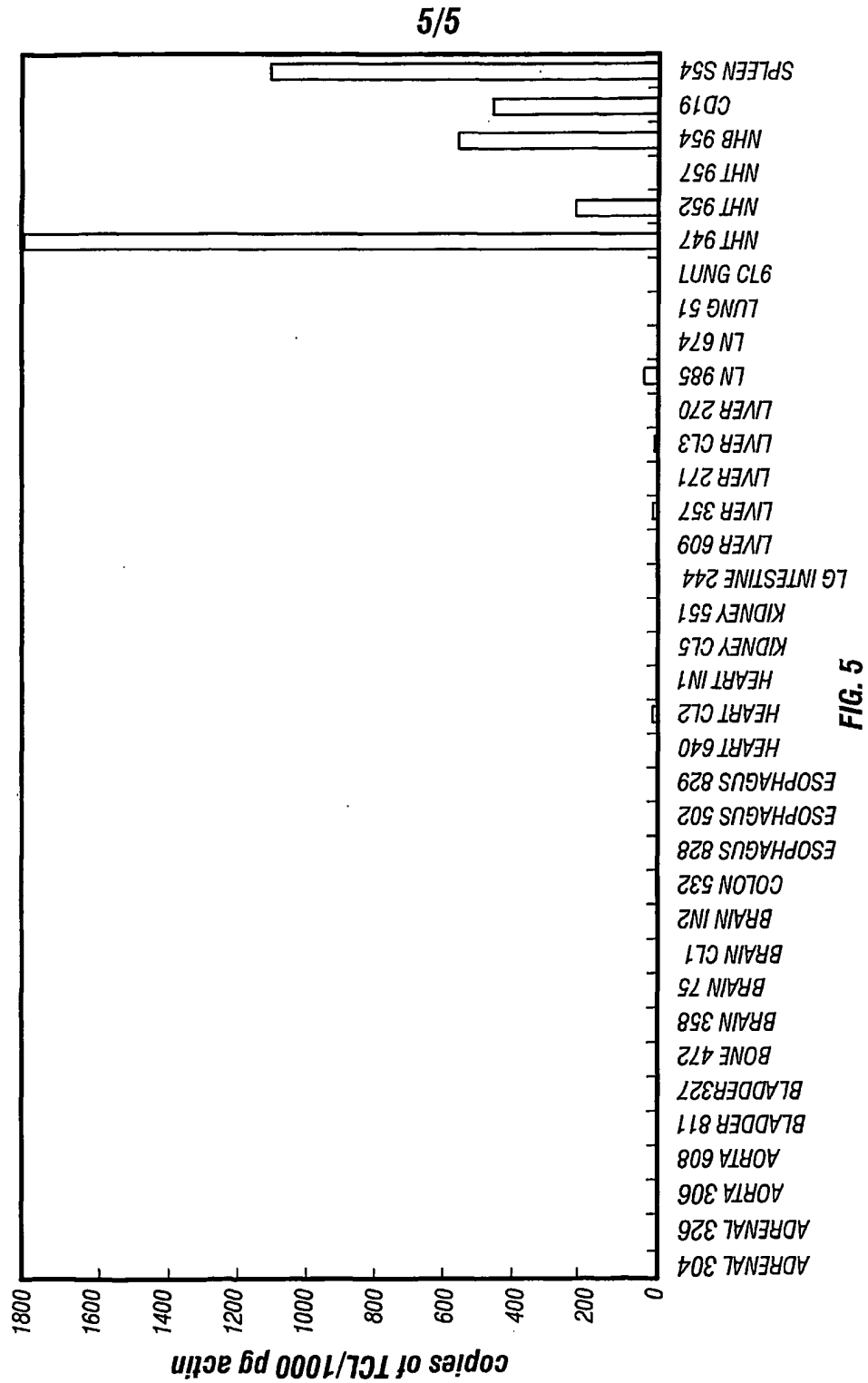


FIG. 3

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SEQUENCE LISTING

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<211> 372
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(372)
<223> n = A,T,C or G

<400> 5
ccacgntgnc catcaacagg gncgaagccg gcgatgaggc cgactattac tgtcaagtgt 60
gggatcgtaa taatgaccat gtcgtcttcg gcggaggagc caaactggcc gtcctaggtc 120
agcccaaggc tgccccctcg gtcactctgt tccccccctc ctctgaggag cttcaagcca 180
acaaggccac actggtgtgt ctcataagtg acttctaccc gggagccgtg acagtggcct 240
ggaaggcana tagcagcccc gtcaaggcgg gagtggagac caccacaccc tccaaacaaa 300
gcaacaacaa gtacgcggcc agcagctatc tgagcctgac gcctgagcag tggaagtccc 360
acanaactac ag 372

<210> 6
<211> 373

<212> DNA
<213> Homo sapiens

<400> 6
ctgtagcttc tgtgggactt cactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttgttgt tgctttgttt ggaggggtgt gtggtctcca ctccgcctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agtgtggcct tgttggcttg aagctcctca gaggagggcg ggaacagagt gaccgagggg 240
gcagccttgg gctgacctag gacggccagt ttggtccctc cgccgaagac gacatggtca 300
ttattacgat cccacacttg acagtaatag tcggcctcat cgccggcttc gaccctgttg 360
atggtcaggg tgg 373

<210> 7
<211> 484
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(484)
<223> n = A,T,C or G

<400> 7
ccttgctca gatccaaggt cactcggaag aggccatgtc taccctcaat gacactcatg 60
gaggaaatgc tgagagaagc attcagatgc atgacacaag agccaatgaa aggccctatt 120
gctatgcaat ctggtccaaa accactcttc aggaggtatgt cttcactggt gggccccacg 180
caaagcttct tcatgaggga atctaagact ttgggggctg tccagattat gaatgggctc 240
ttccacattg ccctgggggg tcttctgatg atcccagcag ggaatctatgc acccatctgt 300
gtgactgggg tgggtaccctc tctggggagg cattatgtat attatttccg gatcactcct 360
ggcagcaacc ggaaaaaaa ctccagggaag tgtttgggtca aaggaaaaaa tgataatgaa 420
ttcattggnc cctctttgct tgccttttct ggaaagaatt cttttcaaat catgggacca 480
tact 484

<210> 8
<211> 457
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(457)
<223> n = A,T,C or G

<400> 8
cctggggggtc agcacggagg ggactggagc tggagagtga ctgtagagcc tcaggactca 60
ggtacttctg ccctcccttt ggtctccctg ttcttctatg tggtgacaga tggcaaggaa 120
gtcctactac cagaggtttg ggccaagggg cagttgaagt ttatcagtgg gcacaccagt 180
gaacttggta acttccgctt tacacttttg ccaccaacca gtccagggga tacagccccc 240
aagtatggca gctacaatgt cttctggacc tccaaccag gactgcccct gctgacagag 300
atggtaaaga gtcgcctaaa tagctggttt cagcatcggc ccccgagggc ctcccctgaa 360
cgctacctcg gcttgccagg atccctgaag tgggaggaca gangtccaag tgggcaaggg 420
canggggcag ttcttgatac agcaggtgac ccttgaa 457

<210> 9
<211> 364
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(364)
<223> n = A,T,C or G

<400> 9
ggcatcatac tcctatngtn atgagaagcc ctctgccatc cagcagcgag ccattctacc 60
ttgtatcaag ggttatgatg tgattgctca agcccaatct gggactggga aaacggccac 120
atttgccata tcgattctgc ancagattga attagatcta aaagccaccc aggccttggg 180
cctagcacc cctcgagaat tggctcagca gatacagaag gtggtcatgg cactaggaga 240
ctacatgggc gcctcctgtc acgcctgtat ccggggcacc aacgtgcngt gctgacgtgc 300
ataaactgca natggaactc cccacatcat cgtgggtacc cctggccgng tgtnttgaaa 360
tgcn 364

<210> 10
<211> 382
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(382)
<223> n = A,T,C or G

<400> 10
tcaggacaca gcatggacat gagggcccc gctcagctcc tggggctcct gctgctctgg 60
ctcccaggtg ccaaattgta catccagatg acccaatctc cttccaccct gtctgcatct 120
gtcggagata caagttacaa taagtgtctg ggcctctcag aatatagatc ggtgggtggc 180
ctggcatcaa cagaaaccag gcaaagcccc taatgtccta atttatgcga cttccagttt 240
agaagaaggg gtctcattaa gatttactgg cagtggatct gggacacaat tcaatttaac 300
catcaccagt ctgcagcctg acgattcagc aacttattat tgncaacatt attctgcatc 360
tcttcgcagt ttttgacct cg 382

<210> 11
<211> 292
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(292)
<223> n = A,T,C or G

<400> 11
ctgtggctgc tgtgggactt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttgttgt tgctttgttt ggaggggtgt gtggnctcca ctccgcctt gacggggctt 120
gctatctgcc ttccaggcca ctgtcacngc tcccgggtag aagtcactta tgagacacac 180
cagngtggcc ttgttggcct gaagctcctc anaggagggc gggaaacaga atgaccgagg 240
gggcagnctt gggctgacct angacggcca gtttgggtcc ctcccccaag ac 292

<210> 12
<211> 465
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(465)
<223> n = A,T,C or G

<400> 12
ccaccctgac catcaacagg gtcgaagccg gcgatgaggc cgactattac tgtcaagtgt 60
gggatcgtaa taatgaccat gtcgtctctg gcgaggaggc caaactggcc gtccctaggtc 120
agcccaaggc tgccccctcg gtcactctgt tcccgcctc ctctgaggag cttcaagcca 180
acaaggccac actgggtgtg ctcataagtg acttctaccc gggagccgtg acagtggcct 240
ggaaggcaga tagcagcccc gtcaaggcgg gagtggagac caccacaccc tccaacaaa 300
gcaacaacaa gtacgcggcc agcagctatc tgagcctgac gcctgagcag tggaaagtccc 360
acagaagcta cagacctgcc cgggcggcca agggcgaatt ccagcacact tggcgccgtt 420

actatggatc cnactcggta ccaacttggc gtaatcatgg ncata 465

<210> 13
<211> 206
<212> DNA
<213> Homo sapiens

<400> 13
ccatggatat ggctaggtta ggtattcata tccaaatata tgaactctaa cctaattgtg 60
atatgattct gtagcattat attaaaagct atgatgatgc aatgcaggaa ataacctttc 120
attctccccc ctagaggatc acgacaggtg cttcaatgcc tgccttatct atgggacagt 180
agtgtgattc tcagtggagag tgaagg 206

<210> 14
<211> 378
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)... (378)
<223> n = A,T,C or G

<400> 14
ccaccctgac catcaacagg gtcgaagccg gcgatgaggc cgactattac tgtcaagtgt 60
gggatcgtaa taatgaccat gtcgtcttcg gcggagggac caaactggcc gtcctaggtc 120
agcccaaggc tgccccctcg gtcactctgt tcccgccctc ctctgaggag cttcaagcca 180
acaaggccac actggtgtgt ctcataagt acttctaccc gggagccgtg acagtggcct 240
ggaaggcaga tagcagcccc gtcaaggcgg gaggggagac caccacacc tccaaacaaa 300
gcaacaacaa gtacgcggcn cagcagctat ctgaagcctt gacccttgag caggtggaaa 360
gtccacacaga agctacag 378

<210> 15
<211> 170
<212> DNA
<213> Homo sapiens

<400> 15
ccgccgcggg tccgtgcgcc cagcgtccca gggcccaggc cgagcagaca aagatcattc 60
cactcagcct gggacgatgg ggaggaaaaa aatccagatc tcccgcaccc tggaccaaag 120
gaatcggcag gtgacgttca ccaagcggaa gttcgggctg atgaagaagg 170

<210> 16
<211> 462
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)... (462)
<223> n = A,T,C or G

<400> 16
ccagtacacc catgaatttg atggagatga gcagttctac gtggacctgg ggaggaagga 60
gactgtctgg tgtttgcctg ttctcagaca atttagattt gaccgcgaat ttgactgac 120
aaatatcgct gcctaaaaca taacttgaac agtctgatta aacgctccaa ctctaccgct 180
gctaccaatg aggnctcctga ggtcacagt ttttccaagt ctcccgtgac actgggtcag 240
ccaacatcc tcatctgtct tgtggacaac atctttcctc ctgtggncaa catcacatgg 300
ctgagcaatg ggcactcagt cacagaangt gtttctgaga ccagcttcct ctccaagagt 360
gatcattcct tcttcaagat cagtacctca ccctcctccc ttctggntga ggagagttat 420
gactgcaagg nggancactg gggactggga caagcctctt ct 462

<210> 17

<211> 207
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(207)
<223> n = A,T,C or G

<400> 17
ggcaagtcct gggctggcctt acctgggcac cgtgggcatg ggggaggtgt gtcacaagat 60
ttgggctctg cagagagaag attgggagtt acggggatct gggatggagg tggatgcgtc 120
agcaccctgc tggggcctgt ccctggactc gggccactct agggctcttg tcccgccttg 180
agctggaggg cgaggacctc ngccgcn 207

<210> 18
<211> 294
<212> DNA
<213> Homo sapiens

<400> 18
ccatgtcccc agaattgaag ccagagaatc gctcagatat ccctgagggc cggtcgttat 60
caaaagagat gattaggaca ggggcctggc ctggcttctg gtaataccag tgtacattgt 120
tactcccaat attgtttccc ccacaggtaa tcttgccgt ctttcctggg gccactgaca 180
ctgaggggtg ctgagtcaac acataggagg tcacagagtc tgtgcagtga gagaggaggc 240
cgaggaggag aacgggtccag gccatggctg aggcaccacc agtgctgctt cctt 294

<210> 19
<211> 197
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(197)
<223> n = A,T,C or G

<400> 19
caagccngcg atgaggccga ctattactgt caagngtggg atcgtaataa tgaccatgtc 60
gtcttcgcg gagggaccaa actggccntc ctangtcanc ccaacgctgc cccctcagnc 120
actctgttcc cggcctcctc tgaggagctt caagccaaca angccacact nggtgtgtctc 180
ataantgact tctaccc 197

<210> 20
<211> 387
<212> DNA
<213> Homo sapiens

<400> 20
aaatttctca aataactaag tcttcactaa ggcagcagtt caaaactggt ccaggaatta 60
aaatatattc ccatttgagg agtcttcctt cacaccttca cctcctcagc cttaagtata 120
tacacacaca cccaacaccc tcaatacttg actagcaaca ggctttacca tctttacctg 180
acaatgaccc cagggcggag atcgaaattc ttcttcacaa tctctaatag ctctctctca 240
ctcttctgag aggtaccata atggaaaatg gagatagata atggatgaga aactccaata 300
gcataagaga cctgaacaag aaccctccgg cacagacctc ctttaacaag ggattttgcc 360
accacaacgag cagcataagc agacctg 387

<210> 21
<211> 290
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (1)...(290)
<223> n = A,T,C or G

<400> 21
aagcagcact ggtggtgcct cagccatggc ctggaccgtt ctctcctcgc gcctcctctc 60
tcactgcaca gactctgtga cctcctatgt gttgactcag acaccctcag tgtcagtggc 120
cccangaaaag acggccaaga ttacctgtgg gggaaacaat attgggagtt acagtgtaca 180
ctgggtattac caaaagccag gccaggcccc tgcctaatac atctcttttg atgacnaccg 240
gccctcangg atatctgagc gattctctgg gcttcaattc tgggggacat 290

<210> 22
<211> 148
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(148)
<223> n = A,T,C or G

<400> 22
ctgtagcttc tgtgggactt ccactgctca ggcgtcaggc tcaganagct gctggccgcg 60
tacttggtgt tgctttgttt ggagggtgtg gtggtctcca ctccgcctt gacggggctg 120
ctatctgcct tncangccac tgtcacgg 148

<210> 23
<211> 265
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(265)
<223> n = A,T,C or G

<400> 23
ctgtagcttc tgtgggactt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt ggagggtgtg gnggtctcca ctccgcctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agtgtggcct tgttggcttg aagctcctca caggagggcg ggaacagagt gaccgagggg 240
gcagccttgg gctgacctag gacgg 265

<210> 24
<211> 377
<212> DNA
<213> Homo sapiens

<400> 24
agggccaccc tgaccatcaa cagggtcgaa gccggcgatg aggccgacta ttactgtcaa 60
gtgtgggatc gtaataatga ccattgtcgc ttcggcggag ggaccaaact ggccgtccta 120
agtcagccca aggtcgcccc ctcggtcact ctgttccgc cctcctctga ggagcttcaa 180
gccaacaagg ccacactggt gtgtctcata agtgacttct acccgggagc cgtgacagtg 240
gcctggaagg cagatagcag ccccgtaag gcgggagtgg agaccaccac accctccaaa 300
caaagcaaca acaagtacgc ggccagcagc tatctgagcc tgaccctga gcattggaag 360
tcccacaaaa gctacag 377

<210> 25
<211> 323
<212> DNA
<213> Homo sapiens

<400> 25

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cctgggagga acctgctcag tctgggccta aggaagcagc actggtggtg cctcagccat 60
ggcctggacc gttctcctcc tcggcctcct ctctcactgc acagactctg tgacctccta 120
tgtgttgact cagacaccct cagtgtcagt ggccccagga aagacggcca agattacctg 180
tgggggaaac aatattggga gtaacaatgt acactggtat taccagaagc caggccaggc 240
ccctgtccta atcatctctt ttgataacga ccggccctca gggatatctg agcgattctc 300
tggcttcaat tctggggaca tgg                                     323
```

<210> 26
<211> 433
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(433)
<223> n = A,T,C or G

```
<400> 26
ccaccctgac catcaacagg gtcgaagccg gcgatgaggc cgactattac tgtcaagtgt 60
gggatcgtaa taatgaccat gtcgtcttcg gcggaggagc caaactggcc gtcctaggtc 120
agcccaaggc tgccccctcg gtcactctgt tcccggccctc ctctgaggag cttcaagcca 180
acaaggccac actggtgtgt ctcataagtg acttctaccc gggagccgtg acagtggcct 240
ggaaggcaga tagcagcccc gtcaaggcgg gagtggagac caccacaccc tccaaacaaa 300
gcaacaacaa gtacgcggcc agcagctatc tgannctgac gcctgagcag tggaagtccc 360
acagaagcta cagcctgggc ttggcttacc ttgggcaccc gtggggcaat gggggaangt 420
gtgtcacaaa aat                                     433
```

<210> 27
<211> 419
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(419)
<223> n = A,T,C or G

```
<400> 27
ngcggccnag gtccagaaca cacatttggc tggaacagcc tgagggacca aaaggcccca 60
gtatcccaca gagctgagga gccaggccag aaaagtaacc ccagagtctg ctgtgcaggg 120
gagacacaga gctctcttta tctgtcagga tggcaggagg ggacagggtc agggcgctga 180
gggtcanatg tcggtgttgg gggccaaggc cccgagagat ctgaggacag gtggtcaggt 240
gtctaaggta aaacagctcc ccgtgcagat cagggcatag tggaaaacac cctgacccct 300
ctgcctggca tagaccttca gacacagagc ccctgaacaa nggcacccca acacctcatc 360
ataactagag ggcaggggct ccccagggtg acaccaggac tctgaccccc ttgcccctc 419
```

<210> 28
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(201)
<223> n = A,T,C or G

```
<400> 28
gctgccccct cggctactct gttccccgcc tcctctgagg agcttcaagc caacaaggcc 60
acactggtgt gtctcataag tgacttctac ccgggagccg tgacagtggc ctggaangca 120
gatagcacc cctcaaggc gggagtggag accaccacac cctncaaca aagcaacaac 180
aagtaccgg ccagcagcta t                                     201
```

<210> 29

<211> 292
<212> DNA
<213> Homo sapiens

<400> 29
ccatgtcccc agaattgaag ccagagaatc gctcagatat ccctgagggc cggtcgttat 60
caaaagagat gattaggaca ggggcctggc ctggcttctg gtaataccag tgtacattgt 120
tactcccaat attgtttccc ccacaggtaa tcttggccgt ctttctggg gccactgaca 180
ctgaggggtg ctgagtcaac acataggagg tcacagagtc tgtgcagtga gagaggaggc 240
cgaggaggag aacgggtccag gccatggctg aggcaccacc agtgctgctt cc 292

<210> 30
<211> 417
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(417)
<223> n = A,T,C or G

<400> 30
ngtccttgnc tnagatccaa ggtcactcgg aagaggccat gtctaccctc aatgacactc 60
atggaggaaa tgctgagaga agcattcaga tgcattgacac aaggtaagac tgccaaaaaa 120
tcttgttctt gctctcctca ttttgttatt tgttttattt ttangagttt tgagagcaaa 180
atgacaacac ccagaaatcc agtaaatggg actttcccg cagagccaat gaaaggncct 240
attgctatgc aatctggtcc aaaaccactc ttcaggagga tgtcttctact ggtgggcccc 300
acgcaaaagt tcttcatgag ggaatctaag actttggggg ctgtccagat tatgaatggg 360
ctcttccaca ttgccctggg gggncctctg atgatccan cagggatnta tgccccc 417

<210> 31
<211> 454
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(454)
<223> n = A,T,C or G

<400> 31
ctgtagcttt tgtgggactt ccactgctca ggcgtcaggc tcaggtagct gctggccgcg 60
tacttgttgt tgctttgttt ggagggtgtg gtggtctcca ctcccgcctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agtgtggcct tgttggtctg aagctcctca naggaggcg ggaacagagt gaccgagggg 240
gcagccttg gctgacctgc ggggtggatg aggggcaggg ggtcaaagtc ctggtgtcca 300
cctgggggagc ccctgacctc agtatatgat gaggtgttgg ggtgcccttg ttcaggggct 360
ctgtgtctga aggtctatgc caggcagagg ggtthanggtg ttttctactat gccctgattt 420
gcccgggagc tgcttacctt agaccctgac ancn 454

<210> 32
<211> 482
<212> DNA
<213> Homo sapiens

<400> 32
aaatcacagc ttttacctat ttgttaggct atagtgtttt gtaaaacttct gtttctattc 60
acatcttctc cacttgagag agacacaaa atccagtcag tatctaactc ggcttttgtt 120
aacttccctc aggagcagac attcatatag gtgatactgt atttcagtc tttcttttga 180
ccccagaagc cctagactga gaagataaaa tggtcagggt gttggggaaa aaaaagtgcc 240
aggctctcta gagaaaaatg tgaagagatg ctccaggcca atgagaagaa ttagacaaga 300
aatacacaga tgtgccagac ttctgagaag cacctgccag caacagcttc cttctttgag 360
tctaggtgag caggattctg gggtttggga tttctagtga tgggctatgg aaagggtgac 420

tgtgcctggg gacaaagcga ggtcccaagg ggacagcctg aactccctgc tcatagtagt 480
gg 482

<210> 33
<211> 383
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(383)
<223> n = A,T,C or G

<400> 33
ngtccaccct gaccatcaac agggncgaag cggcgatga ggccgactat tactgtcaag 60
tgtgggatcg taataatgac catgtcgtct tcggcggagg gaccaaactg gccgtcctag 120
gtcagcccca aggctgcccc ctccgtcact ctgttcccg cctcctctga ggagcttcaa 180
gccaacaagg ccacactggt gtgtctcata agtgacttct acccgggagc cgtgacagt 240
gcctggaagg cagatagcag ccccgtaag gcgggagtgg agaccaccac accctccaaa 300
caaancaaca acaagtacnc ggccagcagc tatctgagcc tgacgcctga gcagtggaa 360
tnccacataa gctacanacc tcn 383

<210> 34
<211> 246
<212> DNA
<213> Homo sapiens

<400> 34
aaatctttag agataccata aatcaacatt taatctttgt aacacatctg aaggaatatt 60
cttgaaatag cgtgatgatg gtctttaagg attctagaaa gggagtgatg agtcagaatt 120
tgccagaatg tcccagcata gtcaggagaa agagaacctc tctggtcgat gtacatgttc 180
taatcccatg gagattaggg caccagacta tgagatttgg taacatttgc tatcaagatg 240
aaccag 246

<210> 35
<211> 309
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(309)
<223> n = A,T,C or G

<400> 35
gcgcggtcga ngtggctctc cgatccccc aggcccttgc ccatacacg ggctccagaa 60
cacacatttg gctggaacag cctgaggac caaaaggccc cagtatcca cagagctgag 120
gagccaggcc agaaaagtaa cccagagtt cgctgtgcag gagagacaca gagctctctt 180
tatctgtcag gatggcagga ggggacaggg tcagggcact gagggtcana tgctcgtgtg 240
gggggccaaag gccccgagag atctcaggac angtggncat gtgtctaang taaaanagct 300
tccccgtgc 309

<210> 36
<211> 363
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(363)
<223> n = A,T,C or G

<400> 36

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atggacatga ggggtccccgc tcagctcctg gggctcctgc tgctctggct cccaggtgcc 60
aaatgtgaca tccagatgac ccaatctcct tccaccctgt ctgcatctgt cggagataga 120
gttacaataa gttgtcgggc ctctcagaat atagatcggt ggttggcctg gcatcaacag 180
aaaccaggca aagccccctaa tgtccctaat tatgcgactt ccagtttaga agaaggggtc 240
tcattaagat ttactggcag tggatctggg acacaattca atttaaccat naccaggtct 300
gcagcctgac gattcancaa cttattattg tnaacattat tctgcatctn ttncagttt 360
tgg

```

```

<210> 37
<211> 416
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(416)
<223> n = A,T,C or G

```

```

<400> 37
ccagtacacc catgaatttg atggagatga gcagttctac gtggacctgg ggaggaagga 60
gactgccttg tgtttgcctg ttctcagaca atttagattt gacccgcaat ttgcactgac 120
aaacatcgct gtcctaaaac ataacttgaa cagtctgatt aaacgctcca actctaccgc 180
tgctaccaat gaggttcctg aggtcacagt gttttccaag tctcccgtga cactgggtca 240
gccaacatc ctcatctgtc ttgtggacaa catctttcct cctgtgggna acatcacatg 300
gctgagcaat gggcactcag tcacanaang tgttcttgag accagcttcc tctccaagag 360
tgatcattn cttctcaana tcagntaccc caccctcctc cttctctctg aggaga 416

```

```

<210> 38
<211> 253
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(253)
<223> n = A,T,C or G

```

```

<400> 38
gtctgtagct tctgtgggac ttccactgct caggcgctcag gctcagatag ctgctgggccg 60
cgtaacttgtt gttgctttgt ttggaggggtg tgggtggnctc cactcccggc ttgacggggg 120
tgctatctgn cttccaggcc actgtcacgg ctcccgggta gaagtcactt atgagacaca 180
ccagtgtggc cttgttggtt tgaanctcct catangaggg cggggaacaga gtgaccgang 240
gggcagcctt ggg

```

```

<210> 39
<211> 178
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(178)
<223> n = A,T,C or G

```

```

<400> 39
gcccnggnag gtccaaatgt ctgagacacc ttcaaattggg cccagtgcca gccaaactggg 60
ctcctcactg gcaccacgtc ccagatgccc ttctctgccc acaccctgca ggctgaggcc 120
agaggaggnc acccctccgg agatggggna tgtgngtggt tgtgngtatg ttctgcgn 178

```

```

<210> 40
<211> 156
<212> DNA
<213> Homo sapiens

```


<220>
<221> misc_feature
<222> (1)...(156)
<223> n = A,T,C or G

<400> 40
ccaaaagaag taagacagct tgctgaagat ttcctgaaag actatatattca tataaacatt 60
ggtygcacttg aactgantgc aaaccacaac attcttcana ntgtggatgt gtgtcatgac 120
ntanaaaagg atgaaaaact tattcgtcta atggaa 156

<210> 41
<211> 287
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(287)
<223> n = A,T,C or G

<400> 41
ccatgtcccc agaattgaag ccagagaatc gctcagatat ccctgagggc cggtcgttat 60
caaaaagagat gattaggaca ggggcctggc ctggcttctg gtaataccag ngtagcattgt 120
tactcccaat attgtttccc ccacaggtaa tcttgccgcg ctttcctggg gccactgaca 180
ctgaggggtgt ctgagtcaac acataggagg ncacagagtn tgtgcagtga gagaggaggc 240
cgaagaggag aacggcccan gccatggctg angcncacc agtgctg 287

<210> 42
<211> 272
<212> DNA
<213> Homo sapiens

<400> 42
gtgctcacag tcatcaatta tagacccac aacatgcgcc ctgaagacag aatgttccat 60
atcacagctg tgatcttgag agccctctcc ttggctttcc tgctgagtct ccgaggagct 120
ggggccatca aggcggacca tgtgtcaact tatgccgcgt ttgtacagac gcatagacca 180
acaggggagt ttatgtttga atttgatgaa gatgagatgt tctatgtgga tctggacaag 240
aaggagaccg tctggcatct ggaggagttt gg 272

<210> 43
<211> 533
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(533)
<223> n = A,T,C or G

<400> 43
cttgccctgt gctctggccc ctggctcctgt cctgttctcc agcatgggtgt gtctgaggct 60
ccctggaggc tcctgcatgg cagttctgac agtgacactg atgggtgctga gctccccact 120
ggctttggct ggggacacca gaccacgttt cttggagtag tctacgtctg agtgteattt 180
cttcaatggg acggagcggg tgcggttcct ggacagatac ttctataacc aagaggagta 240
cgtgcgcttc gacagcgacg tgggggagtt ccgggcggtg acggagctgg ggcggcctga 300
tgaggagtac tggaacagcc agaaggactt cctggaagac aggcggggccg cgggtggacac 360
ctactgcaga cacaactacg ggggttggtga gagcttcaca gtgcagcggc gagtccatcc 420
taagggtgact gtgtatcctt caaagaccca cccctgcagc accacaacct cctgggtctgt 480
tctgnagatg gtttctatcc aggcagcatt gaatcangtg gttccggaat ggn 533

<210> 44
<211> 332

<212> DNA

<213> Homo sapiens

<400> 44

```
tcgccctgaa cgaggacctg cgctcttgga ccgcggcgga catggcggct cagatcacca 60
agcgcaagtg ggaggcggcc catgaggcgg agcagttgag agcctacctg gatggcacgt 120
gctgtgagtg gctccgcaga tacctggaga acgggaagga gacgtgcag cgcacggacc 180
ccccaagac acatatgacc caccaccca tctctgacca tgaggccacc ctgaggtgct 240
gggccctggg cttctaccct gcggagatca cactgacctg gcagcgggat ggggaggacc 300
agacccagga cacggagctc gtggagacca gg 332
```

<210> 45

<211> 391

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(391)

<223> n = A,T,C or G

<400> 45

```
ctgtngctnc tgtgggactt ccactgctca ggcgtcaggc tcanatagct gctggccgcg 60
tactttgtgt tgctttgttt ggagggtgtg gtggtctcca ctcccgcctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agtgtggcct tgttggttg aagctcctca gaggagggcg ggaacagagt gaccgagggg 240
gcagncttgg gctgacttag gacggccagt atggtccctc cgccgaagac gacatgggta 300
ttattacnat ccncacttg acagtaatag tcngccttca tcgccggctt ctgacccttt 360
tgatggttca gggngggacc tttggcccg n 391
```

<210> 46

<211> 478

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(478)

<223> n = A,T,C or G

<400> 46

```
ccaccctgac catcaacagg gtcgaagccg gcgatgaggc cgactattac tgtcaagtgt 60
gggatcttaa taatgaccat gtcgtcttcg gcggaggaac caaactggcc gtcctaggtc 120
agcccaaggc tgccccctcg gtcactctgt tcccgccctc ctctgaggag cttcaagcca 180
acaaggccac actggtgtgt ctcataagtg acttctaccc gggagccgtg acagtggcct 240
ggaaggcaga tagcagcccc gtcaaggngg gagtggagac caccacacc tncaaacaaa 300
gcaacaacaa gtacgcggcc agcagctatc tnagcctgac gcctgagcag tggaagtccc 360
acagaancta cagacctgcc cgggcgggna anggcgaatt ccagcacact ggggggcgtt 420
actagtggat ncgagctcgg taccaagctt ggcgnaatca tggncatagc tggtttcc 478
```

<210> 47

<211> 244

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(244)

<223> n = A,T,C or G

<400> 47

```
ccacggtnnc cntcaacagg ggcgaagccg gcgatgaggc cgactattac tgtcaagtgt 60
gggatcttaa taatgaccat gtcgtcttcg gcggagggac caaactggnc gtcctaggtc 120
```

agcccaaggc tgccccctcg gtcactctgt tcccgccctc ctctgaggag cttcaagcca 180
acaaggccac actggtgtgt ctcataagtg acttntaccc gngagccgtg acagtggcct 240
ggaa 244

<210> 48

<211> 343

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(343)

<223> n = A,T,C or G

<400> 48

cccggcaggn aaatgccact gctgnggaca aaaaactgaa tgaantctat tagaagcttc 60
tgaaaaatgt taaatgttaa atcctgctat ggtctgatna gaanaactca agacttagaa 120
ttagatattt tcttccttcg aattatgtat tagattatct ccctacatat tttctcccag 180
ccataagtaa ctgagttatg ctggaaaaaa aaacacanaa atcttaagat ctctttttct 240
actggtgaaa ttgggggttt gataataatt tttagagaaa aatctanaat tctctgtgta 300
tagctggtca acncataaac cangtaaat ttgattttct tgg 343

<210> 49

<211> 373

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(373)

<223> n = A,T,C or G

<400> 49

ccaccctgac catcaacagg gtcgaagccg gcgatgaggc cgactattac tgtcaagtgt 60
gggatcgtaa taatgaccat gtcgtcttcg gcggagggac caaactggcc gtcctaggtc 120
agcccaaggc tgccccctcg gtcactctgt tcccgccctc ctctgaggag cttcaagcca 180
acaaggccac actggtgtgt ctcataagtg acttntaccc gngagccgtg acagtggcct 240
ggaaggcaga tagcagcccc gtcaaggcgg gagtggagac caccacacc tccaaacaaa 300
gcaacaacaa gtacgcggcc agcagctatc tgagcctgac gcctgagcag tggaagtccc 360
acagaagcta cag 373

<210> 50

<211> 375

<212> DNA

<213> Homo sapiens

<400> 50

ccaaaactgc gaagagatgc agaataatgt tgacaataat aagttgctga atcgtcaggc 60
tgcagactgg tgatggttaa attgaattgt gtcccagatc cactgccagt aaatcttaat 120
gagaccctt cttctaaact ggaagtcgca taaattagga cattaggggc ttgacctggt 180
ttctgttgat gccaggccaa ccaccgatct atattctgag aggcccgaca acttattgta 240
actgtatctc cgacagatgc agacaggggtg gaaggagatt gggtcacatc gatgtcacat 300
ttggcacctg ggagccagag cagcaggagc cccaggagct gagcggggac cctcatgtcc 360
atgctgtgtc ctgac 375

<210> 51

<211> 347

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(347)

<223> n = A,T,C or G

<400> 51
ccaccctgac catcaatagg gtcgaagccg gcgatgaggc cgactattac tgtcaagtgt 60
gggacgtaaa taatgaccat gtcgtcttcg gcggaggagc caaactggcc gtcctaggtc 120
agcccaaggc tgccccctcg gtcactctgt tcccgccttc ctctgaggag cttcaagcca 180
acaagggcac actgggtgtgt ctcataagtg acttctaccc gggagccgtg acagtggcct 240
ggaagggnaga tagcagcccc gtcaaggcgg gagtggagac caccacacc tccaacaaaa 300
gcaacaacaa gtaccgcggg cagcagctat ctgagcctga cgcctga 347

<210> 52

<211> 449

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(449)

<223> n = A,T,C or G

<400> 52
aaaattgatc acaacnaggg aaaacaaaat aaaattaggg ggcaaagggt aggagtatgg 60
ggggaggggg gagcaaacct atcgaatata tcttagaatt ttgctcagaa atcactgctg 120
cctctcaagt gttgcattgt ccctgcctaa accaagaagg ctaaacaaaag cccctcctgt 180
ttgaattcct aaggtaagaa atttctaagc taagaaaaca ctattgccta aaaccaatga 240
tagtgaggct catttacaac taggcattgc tcacacacac agtccaaagg caagacactg 300
gctttgaaat taggctcatg atgtgattcc tattatatgt acctgatttt tttaggcccc 360
aggatatgtg accagagtta atgtcatgac tcttcaaaga tatgatgaaa agttgcccta 420
gaaatctaga gatgcatgtt tatttaatt 449

<210> 53

<211> 199

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(199)

<223> n = A,T,C or G

<400> 53
ccaccctgac catcaacagg gtcgaagccg gcgatggggc cgactattat tgtcaagtgt 60
gggacgtaaa taatgaccat gtcgtcttcg gcggaggagc caaactggcc gtcctaagtc 120
agcccaaggc tgccccctcg gncactctgt tcccgccttn ctctgangag cttnaagcca 180
acaaggncac actgggtgtg 199

<210> 54

<211> 79

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(79)

<223> n = A,T,C or G

<400> 54
ctgtagcttc tgnncgactt ccactgctca ggcgtcaggc tcanatagct gctggcccg 60
tacttggtgt tgctttgtt 79

<210> 55

<211> 93

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(93)

<223> n = A,T,C or G

<400> 55

ctgtagcttt tgtnggnctt ccactgctca ggcgtcaggg tcaggtagct gctggccggn 60
tacttggtgn tnccttgntt ggagggtgtg gtg 93

<210> 56

<211> 426

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(426)

<223> n = A,T,C or G

<400> 56

gtgaaccanc taatccctct gagaaaaact ccccatctac ccaatactgt tacagcatat 60
aatctctgtt cttgggcatt ttgtcagtga tgctgatctt tgccttcttc cagggaacttg 120
taatagctgg catcggtgag aatgaatgga aaagnncgtg ctccanaccc aaatctaaca 180
tagttctcct gtcagnagaa gaaaaaaaaa aacagactat tgaaataaaa gaagaagtgg 240
ttgggctaac tgaaacatct tcccaaccaa agaatagaaga agacattgaa attattccaa 300
tccaagaaga ggaagaagaa gaaacagaga cgaactttnc agaacctccc caagatcagg 360
aatcctcacc aatagaaaat gacagctctc ctnaagtgat ttcttctgnt ttctgnntcc 420
tttttt 426

<210> 57

<211> 232

<212> DNA

<213> Homo sapiens

<400> 57

gctaaaccaa aagaagcctc cagacagccc tgagatcacc taaaaagctg ctaccaagac 60
agccacgaag atcctaccaa aatgaagcgc ttctctctcc tcctactcac catcagcctc 120
ctggttatgg tacagatata aactggactc tcaggacaaa acgacaccag ccaaaccagc 180
agcccctcag catccagcag catgagcgga ggcattttcc tttctctcgt gg 232

<210> 58

<211> 191

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(191)

<223> n = A,T,C or G

<400> 58

ccttgctca gatccaannt cactcgnaag aggccatgtc taccctnaat gacactcatg 60
gaggaaatgc tgagagaagc attcanatgc atgacacaag gtaagactgc caaaaatctt 120
gttcttgctc tcctcathtt gttatttggt ttatttttag gagttttgag agcaaaatga 180
caacaccag a 191

<210> 59

<211> 259

<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(259)
<223> n = A,T,C or G

<400> 59
ctgtagcttc tgtgggactt ccaactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt ggaggggtgtg gtgggtctcca ctccgcctt gacggggctg 120
ctatctgcct tncagggcac tgtcacggnt nccgggtaga agtcacttat gagacacacc 180
agtgtgggctt tgttggttg aagctcntna naggagggcg ggaacanagt gaccgagggg 240
gcagccttg gctgaccta 259

<210> 60
<211> 410
<212> DNA
<213> Homo sapiens

<400> 60
cctgggtcaaa tgtcacctcc actgggaagc cctccttgat ctcccaggct gttaggggcc 60
tgccccaggt tcctgcagac tccctgcttc tctccatcac aaacctgagc agtgtggggc 120
tgtcattatc atgtgtgagg ttttagtacc aggaagtggg gtactaccat agcaaatacc 180
caaaaatggg gaaatggcct ggggaatgga aagaattgga caatgagcac ttgatagaaa 240
aagcctagat tgccctgaag aggtgggtcag tagaaatatg gatgttaaag gtgcccctgc 300
tgaggtccta ggaggaaatg agggacatga cattggacgt gaagatggag gtggggactg 360
cagtgatgca tccacagatc tgggagacca ggatgctgca gccatcacag 410

<210> 61
<211> 361
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(361)
<223> n = A,T,C or G

<400> 61
cttctgtggn acttccactg ctacgcgtn aggcctcagat agctgctggc cgcgtacttg 60
ttgttgcttt gnttggaggg tgtggtggtc tccacccccg ccttgacggg gctgctatct 120
gccttccagg ccaactgtcac ggctcccggg tagaagtcac ttatgagaca caccagtgtg 180
gccttggttg cttgaagctc ctcanaggag ggcgggaaca gagtgaccga gggggcagcc 240
ttgggctgac ctaggacggc cagtttggtc cctccgccga anacgacatg gtcattatta 300
cgatcccaca cttgacagta atagtcggcc tcatcgccg cttcgaccct gttgatggtc 360
a 361

<210> 62
<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(368)
<223> n = A,T,C or G

<400> 62
ctgtagcttc tgtgggactt ccaactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt ggaggggtgtg gtgggtctcca ctccgcctt gacggggctg 120
ctatctgcct tccagggcac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agtgtggcct tgttggttg aagctcctca naggagggcg ggaacagagt gaccgagggg 240
gcanccttg gctgacctag gacggccagt ttgggtccctc cgccgaagac gacatggtca 300
ttattacgat cccacacttn acagttnata gtcngcctca tngccggntt cgaccctggt 360
gatggtca 368

<210> 63
<211> 383
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(383)
<223> n = A,T,C or G

<400> 63
ctgtagcttc tgtgggactt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt ggagggtgtg gtggtctcca ctccgcctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agtgtggcct tgttggcttg aagctcctca gaggagggcg ggaacagagt gaccgagggg 240
gcagccttgg gctgacctan gacggccagt ttggtccctc cgccgaagac gacatggtca 300
ttattacgat cccacacttg acagtaatag tcggcctcat cgccggcttc gaccctgttg 360
atggtcaggg tggacctcgg ccg 383

<210> 64
<211> 373
<212> DNA
<213> Homo sapiens

<400> 64
ctgtagcttc tgtgggactt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt ggagggtgtg gtggtctcca ctccgcctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agtgtggcct tgttggcttg aagctcctca gaggagggcg ggaacagagt gaccgagggg 240
gcagccttgg gctgacctag gacggccagt ttggtccctc cgccgaagac gacatggtca 300
ttattacgat cccacacttg acagtaatag tcggcctcat cgccggcttc gaccctgttg 360
atggtcaggg tgg 373

<210> 65
<211> 334
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(334)
<223> n = A,T,C or G

<400> 65
ctgtagcttc tgtgggactt ccactgctcg ggcgtcaggc tcaggtagct gctggccgcg 60
tacttggtgt tgctctgttt ggagggtttg gtggtctcca ctccgcctt gacggggctg 120
ccatctgcct tccaggccac tgtcacagct cccgggtaga agtcacttat gagacacacc 180
agngtggcct tnntggcttg aanctcctca naggagggcg ggaacanngt gaccnagggg 240
gcanncttgg gctgacctag gacggccagt ttggtccctc cgccgaagac gacatggtca 300
ttattacgat ccnacacttg acagtaatag tcgg 334

<210> 66
<211> 377
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(377)
<223> n = A,T,C or G

<400> 66

```
ctgtagcttc tgtgggactt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt ggaggggtgt gtggtctcca ctccgcctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agtgtggcct tgttggttg aagctcctca gaggaggcg ggaacagagt gaccgagggg 240
gcagccttgg gctgacctag gacggccagt ttggtccctc cgccgaagac gacatggtca 300
ttattacgat cccacacttg acagtaatag tcggnctcat cgtcggcttc gaccctgttg 360
atggtcaggg tggacct
```

```
<210> 67
<211> 392
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(392)
<223> n = A,T,C or G
```

```
<400> 67
ngtcttgctt gctgctctgg cccctgggtc tgcctgttc tccagcatgg tgtgtctgag 60
gctccctgga ggctcctgca tggcagttct gacagtgaca ctgatgggtg tgagctcccc 120
acttgctttg ggctggggac accagaccac gtttcttga gtactctacg tctgagtgac 180
atttcttcaa tgggacggag cgggtgcggt tcctggacag atacttctat aaccaagagg 240
agtacgtgag cttcgacagc gacgtggggg agttccgggc ggtgacngag ctggggcggg 300
ctgatgagga gtactggaac agccannaag gacttcctgg aanacaggcg ggcgcgggtg 360
gacacctact gcanacacaa ctacgggggt gg 392
```

```
<210> 68
<211> 446
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(446)
<223> n = A,T,C or G
```

```
<400> 68
naaaaatgga gagtctgaat tttattagag ctcacacacc atatattaac atatacaact 60
gtgaaccacc taatccctct gagaaaaact ccccatctac ccaatactgn tacagcatat 120
aatctctgtt ctggggcatt ttgtcagtga tgctgatctt tgccttcttc caggaaactg 180
taatanctgg catcgttgac aatgaatgga aaagaacgtg ctccagaccc aaatctaaca 240
tagttctcct gtcagcagaa gaaaaaaaaa aacanactat tgaaataaaa gaagaagtgg 300
ttgggctaac tgaaacatct tccaaccaa agaatgaaga anacattgaa attattccaa 360
tncaagaaga ggaagaagaa agaaacngga gacgaacttt ccagaacctn ccaagatcag 420
gaatcctcac caatagaaaa tgacag 446
```

```
<210> 69
<211> 180
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(180)
<223> n = A,T,C or G
```

```
<400> 69
ctgctgccac agccagtatt gccggggctc caaccagta cccacctggc cgtgggggtc 60
ctccccacc tatgggcca gaaacacccc ctccaggcat gatgggcca cctcccnggt 120
ttganacctc ctatgggtgc ccccaatggg ggatcccccn tggaaganga ctccaatggg 180
```

```
<210> 70
```


<211> 113
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(113)
<223> n = A,T,C or G

<400> 70
nccatgtccc cagaattgaa gccagagaat cgctcanata tccctgaggg ccggtcgtta 60
tcaaaagaga tgattaggac aggggcctgg cctggccttct ggtaatacca acg 113

<210> 71
<211> 117
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(117)
<223> n = A,T,C or G

<400> 71
ngtaaattcc tgtaataaaa gggaaattga gggcagagca atcaggettg agttgcaagg 60
accaggggga tcacctaata ccagaagcca gccatccaaa actctgtttg tcaaagg 117

<210> 72
<211> 247
<212> DNA
<213> Homo sapiens

<400> 72
ccactgcaac agtgagtcaa actctcctcg catgaccaca aagtataggg acaggtgtga 60
ccccctccct gacctatccc cattcaggta tgctctagca cagagccggg agccacagcg 120
ggttgggtga gaaggactgg ctgaagatgg aactgtgttg cccatccacc gcctctctct 180
tcttcatctt gtaatctgtc accttccaaa tgagccttcc attatagcaa gtaccctcca 240
gcagttt 247

<210> 73
<211> 373
<212> DNA
<213> Homo sapiens

<400> 73
ctgtagcttc tgtgggactt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt ggagggtgtg gtggtctcca ctcccgcctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agtgtggcct tgttggttg aagctcctca gaggagggcg ggaacagagt gaccgagggg 240
gcagccttgg gctgacctag gacggccagt ttggtccctc cgccgaagac gacatggtca 300
ttattacgat cccacacttg acagtaatag tcggcctcat cgccggcttc gaccctgttg 360
atggtcaggg tgg 373

<210> 74
<211> 371
<212> DNA
<213> Homo sapiens

<400> 74
ggacacagca tggacatgag ggtccccgct cagctcctgg ggctcctgct gctctggctc 60
ccagggtgcc aatgtgacat ccagatgacc caatctcctt ccaccctgtc tgcactctgc 120
ggaaatacag ttacaataag ttgtcgggcc tctcagaata tagatcgggtg gttggcctgg 180
catcaacaga aaccaggcaa agcccctaata gtcctaattt atgcgacttc cagtttagaa 240

gaaggggtct cattaagatt tactggcagt ggatctggga cacaattcaa tttaaccatc 300
accagtctgc agcctgacga ttcagcaact tattattgtc aacattattc tgcattctctt 360
cgcagttttg g 371

<210> 75
<211> 293
<212> DNA
<213> Homo sapiens

<400> 75
ggaagcagca ctggtggtgc ctcagccatg gcctggaccg ttctcctcct cggcctcctc 60
tctcactgca cagactctgt gacctcctat gtgttgactc agacaccctc agtgtcagtg 120
gccccagga aagacggcca agattacctg tgggggaaac aatattggga gtaacaatgt 180
acactggtat taccagaagc caggccaggc ccctgtccta atcatctctt ttgataacga 240
ccggccctca gggatatctg agcgattctc tggcttcaat tctggggaca tgg 293

<210> 76
<211> 209
<212> DNA
<213> Homo sapiens

<400> 76
aagcagcact ggtggtgcct cagccatggc ctggaccgtt ctcctcctcg gcctcctcctc 60
tctactgcaca ggtgatcccc ccagggtctc accaacctgc ccagcccaag gcttctgggt 120
ccagcgtgtc cttaattctg agctcaggag ggccttctct gtggtgggca ggatgctcat 180
gaccctggtg caaggtggga aggttgggg 209

<210> 77
<211> 396
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(396)
<223> n = A,T,C or G

<400> 77
ctgtagcttc tgtgggactt ccaactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttgttgt tgctttgttt ggaggggtgt gtggtctcca ctcccgctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agcgtggcct tgttggcttg aaactcctca nangaaggcg ggaaacagaa ngaccgaggg 240
gcanccttgg gctgactagg acggcagttt ggtcctccgc caaacacatg gcattattac 300
gatccacact tgacagtaat agtcngctca tcgncggctt caccctgtga tggtcagggt 360
ggactcggcc ccgacaccta agggcgaatc cancac 396

<210> 78
<211> 202
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(202)
<223> n = A,T,C or G

<400> 78
cctcggatga tgaagacagt gcccaccaca atgccacga ggccacaga caaccccag 60
gcgcagacca cagtctctgt gagctctgac ataggggctg gaatctcagg ctcccagtgt 120
ttcagaagag gcttgtccag tcccagtg tccacctg agtcatanct ctcctcanct 180
gaagggaggga gggtaggna ac 202

<210> 79

<211> 356
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(356)
<223> n = A,T,C or G

<400> 79
ccaaaactgc gaagagatgc agaataatgt tgacaataat aagttgctga atcgtcaggg 60
tgagactgg tgatggtaa attgaattgt gtcccagatc cactgccagt aaatcttaat 120
gagaccctt cttctaaact ggaagtcgca taaattagga cattaggggc ttgacctggt 180
ttctgttgat gccaggccaa ccaccgatct atattctgag agggcccgac aacttattgt 240
aactggatc tccgacagat gcagacaggg tggaaggaga ttgggtcatc tggatgtcac 300
atttggcacc tgggagccag agcagcagga gccccangag ctgagcgggg accctc 356

<210> 80
<211> 149
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(149)
<223> n = A,T,C or G

<400> 80
ccagnacncc catgaantt atgganatga gcacttntac gtggacctgg ggaggaagga 60
gactgtctgg tgtttgcctg ttctcataca atttagattt gaccgcgaat ttgncctgac 120
aaacactggc tgttctaaaa cataacttg 149

<210> 81
<211> 292
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(292)
<223> n = A,T,C or G

<400> 81
ggaagcagca ctggtggtgc ctacgccatg gcctggaccg ttctcctcct cggcctcctc 60
tctcactgca cagattctgt gacttcctat gtgttgactc agacaccctc agtgtcagtg 120
gccccaggaa agacggccaa gattacctgt gggggaaaca atattgggag tcacaatgta 180
cactggtatt accagaagcc aggcaggcc cctgtcctaa tcatctcttt tgataacgac 240
cggnccctcan ggatatctga gcgattctct ggcttcaatt ctggggacat gg 292

<210> 82
<211> 284
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(284)
<223> n = A,T,C or G

<400> 82
aatgaaaagg ccctattgct atgcaatctg gtccaaaacc actcttcagg aaggatgtct 60
tcactggtgg gccccacgca aagcttcttc atgagggaat ctaagacttt gggggctgtc 120
cagattatga atgggctcct ccacattgcc ctggggggtc ttctgatgat cccagcaggg 180

```
atctatgcac ccatctgtgt gactgtgtgg taccctctct ggggaggcat tatgtatatt 240
atttccggat cactcctgca ncaacggaaa aaactccagg aagt 284
```

```
<210> 83
<211> 374
<212> DNA
<213> Homo sapiens
```

```
<400> 83
cctaggcatg acaatcggag gactcgaggg ggatggagga ctagtgatcg gctggctgct 60
tccagtcgat tagagaggtg aaaaagctga acgtgtgcc aatacttca aaaggcagaa 120
catatcacct ctgccccgta aactgttctc tccgagggaa aaaatggaag ttatcctcac 180
agttcactgc cgtgggtatt cttcttgtcc catcttttgc atgacttgcc atggtacagc 240
cttgtttcaa actgttccact gtgatctgtg ggtctttgag tttcagtgag tttgctgaaa 300
tgtcgaagaa gtagttccaa acttcaatgt tcaatgaaat tttgtttcaa gtttgaaatg 360
gagagagcag cttt 374
```

```
<210> 84
<211> 357
<212> DNA
<213> Homo sapiens
```

```
<400> 84
catgaggggc cccgctcagc tcctggggct cctgctgctc tggctcccag gtgccaaatg 60
tgacatccag atgaccaaat ctccctccac cctgtctgca tctgtcggag atacagttac 120
aataagttgt cgggcctctc agaatataga tcggtggttg gcctggcatc aacagaaacc 180
aggcaaagcc cctaattgct taatttatgc gacttccagt ttagaagaag ggggtctcatt 240
aagatttact ggcagtggat ctgggacaca attcaattta accatcacca gtctgcagcc 300
tgacgattca gcaacttatt attgtcaaca ttattctgca tctcttcgca gttttgg 357
```

```
<210> 85
<211> 372
<212> DNA
<213> Homo sapiens
```

```
<400> 85
ccaccctgac catcaacagg atcgaagccg gcgatgaggc cgactattac tgtcaagtgt 60
gggatcttaa taatgaccat gtcgtcttcg gcggaggaac caaactggcc gtcctaggtc 120
agcccaaggc tgccccctcg gtcactctgt tcccgcctc ctctgaggag cttcaagcca 180
acaaggccac actggtgtgt ctcataagtg acttctaccc gggagccgtg acagtggcct 240
ggaaggcaga tagcagcccc gtcaaggcgg gagtggagac caccacaccc tccaacaaa 300
gcaacaacaa gtacgcggca gcagctatct gagcctgacg cctgagcagt ggaagtccca 360
cagaagctac ag 372
```

```
<210> 86
<211> 111
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(111)
<223> n = A,T,C or G
```

```
<400> 86
cgaagtcctg ggaggaacct gtcantctg ggcctaanga ancagcactg gtggtgcctn 60
anccatngac tggaccgttc tnactcctcn gncttctctt teactncaca n 111
```

```
<210> 87
<211> 357
<212> DNA
<213> Homo sapiens
```

<220>
<221> misc_feature
<222> (1)...(357)
<223> n = A,T,C or G

<400> 87
ccaccctgac catcaacagg gtcgaagccg gcgatgaggc cgactattac tgtcaagtgt 60
gggatcttaa taatgaccat gtcgtcttcg gcggagggaac caaactggcc gtcctaggtc 120
agcccaaggc tgccccctcg gtcactctgt tccccccctc ctctgaggag cttcaagcca 180
acaaggccac actggtgtgt ctcataagtg acttctaccc gggagccgtn acagtggcct 240
ggaaggcaga tagcagcccc gtcaaggcgg gagtggagac caccacaccc tncaaacaaa 300
gcaacaacaa gtacgcggcc agcagctatc tgagcctgac gcctgagcag tggaaagt 357

<210> 88
<211> 308
<212> DNA
<213> Homo sapiens

<400> 88
ctcagtctgg gcctaaggaa gcagcactgg tggcgcctca gccatggcct ggaccgttct 60
cctcctcggc ctcctctctc actgcacaga ctctgtgacc tcctatgtgt tgactcagac 120
accctcagtg tcagtggccc caggaaagac ggccaagatt acctgtgggg gaaacaatat 180
tgggagtaac aatgtacact ggtattacca gaagccaggc caggccccctg tcctaatacat 240
ctcttttgat aacgaccggc cctcagggat atctgagcga ttctctggct tcaattctgg 300
ggacatgg 308

<210> 89
<211> 206
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(206)
<223> n = A,T,C or G

<400> 89
ccaccctgac catcaacagg gtcgaagccg gcgatgaggc cgactattac tgtcaagtgt 60
gggatcgtaa taatgaccat gtcgtcttcg gcggagggaac caaactggcc gtcctaggtc 120
agcccaaggc tgccccctcg gnnactctgt tccccccctc ctctgaggag cttcaagcca 180
acaaggccac actggtgtgt ctcata 206

<210> 90
<211> 373
<212> DNA
<213> Homo sapiens

<400> 90
ctgtagcttc tgtgggactt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tactttgtgt tgctttgttt ggagggtgtg gtggtctcca ctcccgcctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agtgtggcct tgttggcttg aagctcctca gaggaggcgg ggaacagagt gaccgagggg 240
gcagccttgg gctgacctag gacggccagt ttggtccctc cgccgaagac gacatgggtca 300
ttattatgat cccacacttg acagtaatag tcggcctcat ccccggttc gaccctgttg 360
atggtcaggg tgg 373

<210> 91
<211> 347
<212> DNA
<213> Homo sapiens

<400> 91
cccgtcagc tcctggggct cctgctgctc tggctcccag gtgccaaatg tgacatccag 60

```

atgacccaat ctccttccac cctgtctgca tctgtcggag atacagttac aataagttgt 120
cgggcctctc agaatataga tcggtggttg gcctggcatc aacagaaacc tggcaaagcc 180
cctaattgtc taatttatgc gacttccagt ttagaagaag gggctctcatt aagatttact 240
ggcagtggtt ctgggacaca attcaattta accatcacca gtctgcagcc tgacgattca 300
gcaacttatt attgtcaaca ttattctgca tctcttcgca gtttttg 347

```

```

<210> 92
<211> 421
<212> DNA
<213> Homo sapiens

```

```

<400> 92
ctgtagcttc tgtgggactt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt ggaggggtgt gtggtctcca ctccgcctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agtgtggcct tgttggcttg aagctcctca gaggaggcgg ggaacagagt gaccgagggg 240
gcagccttgg gctgacctag gacggccagt ttggtccctc cgccgaagac gacatgggtca 300
ttattacgat cccacacttg acagtaatag tcggcctcat cgccggcttc gaccctgttg 360
atggtcaggg tggccatgtc cccagaattg aagccaggcc agggccctgt cctaatactc 420
t 421

```

```

<210> 93
<211> 324
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(324)
<223> n = A,T,C or G

```

```

<400> 93
ctgtagcttc tgtgggactt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt ggaggggtgt gtggtctcca ctccgcctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
annngngcct tgntggcttg aagctcctna gaggaggcgg ggaacagagt gaccgagggg 240
gcagccttgg gctgacctag gacggccagt ttggtccctn cgccnaaanac gacntgggtca 300
ttattacnga tccacactt gaca 324

```

```

<210> 94
<211> 150
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(150)
<223> n = A,T,C or G

```

```

<400> 94
ctgtagcttc tgtgggactt ccactgctca ngcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt gnaggggtgt nnggtctcca ctccgnntt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct 150

```

```

<210> 95
<211> 167
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(167)
<223> n = A,T,C or G

```

```

<400> 95
ctgtagcttc tgcnggactt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtgn tgctttgttt ggagggtgtg gtggntcca ctcccgnctt gacggggctg 120
nnatctgcct tccaggccac tgtcacggnt cccggntaga agtcact 167

```

```

<210> 96
<211> 307
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(307)
<223> n = A,T,C or G

```

```

<400> 96
ctgtagcttc tgtgggnctt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt ggagggtgtg gtggntcca ctcccgcctt gacggggctg 120
ctatctgcct tccangccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agtgtggcct tgttggcttg aagctcctca naggangggc gnaacagagt gaccgagggg 240
gcanccttgg gctgacctan gacggccagt tnggtccctc cgccgaanac gacatgggtca 300
ttattac 307

```

```

<210> 97
<211> 571
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(571)
<223> n = A,T,C or G

```

```

<400> 97
ctgtagcttc tgtgggactt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt ggagggtgtg gtggntcca ctcccgcctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agtgtggcct tgttggcttg aagctcctca gaggagggcg ggaacagagt gaccgagggg 240
gcagccttgg gctgacctca atctgggtct ggatcctggc tctgggtccc agctctgtga 300
ttcccagaca tcagccccga gggcactggg tccttctaaa gtctcccang aggtgcctcc 360
ctcagacccc ttgttcccaa ttccccagga gatggaaccc acgtaaccca agggtaaacc 420
tggtccgaca agaaccaga ctgagggggc cagaacagaa caaggcttan agaccagtc 480
tgcgcctgtc agacacacaa agagacaaac agagagagag agacagacag acagacngac 540
agacgaggct cagtaggtca ttctatctag t 571

```

```

<210> 98
<211> 337
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(337)
<223> n = A,T,C or G

```

```

<400> 98
ctgtagcttc tgtgggnctt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt ggagggtgtg gtggntcca ctcccgcctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agtgtggcct tgttggcttg aagctcctca gaggagggcg ggaacagagt gaccgagggg 240
gcagccttgg gctgacctag gacggccagt ttggtccctc cgccgaagac gacatgggtca 300
ttattacnat cccacacttn acagtaatag tcggcct 337

```

<210> 99
<211> 342
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(342)
<223> n = A,T,C or G

<400> 99
ccaccctgac catcaacagg gtcgaagccg gcgatgaggc cgactattac tgtcaagtgt 60
gggatcgtaa taatgaccat gtcgtcttcg gcggannaac caaactggcc gnnctagggtc 120
agcccaannc tgccccctng gtnactcatg ntcnngccct cctctgagga gcttcaagcc 180
aacaaggcca cactgggtgtg tctcataant gacttctacc cgggagccgt gacagtggcc 240
tggaaggcan atagcancnc cgtcaaggcg gnagtggana ccacnacanc ctccaaacaa 300
agcaacaaca agtacgcggg cagnagctat ctgagtcctg ac 342

<210> 100
<211> 366
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(366)
<223> n = A,T,C or G

<400> 100
ctgtagcttc tgtgggactt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt ggagggtgtg gtggtctcca ctccgcctt gacggggctg 120
ctatctgcct tccagggcac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agtgtggcct tgttggcttg aagctcctca gaggagggcg ggaacagagt gaccgagggg 240
gcagccttg gctgacctag gacggccagt tttggtccct ccgtcgaaga cnacatgggtc 300
attattacga tcccacactt gacagtaata gncgggntca tcgcccggctt cnaccctgtt 360
gatggt 366

<210> 101
<211> 131
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(131)
<223> n = A,T,C or G

<400> 101
ctgtagcttc tgtgggnctt ccactgctca ngcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt ggagggtgtg gnggtctcca ctccgcctt gacggggctg 120
ctatctgcct t 131

<210> 102
<211> 330
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(330)
<223> n = A,T,C or G

<400> 102
ctgtagcttc tgtggnactt ccaactgctca ggcgtnaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt ggagggtgtg gtggtctcca ctcccgctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agtgtggcct tgttggttg aagctcctca gaggagggcg ggaacanagt gaccgagggg 240
gcanncttgn gctgacctan gacggccagt ttggtccctc cgccgaagac gacatggtea 300
ttattacgat cccacacttg acagtaatag 330

<210> 103
<211> 369
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(369)
<223> n = A,T,C or G

<400> 103
cttctgtggg acttccactg ctcaggcgtn aggcctcanat agctgctggc cgcgtacttg 60
ttgttgcttt nnttggaggg tgtggtggtc nncactcccg ccttgacggg gctgctatct 120
gccttccagg ccactgtcac ggctcccggt tagaagtcac ttatgagaca caccantgtg 180
gccttggttg cttgaagctc ctcanaggag ggcgggaaca gagtgaccga gggggcagcc 240
ttgggctgac ctaggacggc cagtttggtc cctccgcccga agacgacatg gtcattatta 300
cgatcccaca cttgacagta atagtcggcc tcatcgccgg cttcgaccct gttgatggtc 360
agggtggcc 369

<210> 104
<211> 254
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(254)
<223> n = A,T,C or G

<400> 104
ccaccctgac catcaacagg gtcgaagccg gcgatgaggc cgactattac tgtcaagtgt 60
gggatcgtaa taatgaccat gtctctctcn gnggagggac caaactggcc gtcctaggtc 120
agcccaaggc tgccccctcg gtcactctgt tcccgccctc ctctgaggag cttcaagcca 180
acaaggccac actggtgtgt ctcataagtg acttctaccc gggagccgtg acagtggcct 240
ggaaggcaga tagc 254

<210> 105
<211> 366
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(366)
<223> n = A,T,C or G

<400> 105
caggacacag catggacatg aggggtccccg ctcagctcct ggggctcctg ctgctctggc 60
tcccagggtg caaatgtgac atccagatga cccaatctcc tccaccctg tctgcatctg 120
tcggagatac agttacaata agttgncggg cctctcanaa tatagatcgg tggttggcct 180
ggcatcaaca gaaaccaggc aaagccccta atgtcctaata ttatgcgact tccagtttag 240
aagaaggggt ctcattaaga tttactggca gtggatctgg gacacaattc aatttaacca 300
tcaccagtct gcagcctgac gattcagcaa cttattattg tcaacattat tntgcatctc 360
ttnnga 366

<210> 106
<211> 485
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(485)
<223> n = A,T,C or G

<400> 106
aaaaatggag agtctgaatt ttattagagc tcacacacca tatattaaca tatacaactg 60
tgaaccagct aatccctctg agaaaaactc cccatctacc caatactgtt acagcatata 120
atctctgttc ttgggcattt tgtcagtgat gctgatcttt gccttcttcc aggaacttgt 180
aatagctggc atcggttgaga atgaatggaa aagaacgtgc tccagaccca aatctaact 240
agttctcctg tcggcagaag aaaaaaaga acagactatt gaaataaaa aagaagtgg 300
tgggctaact gaacatctt cccaaccaa gaatgaagaa gacattgaaa ttattccaat 360
ccaagaagag gaagaagaag aaacagagac gaactttcca gaaactcccc aagatcagga 420
atcctcacca atagaaaatg acagctctcc ttaagtgatt tcttctgttt tctgnttcct 480
ttttt 485

<210> 107
<211> 373
<212> DNA
<213> Homo sapiens

<400> 107
ccaccctgac catcaacagg gtcgaagccg gcgatgagc cgactattac tgtcaagtgt 60
gggatcgtaa ttatgaccat gtcgtcttcg gcggaggagc caaactggcc gtcctaggtc 120
agcccaaggc tgccccctcg gtcactctgt tcccgccctc ctctgaggag cttcaagcca 180
acaaggccac actggtgtgt ctcataagtg acttctacce gggagccgtg acagtggcct 240
ggaaggcaga tagcagcccc gtcaggcggg gagtggagac caccacacc tccaaacaaa 300
gcaacaacaa gtacgcggcc agcagctatc tgagcctgac gcctgagcag tggaagtccc 360
acagaagcta cag 373

<210> 108
<211> 75
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(75)
<223> n = A,T,C or G

<400> 108
ctgtagcttc tgtgggactt ccactgctca ggcgtcagc tcanatanct gctggccgcg 60
tacttggtgt tgctt 75

<210> 109
<211> 485
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(485)
<223> n = A,T,C or G

<400> 109
aaaaatggag agtctgaatt ttattagagc tcacacacca tatattaaca tatacaactg 60
tgaaccagct aatccctctg agaaaaactc cccatctacc caatactgtt acagcatata 120
atctctgttc ttgggcattt tgtcagtgat gctgatcttt gccttcttcc aggaacttgt 180

aatagctggc atcgttgaga atgaatggaa aagaacgtgc tccagaccca aatctaacat 240
agttctcctg tcagcagaag aaaaaaaga acagactatt gaaataaaag aagaagtggg 300
tgggctaact gaaacatctt cccaaccaa gaatgaagaa gacattgaaa ttattccaat 360
ccaagaagag gaagaagaag aaacagagac gaactttcca gaacctccc aagatcagga 420
atcctcacca atagaaaatg acagctctcc ttaagtgatt tcttctgttt tctgnttcct 480
ttttt 485

<210> 110
<211> 561
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(561)
<223> n = A,T,C or G

<400> 110
aaggaaagcag cactggtggg gcctcagcca tggcctggac cgttctcctc ctccgcctcc 60
tctctcactg cacagggtgat cccccaggg tctcaccaac ctgccagcc caaggcttct 120
gggtccagcg tgtccttaat tctgagctca ggagggccct tctgtgtgtg ggcaggatgc 180
tcattgacct ggtgcagggt gggaggctgg tggggctgaa ttcccccaa actgtgctca 240
aggacttgtg agaacctgag ggactgcacc tgccaagaga aagtagtgag tttcagttc 300
gaagtctcca tacaacagga catttgtggg ccactggggc tacggctgat tgcaggggat 360
accctgaggg ttacagact ctctggattt tgtctgggac agcaggacaa gggatttcaa 420
aaggaaatcc ttctacttgg aaggcaacct ctctgncatt tattctttt nttatttatt 480
tattttttta ttattcttta tctttgcaga ctctgtgacc tcctatgtgt tgactcagac 540
accctcagtg tcagtggccc c 561

<210> 111
<211> 255
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(255)
<223> n = A,T,C or G

<400> 111
ccaccctgac catcaacagg gtcgaagccg gcgatgaggg cgactattac tgtcaagtgt 60
gggatcgtaa taatgacct gtcgtcttcg gcggagggac caaactggcc gtcctaggctc 120
agcccaaggc tgccccctcg gtcactctgt tcccgcctc ctctgaggag cttcaagcca 180
acaaggccac actgggtgtgt ctcataagtg acttctaccc ggnagccgtg acagtggcct 240
ggaaggcana tagca 255

<210> 112
<211> 365
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(365)
<223> n = A,T,C or G

<400> 112
ctgtagcttc tgtgggactt ccactgctca ngcgtcangc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt ggagggtgtg gtggtctcca ctcccgcctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agtgtggcct tgttggcttg aagctcctca taggagggcg gnaacagant gaccganggg 240
gcagccttgn gctgacctag gacggccagt ttggtccctc cgccgaagac gacatggtca 300
ttattacgat cccacacttg acagtaatat tcggcctcat ngccggcttc gacctgttg 360

atggt 365

<210> 113
<211> 66
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(66)
<223> n = A,T,C or G

<400> 113
ctgtagcttc cncggactt ccactgctca ngcgtcaggc tcagatagct gctggccgcg 60
tacttg 66

<210> 114
<211> 94
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(94)
<223> n = A,T,C or G

<400> 114
ctgtagcttc tgtnggactt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtat tgctttgntt ggagggngtg gtgg 94

<210> 115
<211> 386
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(386)
<223> n = A,T,C or G

<400> 115
ctgtagcttc tgtgggactt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt ggaggggtgt gtgggtctcca ctccgcctt gacggggctg 120
ctatctgcct tccagggcac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agtgtggcct tgttggtctt aagctcctca gaggagggcg ggaacagagt gaccgagggg 240
gcagccttgg gctgacctan nacggccagt ttgggtccctc cgccnaagac gacatggttc 300
attattacga tcccacactt gacagtaata gtcggcctca tcgccgggctt cnaccctgtt 360
gatggtcagg gtggctgttc atgctt 386

<210> 116
<211> 188
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(188)
<223> n = A,T,C or G

<400> 116
ccaccctgac catcaacagg gtcgaagccg gcgatgaggc cgactattac tgtcaagtgt 60
gggatcgtaa taatgaccat gtcgtcttcn gcggagggac caaactggcc gtcctaggtc 120
ancccaaggc tgccccctcg gtcactctgt tccccccctc ctctgangag cttcaancca 180

acaaggcc

188

<210> 117
<211> 308
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(308)
<223> n = A,T,C or G

<400> 117
ctgtagcttc tgtgggnctt ccactgctca nncgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt ggaggggtgt gtgggtctcca ctcccgctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
antgtggcct tgttggttg aagctcctca gaggagggcg ggaacanant gaccganggg 240
gcagccttgg gctgacctan gacggccagt ttgggtcctc cgccnaanac gacatgggtca 300
attattaa 308

<210> 118
<211> 203
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(203)
<223> n = A,T,C or G

<400> 118
ctgtagcttc tgtgnnnctt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt ggaggggtgt gtgggtctcca ctcccgctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agtgtggcct tgnrtggcttg aag 203

<210> 119
<211> 293
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(293)
<223> n = A,T,C or G

<400> 119
ccaccctgac catcaacagg gtcgaagccg gcgatgaggc cgactattac tgtcaagtgt 60
gggatcgtaa taatgacat gtcgtcttcg gcggagggac caaactggcc gtcctaggtc 120
agcccaaggc tgcccctcg gtcactctgt tcccgccctc ctctgaggag cttcaagcca 180
acaaggccac actggtgtgt ctcataagt actttctacc cgggagccgt gacantggcc 240
tgnaaggcan atagcangnn ccgtcaaggc ggnagtggag accaccacac cct 293

<210> 120
<211> 266
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(266)
<223> n = A,T,C or G

<400> 120
ctaaggaagc agcactgggtg gtgcctcagc catggcctgg accgttctcc tcctcggcct 60
cctctctcac tgcacagact ctgtgacctc ctatgtgttg actcagacac cctcagtgtc 120
agtggcccca ngaaagacgg ccaagattac ctgtggggga aacaatattg ggagtaacaa 180
tgtacactgg tattaccaga agccnngcca ngccccgtt cctaatacctc tcttttgata 240
acgaccggnn ctcagggata tctgag 266

<210> 121
<211> 210
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(210)
<223> n = A,T,C or G

<400> 121
ctgtagcttc tgtnggactt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tactttgttt ggagggtgtg gtggtctcca ctcccgcctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
antgtggcct tgttggttg aagctcctca 210

<210> 122
<211> 292
<212> DNA
<213> Homo sapiens

<400> 122
ccatgtcccc agaattgaag ccagagaatc gctcagatat ccctgagggc cggtcgttat 60
caaaaagagat gattaggaca ggggcctggc ctggcttctg gtaataccag tgtacattgt 120
tactcccaat attgtttccc ccacaggtaa tcttgccgt ctttcctggg gccactgaca 180
ctgagggtgt ctgagtcaac acataggagg tcacagagtc tgtgcagtga gagaggaggc 240
cgaggaggag aacgggtccag gccatggccg aggcaccacc agtgctgctt cc 292

<210> 123
<211> 474
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(474)
<223> n = A,T,C or G

<400> 123
ggaagcagca ctggtggtgc ctcagccatg gcctggaccg ttctcctccc cggcctctc 60
tctcactgca cagactctgt gacctcctat gtgttgactc agacaccctc agtgtcagt 120
gccccaggaa agacggccaa gattacctgt gggggaaaca atattgggag ttacagtgt 180
cactgggtatt accaaaagcc aggccaggcc cctgtcctaa tcatctcttt tgataacgac 240
cggccgcccc ggcagggtcca atgaagatc tccacagttg tatgtggcct gtggtagggg 300
accccgatca tctctgagag tcctaagaca tggacttgag gtgtcagaaa tggctgtttc 360
tgagctacct ggtnacccca aacgctgtct ggacagtgcg tcgacacatt gaagatgagt 420
ttgatgccta catcattgtg tctttcgtga atgccaccct agtgtgtgcc attg 474

<210> 124
<211> 200
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(200)

<223> n = A,T,C or G

<400> 124

```
ccaccctgac catcaacagg gtcgaagccg gcgatgagggc cgactattac tgtcaagtgt 60
gggatcgtaa taatgaccat gtcgtcttcg gcgganngac caaactggcc gtcctaggtc 120
agcccaaggc tgccccctcg gtcactctgt tcccgccctc ctctgaggag cttcaagcca 180
acaaggccac actggtgtgt                                     200
```

<210> 125

<211> 155

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(155)

<223> n = A,T,C or G

<400> 125

```
ctgtagcttc ngccggactt ccaactgctca ggcgtcaggc tcagatagct gctggcccg 60
tacttggtgt tgctttgttt ggaggggtgt gtggtctcca ctccgcctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgg                                     155
```

<210> 126

<211> 160

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(160)

<223> n = A,T,C or G

<400> 126

```
ccaccctgac catcaacagg gtcgaagccg gcgatgagggc cgactattac tgtcaagtgt 60
gggatcgttaa tgatgaccat gtcgtcttcg gcggangaac caaactggcc gtcctaggtc 120
agcccaaggc tgccccctcg gtcactctgt nnccgccctc                                     160
```

<210> 127

<211> 201

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(201)

<223> n = A,T,C or G

<400> 127

```
ccaccctgac catcaacagg gtcgaagccg gcgatgagggc cgactattac tgtcaagtgt 60
gggatcgtaa taatgaccat gtcgtcttcg gcgganngac caaactggcc gtcctaggtc 120
agnccaaggc tgnccccctcg gtcactctgt tcccgccctc ctntgangag cttcaagcca 180
acaaggccac actggtgtgt c                                     201
```

<210> 128

<211> 198

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(198)

<223> n = A,T,C or G

<400> 128
ctgtagcttc tgnngnctt ccactgctca ggcgtcaggc tcanatagct gctggccgcg 60
tacttggtgt tgctttgttt ggaggggtgt gtggtctcca ctccgcctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga agtcacttta tganacacac 180
cantgtggcc ttgttggc 198

<210> 129
<211> 485
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(485)
<223> n = A,T,C or G

<400> 129
aaaaaaggaa acanaaaaca gaagaaatca cttaaggaga gctgtcattt tctattgggtg 60
aggattcctg atcttgggga gggtctggaa agttcgtctc tgtttcttct tcttcctctt 120
cttggattgg aataatttca atgtcttctt cattctttgg ttgggaagat gtttcagtta 180
gccaaccac ttcttctttt atttcaatag tctgttcttt tttttcttct gctgacagga 240
gaactatggt agatttgggt ctggagcacg ttcttttcca ttcatttca acgatgccag 300
ctattacaag ttcttgggaag aaggcaaaaga tcagcatcac tgacaaaatg cccaagaaca 360
gagattgtat gctgtaacag tattgggtag atggggagtt tttctcagag ggattagctg 420
gttcacagtt gtatatgtta atatatggtg tgtgagctct aataaaattc agactctcca 480
ttttt 485

<210> 130
<211> 77
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(77)
<223> n = A,T,C or G

<400> 130
ctgtagcttc tgtnggactt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttg 77

<210> 131
<211> 161
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(161)
<223> n = A,T,C or G

<400> 131
ctgtagcttc tgtnggactt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt ggaggggtgt gtggtctcca ctccgcctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga a 161

<210> 132
<211> 294
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (1)...(294)
<223> n = A,T,C or G

<400> 132
ccaccctgac catcaacagg gtcgaagccg gcgatgaggc cgactattac tgtcaagtgt 60
gggatcataa taatgaccat gtcgtcttcg gcggagggac caaactggcc gtcctaggtc 120
agcccaaggc tgccccctcg gtcactctgt tcccgcctc ctctgaggag cttcaagcca 180
acaagggcac actggtgtgt ctcataagt acttctaccc gggagccgtg acantnncc 240
ggaaggcana tancagcccc gtcaangcgg gagtgganac caccacacc tcca 294

<210> 133
<211> 298
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(298)
<223> n = A,T,C or G

<400> 133
ccaccctgac catcaacagg gtcnaagccg gcgatgaggc cgactattac tgtcaagtgt 60
gggatcgtaa taatgaccat gtcgtcttcg gcggagggac caaactggcc gtcctaggtc 120
agcccaaggc tgccccctcg gtcactctgn tcccgnccctc ctntgangag cttcaagcca 180
acaagggcac actggtgtgt ctcataagt acttctaccc gggagccgtg acagtggcct 240
ggaaggcant atagcagccc cgtcaaggcg ggagtggaga ccaccacacc ctccaaac 298

<210> 134
<211> 373
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(373)
<223> n = A,T,C or G

<400> 134
ctgtagcttc tgtgggactt ccactgttca ggcgtcaggc tcagatagct gctggccgcg 60
tacttgttgt tgctttgttt ggaggggtgtg gtggtctcca ctccgcctt gacggggctg 120
ctatctgcct tccagggcac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agtgtggcct tggtggcttg aagctcctca gaggagggcg ggaacagagt gaccgagggg 240
gcagccttgg gctgacctan gacggccagt ttggtccctc caccgaagac gacatggtea 300
ttattacgat cccacacttg acagtaatag tcggcctcat cgccggcttc gaccctgttg 360
atggtcaggg tgg 373

<210> 135
<211> 487
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(487)
<223> n = A,T,C or G

<400> 135
aaaaatggag agtctgaatt ttattagagc tcacacacca tatattaaca tatacaactg 60
tgaaccagct aatccctctg agaaaaactc cccatctacc caatactgtt acagcataca 120
atctctgttc ttgggcattt tgtcagtgat gctgatcttt gccttcttcc aggaacttgt 180
aatagctggc atcgttgaga atgaatggaa aagaacgtgc tccagaccca aatctaact 240
agttctcctg tcagcagaag aaaaaaaga acagactatt gaaataaaag aagaagtggg 300

tgggctaact gaaacatctt cccaacccaaa gaatgaagaa gacattgaaa ttattccaat 360
ccaagaagag gaagaagaag aaacagagac gaactttcca gaacctcccc aagatcagga 420
atcctcacna atagaaaatg acagctctcc ttaagtgatt tcttctgttt tctgtttttc 480
ctttttt 487

<210> 136
<211> 368
<212> DNA
<213> Homo sapiens

<400> 136
acagcatgga catgaggggc cccgctcagc tcctggggct cctgctgctc tggctcccag 60
gtgccaaatg tgacatccag atgaccaat ctccctccac cctgtctgca tctgtcggag 120
atacagttac aataagtgtg cgggcctctc agaatataga tcggtgggtg gcctggcatc 180
aacagaaacc aggcaaagcc cctaattgtc taatttatgc gacttccagt ttagaagaag 240
gggtctcatt aagatttact ggagtgat ctgggacaca attcaattta accatcacca 300
gtctgcagcc tgacgattca gcaacttatt attgtgcaac attattctgc atctcttcgc 360
agtttttg 368

<210> 137
<211> 59
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(59)
<223> n = A,T,C or G

<400> 137
ctgtagcttc tgtgggnctt ccactgctcg ggcgtcaggc tcaggtagct gctggccgc 59

<210> 138
<211> 357
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(357)
<223> n = A,T,C or G

<400> 138
ccaccctgac catcaacagg gtcgaagccg gcgatgaggc cgactattac tgtcaagtgt 60
gggatcgtaa taatgaccat gtcgtcttcg gcggaggagc caaactggcc gtcctaggtc 120
agcccaaggc tgccccctcg gtcactctgt tcccgcctc ctctgannag cttnaagcca 180
acaaggccac actggtgtgt ctcataagt acttctaccc gggagccgtg acagtggcct 240
ggaaggcaga tagcagcccc gtcaaggcgg gagtggagac caccacacc tccaaacaaa 300
gcaacaacaa gtacncggcc agcanctatc tgagcctgac gcctgagcag tggaagt 357

<210> 139
<211> 79
<212> DNA
<213> Homo sapiens

<400> 139
ctgtagcttc tgtgggactt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttgtgtg tgctttgtt 79

<210> 140
<211> 239
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(239)
<223> n = A,T,C or G

<400> 140
ctgtagcttc tgtgggactt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttgttgt tgctttgttn ngagggtgtg gnngtctcca ctcccgcctt ganngggctg 120
ctatcnnct tccagagcca cnntcacggc tcccgggtag aagtcactta tgagacacac 180
cantgtggcc ttgttngctt naagctcctc agaggagggc gggaacagag tgaccgagg 239

<210> 141
<211> 373
<212> DNA
<213> Homo sapiens

<400> 141
ccaccctgac catcaacagg gtcgaagccg gcgatgaggc caactattac tgtcaagtgt 60
gggatcgtaa taatgaccat gtcgtcttcg gcggaggagc caaactggcc gtcctaggtc 120
agcccaaggc tgccccctcg gtcactctgt tcccgcctc ctctgaggag cttcaagcca 180
acaaggccac actggtgtgc ctcataagtg acttctaccc gggagccgtg acagtggcct 240
ggaaggcaga tagcagcccc gtcaaggcgg gagtggagac caccacaccc tccaaacaaa 300
gcaacaacaa gtacgcggcc agcagctatc tgagcctgac gcctgagcag tggaagtccc 360
acagaagcta cag 373

<210> 142
<211> 373
<212> DNA
<213> Homo sapiens

<400> 142
ccaccctgac catcaacagg gtcgaagccg gcgatgaggc cgactattac tgtcaagtgt 60
gggatcgtaa taatgaccat gtcgtcttcg gcggaggagc caaactggcc gtcctaggtc 120
agcccaaggc tgccccctcg gtcactctgt tcccgcctc ctctgaggag cttcaagcca 180
acaaggccac actggtgtgt ctcataagtg acttctaccc gggagccgtg acagtggcct 240
ggaaggcaga tagcagcccc gtcaaggcgg gagtggagac caccacaccc tccaaacaaa 300
gcaacaacaa gtacgcggcc agcagctatc tgagcctgac gcctgagcag tggaagtccc 360
acagaagcta cag 373

<210> 143
<211> 267
<212> DNA
<213> Homo sapiens

<400> 143
cacagtcac aattatagac cccacaacat gcgccctgaa gacagaatgt tccatatcag 60
agctgtgatc ttgagagccc tctccttggc ttccctgctg agtctccgag gagctggggc 120
catcaaggcg gaccatgtgt caacttatgc cgcgtttgta cagacgcata gaccaacagg 180
ggagtttatg tttgaatttg atgaagatga gatgttctat gtggatcttg acaagaagga 240
gaccgtctgg catctggagg agtttgg 267

<210> 144
<211> 367
<212> DNA
<213> Homo sapiens

<400> 144
cttctgtggg acttccactg ctacaggcgtc aggctcagat agctgctggc cgcgtacttg 60
ttgttgcttt gtttggaggg tgtgtgtgtc tccactcccg ccttgacggg gctgctatct 120
gccttccagg ccactgtcac ggctccggg tagaagtcac ttatgagaca caccagtgtg 180
gccttgctgg cttgaagctc ctacagaggag ggcggaaca gagtgaaccg gggggcagcc 240
ttgggctgac ctaggacggc cagtttgggt cctccgccga agacgacatg gtcattatta 300

agatcccaca cttgacagta atagtcggcc ttatcgccgg cttcgaccct gttgatggtc 360
aggggtgg 367

<210> 145
<211> 90
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(90)
<223> n = A,T,C or G

<400> 145
ccaccctnac catcaacagg gtcgaagccg gggatgaggc cgactattac tgnnaagtgt 60
gggatcataa taatgaccat gtcgnnttcg 90

<210> 146
<211> 291
<212> DNA
<213> Homo sapiens

<400> 146
ccatgtcccc agaattgaag ccagagaatc gctcagatat ccctgagggc cggtcgttat 60
caaaagagat gattaggaca ggggcctggc ctggcttctg gtaataccag tgtacattgt 120
tactcccaat attgtttccc ccacaggtaa tcttgcccg ctttcctggg gccactgaca 180
ctgaggggtgt ctgagtcaac acataggagg tcacagagtc tgtgcagtga gagaggaggc 240
cgaggaggag aacggtccag gccatggctg aggcaccacc agtgctgctt c 291

<210> 147
<211> 244
<212> DNA
<213> Homo sapiens

<400> 147
ccatgtcccc agaattgaag ccagagaatc gctcagatat ccctgagggc cagtcgttat 60
caaaagagat gattaggaca ggggcccggc ctggcttctg gtaataccag tgtacattgt 120
tactcccaat attgtttccc ccacaggtaa tcttgcccg ctttcctggg gccactgaca 180
ctgaggggtgt ctgagtcaac acataggagg tcacagagtc tgtgcagtga gagaggaggc 240
cgag 244

<210> 148
<211> 513
<212> DNA
<213> Homo sapiens

<400> 148
ccaagccttt tcctttgagg ctcagggcgg gctggctaac attgctatat tgaacaacaa 60
cttgaatacc ttgatccagc gttccaacca cactcaggcc accaacgac cccctgagg 120
gaccgtgttt cccaaggagc ctgtggagct gggccagccc aacaccctca tctgccacat 180
tgacaagtcc ttcccaccag tgctcaacgt cagtggtgctg tgcaacgggg agctgggtcac 240
tgaggggtgc gctgagagcc tcttcctgcc cagaacagat tacagcttcc acaagttcca 300
ttacctgacc tttgtgccct cagcagagga cttctatgac tgcaggggtgg aacactgggg 360
cttgagaccag ccgctcctca agcactggga ggcccaagag ccaatccaga tgcctgagac 420
aacggagact gtgctctgtg ccctgggcct ggtgctgggc ctagtccgga tcatcggtgg 480
caccgtcctc atcataaagt ctctgcgttc tgg 513

<210> 149
<211> 181
<212> DNA
<213> Homo sapiens

<400> 149

```

cttctgtggg acttccactg ctcaggcgctc aggctcagat agctgctggc cgcgtacttg 60
ttgttgcttt gtttggaggg tgtggtggtc tccactcccg ccttgacggg gctgctatct 120
gccttccagg ccactgtcac ggctcccggt tagaagtcac ttatgagaca caccagtgtg 180
g 181

```

```

<210> 150
<211> 373
<212> DNA
<213> Homo sapiens

```

```

<400> 150
ctgtagcttc tgtgggactt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt ggagggtgtg gtggtctcca ctcccgcctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agtgtggcct tgttggttgg aagtcctca gaggagggcg ggaacagagt gaccgagggg 240
gcagccctgg gctgacctag gacggccagt ttggtccctc cgccgaagac gacatggtca 300
ttattacgat cccacacttg acagtaatag tcggcctcat cgccggcttc gaccctgttg 360
atggtcaggg tgg 373

```

```

<210> 151
<211> 252
<212> DNA
<213> Homo sapiens

```

```

<400> 151
cttctgtggg acttccactg ctcaggcgctc aggctcagat agctgctggc cgcgtacttg 60
ttgttgcttt gtttggaggg tgtggtggtc tccactcccg ccttgacggg gctgctatct 120
gccttccagg ccactgtcac ggctcccggt tagaagtcac ttatgagaca caccagtgtg 180
gccttggtgg cttgaagctc ctcagaggag ggcgggaaca gagtgaccga gggggcagcc 240
ttgggctgac ct 252

```

```

<210> 152
<211> 499
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(499)
<223> n = A,T,C or G

```

```

<400> 152
cctcggatga tgaagacagt gcccaccaca atgcccacga ggcccacaga caaccccagg 60
gcgcagacca cagtctctgt gagctctgac ataggggctg gaatctcagg ctcccagtg 120
ttcagaagag gcttgtccag tcccagtg cccaccttgc agtcataact ctccctcagca 180
gaaggaggga gggtagaggta actgatcttg aagaaggaat gatcactctt ggagaggaag 240
ctggtctcan aaacaccttc tgtgactgag tgcccattgc tcanccatgt gatgttgacc 300
acaggaggaa agatgttgtc cacaagacag atgaggatgt tgggctgacc cagtgtcacg 360
ggagacttgg aaaacactgt gacctcagga acctcattgg tagcagcggg agagtgtggag 420
cgtttaatca gactgttcaa gttatgtttt angacagcga tgtttgtcag tgcaaatgac 480
gggtcaaatac taaattgtc 499

```

```

<210> 153
<211> 373
<212> DNA
<213> Homo sapiens

```

```

<400> 153
ctgtagcttc tgtgggactt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt ggagggtgtg gtggtctcca ctcccgcctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agtgtggcct tgttggttgg aagtcctca gaggagggcg ggaacagagt gaccgagggg 240
gcagccctgg gctgacctag gacggccagt ttggtccctc cgccgaagac gacatggtca 300

```

ttattatgat cccacacttg acagtaatag tcggcctcat ccccggttc gaccctgttg 360
atggtcaggg tgg 373

<210> 154
<211> 243
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(243)
<223> n = A,T,C or G

<400> 154
ctgtagcttc tgnnggactt ccaactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt ggagggtgtg gnggtctcca ctcccgctt gacggggctg 120
ctatctgcct tccaggccac tgtcacngct cccgggtana agtcactnn gagacacacc 180
antgtggcct tgntggcttg aanctcctca taggagggcg ggaacagant gaccgagggg 240
gca 243

<210> 155
<211> 307
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(307)
<223> n = A,T,C or G

<400> 155
ccacctgac catcaacagg gtcgaagccg gcgatgaggc cgactattac tgtcaagtgt 60
gggatcgtaa taatgaccat gtcgtcttcg gcggaggagc caaactggcc gtcctaggtc 120
agcccaaaggc tgcccccctcg gtcactctgt tcccggccctc ctctgaggag cttcaagcca 180
acaaggccac actggtgtgt ctcataagtg acttctaccc gggagccgtg acagtggcct 240
ggaaggcaga tagcancccc gtcaaggcgg gagtgaggag caccacaccc tccaaacaaa 300
gnaacaa 307

<210> 156
<211> 502
<212> DNA
<213> Homo sapiens

<400> 156
ccatgtcccc agaattgaag ccagagaatc gctcagatat ccctgagggc cggtcgttat 60
caaaagagat gattaggaca ggggcctggc ctggcttctg gtaataccag tgtacattgt 120
tactcccaat attgtttccc ccacaggtaa tcttgccgt ctttcctggg gccactgaca 180
ctgagggtgt ctgagtcaac acataggagg tcacagagtt actttctctt ggcaggtgca 240
gtccctcagg ttctcacaag tccttgagca cagtttgggg ggaattcagc cccaccagcc 300
tcccaccctg caccagggtc atgagcatcc tgcccaccac aggaagggcc ctctgagct 360
cagaattaag gacacgctgg acccagaagc cttgggctgg gcagggttgg gagaccctgg 420
ggggatcacc tgtgcagtga gagaggaggc cgaggaggag aacggtccag gccatggctg 480
aggcaccacc agtgctgctt cc 502

<210> 157
<211> 538
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(538)
<223> n = A,T,C or G

<400> 157
ctgtcccaaa cgggccagcc ctggggcttt ggggctgggc ctccgtgagg agaggtcagt 60
cggtcagcgg cccgggggtg ctgccctgag cccaggggct ggccctgggg tctgtcagtc 120
cttccccagg ctttccaggt ccagaaggct ttgtggggtc tggggctgtg tcagggtaag 180
gaaagctgcc ttggtggagg aagagaagtc agagaggtca cacatgtggc cttagaacct 240
gctaagtcca acgtcagcat gtgacaggag gggaaagtga gcaagacggc agaaccagg 300
ggaaaaggtg gcagggagtc tgagagtga gttgggagga ccagcatctt ttaggcctg 360
agcaagaagg aggtgaccgg agtcttccag gtatccctcc ctccctagctt ctggaagtgg 420
gagtcgggga gggggctcca gtcagtcang tgtaagctcc atgccatggg gactctgcag 480
gacaggcagg cttgaggagc cactgtgcct ggacaggttc tgcaggctcc cccacttg 538

<210> 158
<211> 373
<212> DNA
<213> Homo sapiens

<400> 158
ctgtagcttc tgtgggactt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttgttgt tgctttgttt ggagggtgtg gtggtctcca ctccgcctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agtgtggcct tgttggcttg aagctcctca gagggaggcg ggaacagagt gaccgagggg 240
gcagccttgg gctgacctag gacggccagt ttggtccctc cgccgaagac gacatgttca 300
ttattacgat cccacacttg acagtaatag tcggcctcat cgccggcttc gacctgttg 360
atggtcaggg tgg 373

<210> 159
<211> 290
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(290)
<223> n = A,T,C or G

<400> 159
ctgtagcttc tgtgggactt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttgttgt tgctttgttt ggagggtgtg gtggtctcca ctccgcctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agtgtggcct tgttggcttg aagctcctca gagggaggcg ggaacagagt gaccgagggg 240
gcagccttgg gctgacctan gacggccagt ttgnccctc cgccgaagac 290

<210> 160
<211> 274
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(274)
<223> n = A,T,C or G

<400> 160
ctgtagcttc tgtgggactt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttgttgt tgctttgttt ggagggtgtg gtggtctcca ctccgcctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
antgtggcct tgttggcttg aagctcctca nagggaggcg ggaacagagt gaccgagggg 240
gcagccttgg gctgacctag gacggccagt ttgg 274

<210> 161
<211> 375
<212> DNA

<213> Homo sapiens

<400> 161

```
gtcaggacac agcatggaca tgaggggtccc cgctcagctc ctgggggtccc tgctgctctg 60
gctcccaggt gccaaatgtg acatccagat gacccaatct ccttccaccc tgtctgcatc 120
tgtcggagat acagttacaa taagctgtcg ggcctctcag aatatagatc ggtgggtggc 180
ctggcatcaa cagaaaccag gcaaagcccc taatgtccta atttatgcga cttccagttt 240
agaagaaggg gtctcattaa gatttactgg cagtggatct gggacacaaat tcaatttaac 300
catcaccagt ctgcagcctg acgattcagc aacttattat tgtcaacatt attctgcatc 360
tcttcgcagt tttgg 375
```

<210> 162

<211> 288

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(288)

<223> n = A,T,C or G

<400> 162

```
ccaccctgac catcaacagg gtcgaagccg gcgatgagggc cgactattac tgtcaagtgt 60
gggatcgtaa taatgaccat gtcgtcttcg gcggaggggac caaactggcc gtcctaggtc 120
agcccaaggc tgccccctcg gtcactctgt tccccccctc ctctgaggag cttcaagcca 180
acaaggccac actgggtgtg ctcataagtg acttctaccc gggagccgtg acagtggcct 240
ggaaggcana tagcancccc gncaaggcgg gaggggagac caccacac 288
```

<210> 163

<211> 297

<212> DNA

<213> Homo sapiens

<400> 163

```
ccaccctgac catcaacagg gtcgaagccg gcgatgagggc cgactattac tgtcaagtgt 60
gggatcgtaa taatgaccat gtcgtcttcg gcggaggggac caaactggcc gtcctaggtc 120
agcccaaggc tgccccctcg gtcactctgt tccccccctc ctctgaggag cttcaagcca 180
acaaggccac actggcgtgt ctcataagtg acttctaccc gggagccgtg acagtggcct 240
ggaaggcaga tagcagcccc gtcaaggcgg gaggggagac caccacaccc tccaaac 297
```

<210> 164

<211> 395

<212> DNA

<213> Homo sapiens

<400> 164

```
ccatgtcccc agaattgaag ccagagaatc gctcagatat ccctgagggc cggtcgttat 60
caaaagagat gattaggaca ggggcctggc ctggcttttg gtaataccag tgtacactgt 120
aactcccaat attgtttccc ccacaggtaa tcttggccgt ctttcctggg gccactgaca 180
ctgaggggtgt ctgagtcaac acataggagg tcacagactc tgtgcagtga gagaggaggc 240
cgaggaggag aacggtcagg gccatggctg aggcaccacc agtgctgctt ccttaggcaa 300
agttatccct gtctgaaatg gtatcttttg tgaggaggtc tgacttgctg aggatattga 360
ctatgaaaga gagaaccttg agtttcctgg gaaag 395
```

<210> 165

<211> 292

<212> DNA

<213> Homo sapiens

<400> 165

```
ccatgtcccc agaattgaag ccagagaatc gctcagatat ccctgagggc cggtcgttat 60
caaaagagat gattaggaca ggggcctggc ctggcttttg gtaataccag tgtacattgt 120
tactcccaat attgtttccc ccacaggtaa tcttggccgt ctttcctggg gccactgaca 180
```

ctgaggggtgt ctgagtcac acataggagg tcacagagtc tgtgcagtga gagaggaggc 240
cgaggaggag aacggtccag gccatggctg aggcaccacc agtgctgctt cc 292

<210> 166
<211> 193
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(193)
<223> n = A,T,C or G

<400> 166
gaaccgnacc cgctccgtcc cattgaagaa atgacactca gacgtagagt actccaagaa 60
acgtggncctg gtgtccccag ccaaagccag tggggagctc ancacatca ntgtcactgn 120
cagaactgnc atgcaggaac ctccaggagg cctnagacac accatgctgg anaacaggac 180
aggaccaggg gcc 193

<210> 167
<211> 373
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(373)
<223> n = A,T,C or G

<400> 167
ctgtagcttc tgtgggactt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt ggagggtgtg gtggtctcca ctccgcctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agtgtggcct tgttggcttg aagctcctca gaggaggggc ggaacagagt gaccgagggg 240
gcagccttgg gctgacctag gacggccagt ttggtccctc cgccgaagac gacatgggtca 300
ttattacgat cccacacttg acagtaatag tcggcctcat ngccggcttc gaccctgttg 360
atggtcaggg tgg 373

<210> 168
<211> 83
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(83)
<223> n = A,T,C or G

<400> 168
ccaccctgac catcaacagg gtcgaagccg gngatgaggc cgactattac tgncaagtgt 60
gggatcgtaa taatgacat gtc 83

<210> 169
<211> 466
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(466)
<223> n = A,T,C or G

<400> 169

```

ccttgccctca gatccaaggt cactcgggaag aggccatgtc taccctcaat gacactcatg 60
gaggaaatgc tgagagaagc attcagatgc atgacacaag gtaagactgc caaaaatctt 120
gttcttgctc tcctcatttt gttattttgt ttatttttag gagttttgag agcaaaatga 180
caacacccag aaattcagta aatgggactt tcccggcaga gccaatgaaa ggccctattg 240
ctatgcaatc tgggtccaaa ccactcttca ggaggatgtc ttcactggtg ggccccacgc 300
aaagcttctt catgagggaa tctaagactt tgggggctgt ccagattatg aatgggctct 360
tccacattgc cctggggggg cttctgatga tcccagcagg gatctatgca cccatctgtg 420
tgactgtgtg gtaccctctc tggggangaa ncggaagcat aaagtg 466

```

<210> 170

<211> 429

<212> DNA

<213> Homo sapiens

<400> 170

```

ccttgccctca gatccaaggt cactcgggaag aggccatgtc taccctcaat gacactcatg 60
gaggaaatgc tgagagaagc attcagatgc atgacacaag gtaagactgc caaaaatctt 120
gttcttgctc tcctcatttt gttattttgt ttatttttag gagttttgag agcaaaatga 180
caacacccag aaattcagta aatgggactt tcccggcaga gccaatgaaa ggccctattg 240
ctatgcaatc tgggtccaaa ccactcttca ggaggatgtc ttcactggtg ggccccacgc 300
aaagcttctt catgagggaa tctaagactt tgggggctgt ccagattatg aatgggctct 360
tccacattgc cctggggggg cttctgatga tcccagcagg aatctatgca cccatctgtg 420
tgactgtgtg 429

```

<210> 171

<211> 553

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(553)

<223> n = A,T,C or G

<400> 171

```

ccttgccctca gatccaaggt cactcgggaag aggccatgtc taccctcaat gacactcatg 60
gaggaaatgc tgagagaagc attcagatgc atgacacaag gtaagactgc caaaaatctt 120
gttcttgctc tcctcatttt gttattttgt ttatttttag gagttttgag agcaaaatga 180
caacacccag aaattcagta aatgggactt tcccggcaga gccaatgaaa ggccctattg 240
ctatgcaatc tgggtccaaa ccactcttca ggaggatgtc ttcactggtg ggccccacgc 300
aaggcttctt catgagggaa tctaagactt tgggggctgt ccagattatg aatgggctct 360
tccacattgc cctggggggg cttctgatga tcccagcagg gatctatgca cccatctgtg 420
tgactgtgtg gtaccctctc tggggaggca ttatgtatat ttttccgga tcaactcctg 480
cagcaacgga gaaaaactcc aggaagtgtt tgggtcaaagg aaaaatgata atgaattcat 540
tnngcctctt tgc 553

```

<210> 172

<211> 421

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(421)

<223> n = A,T,C or G

<400> 172

```

ccaatcatag agatatctgc accagcctgc aaagcttcca tgaacgcttt ggtcccagac 60
ttggcgatag taccaaggtt attgatcaag tcagccttgg tcattccaat tccagtatcc 120
acaatagtga gagttcgatc ttgtttgttc ggtataaggt taatatgcag ctctttctca 180
gagtcataat tactgggcatc tgtcaagctt tcataccgga ttttgtccaa tgcactctgat 240
gaatttgaaa tgagctctct cagaaagatc tctttgttcg agtagaaagt attgatgatc 300
aatgacatca actgggcaat ttctgcctga aaggcgaacg tntnaacctc ctntcctccc 360

```

atcgggttggt cttgggtctg ggtttcctca ngcatntgga acgacaccgc gccggnttac 420
c 421

<210> 173
<211> 481
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(481)
<223> n = A,T,C or G

<400> 173
ccttgcctca natccanggt cactcggaag aggccatgtc taccctcaat gacactcatg 60
gaggaaatgc tganagaagc attcanatgc atgacacaag gtaagactgc caaaaatctt 120
gntcttgctc tcctcatttt gttattngtt ttanttttag gagttntgag agcaaaatna 180
cancacccag aaattcagta aatgggactt tcccggcaga nccaatgaaa ggccctattg 240
ctatgcaatc tgggtccaaaa ccactcttca ggaggatgtt ttcactggtg ggccccacgc 300
aaagcttctt catgagggaa tctaagactt tgggggctgt ccagattatg aatgggctct 360
tccacattgc cctggggggt cttctgatga tcccancagg gatctatgcn cccatctgtg 420
tgactgtgtg gtaccctctc tggggaggca ttatgtatat tatttccgga tcaactctg 480
c 481

<210> 174
<211> 110
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(110)
<223> n = A,T,C or G

<400> 174
ccccggctgg cttacctggg caccgtgggc atgggggagg tgtgtcacia gatttgggct 60
ctgcagagag aanattggga gttacgggga tctgggatng aggtggntgc 110

<210> 175
<211> 372
<212> DNA
<213> Homo sapiens

<400> 175
aggacacagc atggacatga ggggtccccgc tcagctcctg gggctcctgc tgctctggt 60
cccagggtgc aaatgtgaca tccagatgac ccaatctcct tccaccctgt ctgcatctgt 120
cggagataca gttacaataa gttgtcgggc ctctcagaat atagatcggg ggttggcctg 180
gcatcaacag aaaccaggca aagcccctaa tgtcctaatt tatgcgactt ccagtttaga 240
agaaggggtc tcattaagat ttactggcag tggatctggg acacaattca atttaacat 300
caccagtctg cagcctgacg attcagcaac ttattattgt caacattatt ctgcatctct 360
tcgcagtttt gg 372

<210> 176
<211> 373
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(373)
<223> n = A,T,C or G

<400> 176

```
ctgtagcttc tgtgggactt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt ggaggggtgt gtggnctcca ctccgcctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agtgtggcct tgttggttg aagctcctca gaggagggcg ggaacagagt gaccgagggg 240
gcagccttgg gctgacctag gacggccagt ttggtccctc cgccgaagac gacatggtca 300
ttattacgat cccacacttg acagtaatag tcggcctcat cgccggcttc gaccctgttg 360
atggtcaggg tgg 373
```

<210> 177

<211> 373

<212> DNA

<213> Homo sapiens

<400> 177

```
ctgtagcttc tgtgggactt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt ggaggggtgt gtggtctcca ctccgcctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agtgtggcct tgttggttg aagctcctca gaggagggcg ggaacagagt gaccgagggg 240
gcagccttgg gctgacctag gacggccagt ttggtccctc cgccgaagac gacatggtca 300
ttattacgat cccacacttg acaataatag tcggcctcat cgccggcttc gaccctgttg 360
atggtcaggg tgg 373
```

<210> 178

<211> 136

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(136)

<223> n = A,T,C or G

<400> 178

```
cttctgtggg acttccactg ctcaggcgtc aggctcagat agctgctggc cgcgtacttg 60
ttgttgcttt gtttgaggg tgtggtggtc tccactcccn ccttgacggg gctgctatct 120
gccttccagg cactg 136
```

<210> 179

<211> 327

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(327)

<223> n = A,T,C or G

<400> 179

```
ctgtagcttc tgtgggactt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt ggaggggtgt gtggtctcca ctccgcctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agtgtggcct tgttggttg aagctcctca gaggagggcg ggaacagagt gaccgagggg 240
gcagccttgg gctgacctag gacggccagt ttggtccctc cgccgaagac gacatggtca 300
taattacgat cccacacttg ncagtaa 327
```

<210> 180

<211> 192

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(192)

<223> n = A,T,C or G

<400> 180

```
ctgtagcttc tgtgggactt ccaactgctca ngcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt ggagggtgtg gtggtctcca ctccncctt gacggggcnn 120
gctatctgcc ttccangcca ctgncacggc tcccnggtag aagtcactta tgagacacac 180
cantgtggcc tt 192
```

<210> 181

<211> 171

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(171)

<223> n = A,T,C or G

<400> 181

```
ccaccctgac catcaacagg gtcgaagccg gcgatgaggc cgactattac tgtcaagtgt 60
gggatcgtaa taatgaccat gtcgnttctg gcggaggggac caaactggcc gtcctaggtg 120
ancccaaggc tgccccctcg gtcactctgt tccnnccctn ctctgangag c 171
```

<210> 182

<211> 373

<212> DNA

<213> Homo sapiens

<400> 182

```
ctgtagcttc tgtgggactt ccaactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt ggagggtgtg gtggtctcca ctccgcctt gacggggctg 120
ctatctgcct tccaggccac tgtoacggct cccgggtaga agtcacttat gagacacacc 180
agtgtggcct tgttggtctg aagctcctca gaggaggggc ggaacagagt gaccgagggg 240
gcagccttgg gctgacctag gacggccagt ttggtccctc cgccgaagac gacatgggtc 300
ttattaagat cccacacttg acagtaatag tcagcctcat cgccggcttc gaccctgttg 360
atggtcaggg tgg 373
```

<210> 183

<211> 585

<212> DNA

<213> Homo sapiens

<400> 183

```
ccagtacacc catgaatttg atggagatga gcagttctac gtggacctgg ggaggaagga 60
gactgtcttg tgtttgctg ttctcagaca atttagattt gacccgcaat ttgacctgac 120
aaacatcgct gtcctaaaac ataacttgaa cagtctgatt aaacgctcca actctaccgc 180
tgctaccaat gaggttcctg aggtcacagt gttttccaag tctcccgta cactgggtca 240
gccaacatc ctcatctgtc ttgtggacaa catctttcct cctgtggtca acatcacatg 300
gctgagcaat gggcactcag tcacagaagg tgtttctgag accagcttcc tctccaagag 360
tgatcattcc ttcttcaaga tcagttacct caccctcctc ccttctgctg aggagagtta 420
tgactgcaag gtggagcact ggggactgga caagcctctt ctgaaacact gggagcctga 480
gattccagcc cctatgtcag agctcacaga gactgtggtc tgcgccctgg ggttgtctgt 540
gggcctcgtg ggcattgtg tgggactgt cttcatcatc cgagg 585
```

<210> 184

<211> 155

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(155)

<223> n = A,T,C or G

<400> 184
aagcagcact ggtggtgcct cagccatggc ctggaccgtt ctcctnctcg gnetcctctc 60
tcaccgnaca gactctgtga cctcctatgt gttgactcag acaccctnag tgtnagnngc 120
cccagganan acggccaaga ttacctgtgg gggaa 155

<210> 185
<211> 119
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(119)
<223> n = A,T,C or G

<400> 185
ggacacagcn tggacatgag ggtccccgct cagctcctgg ggctcctgct gctctggctn 60
ccaggtgcc aatgtganat ccagatgacc caatctcctt ccaccctgtc tgcattctgt 119

<210> 186
<211> 101
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(101)
<223> n = A,T,C or G

<400> 186
ccaccctgac catnaacagg gtngaagccg gcgatnagcc cgactatnac tgtcaagtgt 60
gggatcgtaa tnatgaccat gtcntctttn gcggaggagac c 101

<210> 187
<211> 239
<212> DNA
<213> Homo sapiens

<400> 187
cccactgtca ctctgttccc gccctcctct gaggagctcc aagccaacaa ggccacacta 60
gtgtgtctga tcagtgaact ctaccggga gctgtgacag tggcctggaa ggcagatggc 120
agccccgtca aggcgggagt ggagaccacc aaaccctcca aacagagcaa caacaagtac 180
gcggccagca gctacctgag cctgacgccc gagcagtgga agtcccacag aagctacag 239

<210> 188
<211> 84
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(84)
<223> n = A,T,C or G

<400> 188
ccaccctgac catcaacagg gtcgaagccg gngatgaggg cgactattac tgncaagngt 60
gggatcgtaa taangaccat gtcg 84

<210> 189
<211> 139
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(139)
<223> n = A,T,C or G

<400> 189
ccaccctgac catcaacagg gtcnaantcc ggcgatgagg cggactatta ctgtcaagtg 60
tgggatcgta ataatgacca tgctgtcttc ggcggaggga ccaaactggc cgnccctagg 120
cagcccaagg ctgccccct 139

<210> 190
<211> 283
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(283)
<223> n = A,T,C or G

<400> 190
ctgtagcttc tgtgggactt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt ggagggtgtg gtggtctcca ctccgcctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agtgtggcct tgttgcttg aagctcctca naggaggcg ggaacagagt gaccgagggg 240
gcagccttgg gctgacctag gacggccngt ttggtccctn cgc 283

<210> 191
<211> 179
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(179)
<223> n = A,T,C or G

<400> 191
aatgtttcat tgnactcaac atgtgaagaa aactattggt nntgncccat gactgtttgc 60
acttntctgn taacctgaca aattcctact ccttcccat gagcattgta aanccttggt 120
cacaaatntga aaacttatga gtgacctgag atnttatcta tcccctanct ttttaccta 179

<210> 192
<211> 90
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(90)
<223> n = A,T,C or G

<400> 192
ctgtagcttc tgtgggactt ccactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgntt ggagggtgtg 90

<210> 193
<211> 585
<212> DNA
<213> Homo sapiens

<400> 193


```

ccagtacacc catgaatttg atggagatga gcagttctac gtggacctgg ggaggaagga 60
gactgtctgg tgtttgcctg ttctcagaca atttagattt gacccgcaat ttgactgac 120
aaacatcgct gtctaaaac ataacttgaa cagtctgatt aaacgctcca actctaccgc 180
tgctaccaat gaggttcctg aggtcacagt gttttccaag tctcccgta cactgggtca 240
gccccacatc ctcatctgtc ttgtggacaa catctttcct cctgtgggtca acatcacatg 300
gctgagcaat gggcactcag tcacagaagg tgtttctgag accagcttcc tctccaagag 360
tgatcattcc ttcttcaaga tcagttacct caccctcctc ccttctgctg aggagagtta 420
tgactgcaag gtggagcact ggggactgga caagcctctt ctgaaacact gggagcctga 480
gattccagcc cctatgtcag agctcacaga gactgtggtc tgcgccctgg gggtgtctgt 540
gggcctcgtg ggcattgtgg tgggactgtt cttcatcatc cgagg 585

```

```

<210> 194
<211> 283
<212> DNA
<213> Homo sapiens

```

```

<400> 194
actggtggtg cctcagccat ggcctggacc gttctcctcc tcggcctcct ctctcactgc 60
acagactctg tgacctccta tgtgttgact cagacaccct cagtgtcagt ggccccagga 120
aagacggcca agattacctg tgggggaaac aatattggga gtaacaatgt acactggtat 180
taccagaagc caggccaggc ccctgtccta atcatctctt ttgataacga ccggccctca 240
gggatattctg agcgattctc tggcttcaat tctggggaca tgg 283

```

```

<210> 195
<211> 54
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(54)
<223> n = A,T,C or G

```

```

<400> 195
ctgtagcttc tgtgggactt ncactgetca ggcgtcaggc tcanatagct gctg 54

```

```

<210> 196
<211> 375
<212> DNA
<213> Homo sapiens

```

```

<400> 196
ccaaaactgc gaagagatgc agaataatgt tgacaataat aagttgctga atcgtcaggc 60
tgcagactgg tgatgggttaa attgaattgt gtcccagatc cactgccagt aaatcttaat 120
gagacccctt cttctaaact ggaagtcgca taaattagga cattaggggc tttgcctggt 180
ttctgttgat gccaggccaa ccaccgatct atattctgag aggccccgaca acttattgta 240
actgtatctc cgacagatgc agacaggggtg gaaggagatt gggtcactctg gatgtcacat 300
ttggcacctg ggagccagag cagcaggagc cccaggagct gagcggggac cctcatgtcc 360
atgctgtgtc ctgac 375

```

```

<210> 197
<211> 130
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(130)
<223> n = A,T,C or G

```

```

<400> 197
atggacatga gggccccgc tcagctcctg gggctcctgc nngctctggc tcccagggtgc 60
caaatgtgac atncagatga cccaatctcc tncacceng tctgcatctg ncggagatac 120

```

anntncaata

130

<210> 198

<211> 191

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(191)

<223> n = A,T,C or G

<400> 198

```
taataatgac catgtcgtct tcggcggagg gaccaaactg gccgtcctag gtcagcccaa 60
ggctgcccc tcggtcactc tgttcccgcc ctncntntgag nagcttcaag ccaacaaggc 120
cacactgggtg tgtctcataa gtgacttcta cccgggagcc gtgacagtgg cctggaaggc 180
anatagcagc c                                     191
```

<210> 199

<211> 282

<212> DNA

<213> Homo sapiens

<400> 199

```
ctgggtgggtgc ctcagccatg gcctggaccg ttctcctcct cggcctcctc tctcaccgca 60
cagattctgt gacttcctat gtgttgactc aaacacctc agtgtcagt gccccaggaa 120
agacggcccaa gattacctgt gggggaaaca atattgggag tcacaatgta cactagtatt 180
accagaagcc aggccaggcc cctgtcctaa tcattctctt tgataacgac cggccctcag 240
ggatatctga gcgattctct ggcttcaatt ctggggacat gg                                     282
```

<210> 200

<211> 464

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(464)

<223> n = A,T,C or G

<400> 200

```
caggcagagg ctctgggtca gtgcaggaag cagagtcaca gccagcgcct tgggggtggg 60
atgaaaggag atgacctggt ggctgcgtga cagccactgt aggactctga tctcagggg 120
acaggctgac acaggcagtt gggaattctg ggcagggaca agcaggcgtt acagaaaagt 180
gataaccaat cccagttaaa atagtctcag gagtcaagtgc aggagccctt tctgactcct 240
gtgatggata ataaggccca ncccaggaa gatgagcccc agcacgaagc ctccaatgcc 300
actcagcatc ttgctctggg cagattcaga ctgagcccg cactccacgg tgatggggtt 360
ctggaggctg ggggtgctcca cgtggcaggt gtagacgtct ccatgctggg gattcatttc 420
cagcatcacc aggatctgga aggnccagtc accgnttcct aata                                     464
```

<210> 201

<211> 373

<212> DNA

<213> Homo sapiens

<400> 201

```
ctgtagcttc tgtgggactt ccaactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttggtt ggagggtgtg gtgggtctcca ctcccgcctt gacggggctg 120
ctatctgcct tcaggccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agtggtggcct tgttggtctg aagctcctca gaggaggcg ggaacagagt gaccgagggg 240
gcagccttgg gctgacctag gacggccagt ttggtccctc cgccgaagac gacatgttca 300
ttattacgat cccacacttg acagtaatat tcggcctcat cgccggcttc gaccctgttg 360
atggtcaggg tgg                                     373
```

<210> 202
<211> 373
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(373)
<223> n = A,T,C or G

<400> 202
ccaccctgac catcaacagg gtcgaagccg gcgatgaggc cgactattac tgtcaagtgt 60
gggatcgtaa taatgaccat gtcgtcttcg gcggaggagc caaactggnc gtnctaggtn 120
agnccaaggc tgccccctcg gtcactctgt tcccgccctc ctctgaggag cttcaagcca 180
acaaggccac actgggtgtgt ctcataaagt acttctaccc gggagccgcg acagtggcct 240
ggaaggcaga tagcagcccc gtcaaggcgg gagtggagac caccacaccc tccaaacaaa 300
gcaacaacaa gtacgcggcc agcagctatc tgagcctgac gcctgagcag tgggaagtccc 360
acagaagcta cag 373

<210> 203
<211> 373
<212> DNA
<213> Homo sapiens

<400> 203
ctgtagcttc tgtgggactt ccaactgctca ggcgtcaggc tcagatagct gctggccgcg 60
tacttggtgt tgctttgttt ggagggtgtg gtggtctcca ctcccgctt gacggggctg 120
ctatctgcct tccaggccac tgtcacggct cccgggtaga agtcacttat gagacacacc 180
agtgtggcct tgttggcttg aagctcctca gaggaggcgg ggaacagagt gaccgagggg 240
gcagccttgg gctgacctag gacggccagt ttggtccctc cgccgaagac gacatgggtca 300
ttattacgat cccacacttg acagtaatag tcggcctcat cgccggcttc gaccctgttg 360
atggtcaggg tgg 373

<210> 204
<211> 565
<212> DNA
<213> Homo sapiens

<400> 204
cagagctcaa gtctgaactc tacctccaga cagaatgaag ttcattctga catctctgct 60
tcttatgctg ctggtcagca gcctctctcc agtccaaggt gttctggagg tctattacac 120
aagcttgagg tgtagatgtg tccaagagag ctcaagtctt atccctagac gttcattga 180
tcgaattcaa atcttgcccc gtgggaatgg ttgtccaaga aaagaaatca tagtctggaa 240
gaagaacaag tcaattgtgt gtgtggaccc tcaagctgaa tggatacaaa gaatgatgga 300
agtattgaga aaaagaagtt cttcaactct accagttcca gtgtttaaga gaaagattcc 360
ctgatgctga tatttccact aagaacacct gcattcttcc cttatccctg ctctggattt 420
tagttttgtg cttagttaaa tcttttccag gaaaaagaac ttccccatac aaataagcat 480
gagactatgt aaaaataacc ttgcagaagc tgatggggca aactcaagct tcttactca 540
cagcacccta tatacacttg gagtt 565

<210> 205
<211> 474
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(474)
<223> n = A,T,C or G

<400> 205
gtgcgaaggt ccagctcagt ggcacaagtg aaagcaatga tcgagactaa gacgggtata 60

```

atccctgaga cccagattgt gacttgcaat ggaaagagac tggaagatgg gaagatgatg 120
gcagattacg gcatcagaaa gggcaactta ctcttcctgg catgttattg tattggaggg 180
tgaccaccct gggcatgggg tggtggcagg gatcaaaaag cttatttctt ttaatctctt 240
actcaacgaa cacatcttct gatgatttcc caaaattaat gagaatgaga tgagtagagt 300
aagatttggg tgggatgggt aggatgaagt atattgcca actctatgtt tctttgattc 360
taacacaatt aattaagtga catgattttt actaatgtat tactgagact agtaataaaa 420
tttttaaggc aaaatagagc attccnaaaa aaaaaaaaaa aaaaaaaaaa aagg 474

```

<210> 206

<211> 237

<212> DNA

<213> Homo sapiens

<400> 206

```

ccagtattcc tggaggatat aacactgaca tcagcagggt tttcaatggc aacaattgca 60
cgagctgccg gcagaagctt ctcccagggt ctcttgagat ttatgatata gatgccatca 120
cttttccttt tatagatgta ctgttccatc tggaagtcaa gattgggtgc acctaagtgg 180
gttctctgctg caaggaactt aaggacatcc tcctccttca ttgcaggac atcaagg 237

```

<210> 207

<211> 585

<212> DNA

<213> Homo sapiens

<400> 207

```

ctcagagctc aagtctgaac tctatctcca gacagaatga agttcatctc gacatctctg 60
cttctcatgc tgctggtcag cagcctctct ccagtcceaag gtgttctgga ggtctattac 120
acaagcttga ggtgtagatg tgtccaagag agctcagtc tttatccctag acgcttcatt 180
gatcgaatcc aaatcttgcc ccgtgggaat ggtgtccaa gaaaagaaat catagtcttg 240
aagaagaaca agtcaattgt gtgtgtggac cctcaagctg aatggataca aagaatgatg 300
gaagtattga gaaaaagaag ttcttcaact ctaccagttc cagtgtttaa gagaagatt 360
ccctgatgct gatatttcca ctaagaacac ctgcattctt cccttatccc tgctctggat 420
tttagttttg tgcttagtta aatcttttcc aggaaaaaga acttccccc atcaataaagc 480
atgaggctat gtaaaaataa ccttgacaga gctgatgggg caaactcaag cttcttctact 540
cacagcacc tatatacact tggagtttgc attcttatc atcag 585

```

<210> 208

<211> 436

<212> DNA

<213> Homo sapiens

<400> 208

```

ctgagcagag ggacctgcac acagagactc cctcctgggc tcctggcacc atggccccc 60
tgaagatgct ggccctgggt accctcctcc tgggggcttc tctgcagcac atccacgcag 120
ctcgagggac caatgtgggg cgggagtgct gcctggagta cttcaaggga gccattcccc 180
ttagaaagct gaagacgtgg taccagacat ctgaggactg ctccagggat gccatcggtt 240
ttgtaactgt gcagggcagg gccatctgtt cggaccccaa caacaagaga gtgaagaatg 300
cagttaaata cctgcaaagc cttgagaggt cttgaagcct cctcacccca gactcctgac 360
tgtctcccgg gactacctgg gacctccacc gtcggtgttc accgccccca ccctgagcgc 420
ctgggtccag gggagg 436

```

<210> 209

<211> 524

<212> DNA

<213> Homo sapiens

<400> 209

```

gctctggccc ctggtcctgt cctgttctcc agcatggtgt gtctgaggct ccctggaggc 60
tcctgcattg cagttctgac agtgacactg atggtgctga gctcccccact ggctttggct 120
ggggacacca gaccacgttt ctggagtagc tctacgtctg agtgatcatt cttcaatggg 180
acggagcggg tcgggttcct ggacagatac ttctataacc aagaggagta cgtgcgcttc 240
gacagcgacg tgggggagtt ccgggcggtg acggagctgg ggcggcctga tgaggagtac 300
tggaacagcc agaaggactt cctggaagac aggcgggccc cgttgagcac ctactgcaga 360

```

cacaactacg ggggtgtgga gagcttcaca gtgcagcggc gagtccatcc taagggtgact 420
gtgtatcctt caaagaccca gccctgcag caccacaacc tcctgggtctg ttctgtgagt 480
ggtttctatc caggcagcat tgaagtcagg tggttccgga atgg 524

<210> 210
<211> 579
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1) ..(579)
<223> n = A,T,C or G

<400> 210
aaagaatatg tagaatctag gtaagtggat aaaaggctctg ggggcagggg aaaggagagc 60
atttcattgt gaatcaagga atttctccac ctgttttaac tcttccatat gacatcaaaag 120
agatgtcact tgcagctagc atttcagtga tgttttcttg ctaataatat cgtgataaaa 180
gaaacattga ctataagaaa taggaatggg tctcataaaa ggaaacagca aaacccccaa 240
actaaaaaac agcgcaggct atttctctct tctctccttt tgcttggcac tcatgagatg 300
ctaggtgtgg aagtcagcca actgaaaaag agaggtggct gaagaagggt gggaggctga 360
agccagttaa ataggatggt ccaattcaca gacggcgagg ctacagtga aataggactc 420
tttcaacttg agcaggacc cattaacttca ctggagttag aaagaaagga gagcgtagac 480
tttttgaact ttctataaga gtgtacctcc ncagtataca gaagacgacg tgaaatttga 540
tctgcaagaa aactgagtcc atattcacat atgtatcaa 579

<210> 211
<211> 556
<212> DNA
<213> Homo sapiens

<400> 211
cagagctcaa gtctgaactc tacctccaga cagaatgaag ttcattctga catctctgct 60
tctcatgctg ctggtcagca gcctctctcc agtccaaggt gttctggagg tctattacac 120
aagcttgagg ttagatgtg tccaagagag ctccagtctt atccctagac gcttcattga 180
tcgaattcaa atcttgcccc gtgggaatgg ttgtccaaga aaagaaatca tagtctggaa 240
gaagaacaag tcaattgtgt gtgtggaccc tcaagctgaa tggatacaaa gaatgatgga 300
agtattgaga aaaagaagtt cttcaactct accagttcca gtgtttaaga gaaagattcc 360
ctgatgctga tatttccact aagaacacct gcattcttcc cttatccctg ctctggattt 420
tagttttgtg cttagttaaa tcttttccag gaaaaagaac ttccccatac aaataagcat 480
gagactatgt aaaaataacc ttgcagaagc tgatggggca aactcaagct tcttactca 540
caacacccta tataca 556

<210> 212
<211> 353
<212> DNA
<213> Homo sapiens

<400> 212
cgcagccatg gctcgtggtc ccaagaagca tctgaagcgg gtggcagctc caaagcattg 60
gatgctggat aaattgaccg gtgtgtttgc tcctcgtcca tccaccggtc cccacaagtt 120
gagagagtgt ctccccctca tcatttttct gaggaacaga cttaagtatg ccctgacagg 180
agatgaagta aagaagattt gcattgcagc gttcattaaa atcgatggca aggtccgaac 240
tgatataacc taccctgctg gattcatgga tgtcatcagc attgacaaga cgggagagaa 300
tttccgtctg atctatgaca ccaagggtcg ctttgctgta catcgtatta cac 353

<210> 213
<211> 513
<212> DNA
<213> Homo sapiens

<400> 213
ctgctactca ttgcttctta tgggtatgct agaagcgaga atccgtatac taaccaacaa 60

```
ttctcagacc ccaatcctaa gccctcagga ggttggtgtct tgtagccagt atgctcaagg 120
ctgtgatggc ggcttcccat accttattgc aggaaagtac gcccagatt ttgggctggg 180
ggaagaagct tgcttccctt acacaggcac tgattctcca tgcaaatga aggaagactg 240
ctttcggtat tactcctctg agtaccacta tgtaggaggt ttctatggag gctgcaatga 300
agccctgatg aagcttgagt tgggtccatca tgggcccacg gcagttgctt ttgaagtata 360
tgatgacttc ctccactaca aaaaggggat ctaccaccac actggtctaa gagacccttt 420
caaccctttt gagctgacta atcatgctgt tctgcttggt ggctatggca ctgactcagc 480
ctctgggatg gattactgga ttgttaaaaa cag 513
```

<210> 214

<211> 538

<212> DNA

<213> Homo sapiens

<400> 214

```
aaacattaaa caacaagtat ataatcaaaa taatcctgta ttacttataa ctgaataact 60
attttcaaag aaactttcct ccctgatgaa taagaatgca aactccaagt gtatataggg 120
tgctgtgagt gaagaagctt gagtttgccc catcagcttc tacaagggtta tttttacata 180
gtctcatgct tatttgtatg gggaagttct ttttcttggg aaagatttaa ctaagcacaa 240
aactaaaatc cagagcaggg ataagggaag aatgcaggtg ttcttagtgg aaatatcagc 300
atcaggggat ctttctctta aacactggaa ctggtagagt tgaagaactt ctttttctca 360
atacttccat cattctttgt atccattcag cttgagggcc cacacacaca attgacttgt 420
tcttttccca gactatgatt tcttttcttg gacaaccact cccacggggc aagatttgaa 480
ttcgatcaat gaagcgtcta gggataaaga ctgagctctc ttggacacat ctacacct 538
```

<210> 215

<211> 588

<212> DNA

<213> Homo sapiens

<400> 215

```
aaacattagt gttcatagct tccaagagac atgctgactt tcatttcttg aggtactctg 60
cacatacgca ccacatctct atctggcctt tgcatggagt gaccatagct ctttctctct 120
tacattgaat gttagagaatg tagccattgt agcagcttgt gttgtcagc ttcttctttt 180
gagcaacttt cttacactga agaaaggcag aatgagtgct tcagaatgtg atttccctact 240
aacctgttcc ttggataggc tttttagtat agtatttttt ttgtcatttt ctccatcaac 300
aaccagggag actgcacctg atggaaaaga tatatgactg ctatcatgaca ttccctaaact 360
atcttttttt tattccacat ctactgtttt ggtggagtcc cttttgcac attgttttaa 420
ggatgataaa aaaaaataac aactagggac aatacagaac ccattccatt tatctttcta 480
cagggctgac attgtggcac attcttagag ttaccacacc ccagtaggga agctctaaat 540
agccaacacc catctgtttt ttgtaaaaac agcatagctt atacatgg 588
```

<210> 216

<211> 580

<212> DNA

<213> Homo sapiens

<400> 216

```
cagagctcaa gtctgaactc tacctccaga cagaatgaag ttcattctga catctctgct 60
tctcatgctg ctggtcagca gcctctctcc agtccaaggt gttctggagg tctattacac 120
aagcttgagg tgtagatgtg tccaagagag ctcatgtctt atccctagac gcttcattga 180
tcgaattcaa atcttgcccc gtgggaatgg ttgtccaaga aaagaaatca tagtctggaa 240
gaagaacaag tcaattgtgt gtgtggaccc tcaagctgaa tggatacaaa gaatgatgga 300
agtattgaga aaaagaagtt cttcaactct accagttcca gtgtttaaga gaaagattcc 360
ctgatgctga tatttccact aagaacacct gcattcttcc cttatccctg ctctggattt 420
tagttttgtg cttagttaaa tcttttccag gaaaaagaac ttccccatac aaataagcat 480
gagactatgt aaaaataacc tcgcagaagc tgatggggca aactcaagct tcttactca 540
cagcacccta tatacacttg gaggttgcat tcttattcat 580
```

<210> 217

<211> 396

<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(396)
<223> n = A,T,C or G

<400> 217
ctgttgactc agattcggca ttttaattac attgtttcca agtatgatat tctgagagtg 60
tctatagcac ttagtgctctg cttcatataa actaccagtt attatatatt tatgatgcaa 120
gtagttttcc aaatgtggtg aaagtctgag tctttttatc cccatgggta aaatctgaat 180
ctggctctct gtgtctctca gtgcttggtt attgctggtc agagagtaaa ttcttgataa 240
aagctgtntg anttggctct cacagtttat gcagacattg gagagacaat ttggttattt 300
caaacatcac aggatttgag taagaagacc tggttatgaa acaaggctct cataattact 360
agttatgact gttgacaagg ttaccttttc ttgttt 396

<210> 218
<211> 426
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(426)
<223> n = A,T,C or G

<400> 218
tggacagncc tgggaaggtgt cgaagtgcag acagactacg tgcccttgct gaactcgtg 60
gcggcctatg gctggcagct cactgtgtg ctaccaactc ccgtcgtcaa gactaccagc 120
gaggggagtg tatccaccaa gcagattgtc tttcttcaga gacctgtct acctcagaaa 180
atcaagaaga aggaatcgaa gtttcagtgg cgattctcca gagaagaaat gcacaacagg 240
cagatgagga aatcaaaagg taaactcagt gccagagaca aacaacaagc agaagaaaat 300
gagaagaact tagaagacca gtcttccaaa gctggagaca tgggaaactg tgtttcagga 360
cagcagcagg aggggtgagtg ctccgaggag atgaagggcc ctgtccaaga ggacaaggga 420
gaacag 426

<210> 219
<211> 431
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(431)
<223> n = A,T,C or G

<400> 219
tcaagtctga actctacctc cagacagaat gaagttcatc tcgacatctc tgcttctcat 60
gctgctggtc agcagcctct ctccagtcca aggtgttctg gaggtctatt acacaagctt 120
gaggtgtaga tgtgtccaan agagctcagt ctttatccct anacgcttca ttgatcgaat 180
tcaaattcttg ccccggtggga atggttgctc aagaaaagaa atcatagtct ggaagaagaa 240
caagtcaatt gtgtgtgtgg accctcaagc tgaatggata caaagaatga tggaagtatt 300
gagaaaaaga agttcttcaa ctctaccagt tccagtgttt aagagaaaga ttccctgatg 360
ctgatatttc cactaagaac acctgcattc ttcccttatc cctgctctgg atttttagtt 420
tgnngcttagt t 431

<210> 220
<211> 286
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(286)

<223> n = A,T,C or G

<400> 220

```
ctgtctcaca ctttacaagc tgtgagagac acatcagagc cctgggcact gtcactgctt 60
gcagcctgag tgtaactccc tccttttcta tctgagctct tcctcctcca catcacggca 120
gcgaccacag ctccagtgat cacagctcca aggagaacca ggccagcaat gatgcccacg 180
atggggatgg tgggctggga agacagctcc catctcangg tgaggggcctt gggcagaccc 240
tcattgctgca catggcaggt gtatctctgc tcctctccag aaggca 286
```

<210> 221

<211> 536

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(536)

<223> n = A,T,C or G

<400> 221

```
ctcaagtctg aactctacct ccagacagaa tgaagttcat ctgcacatct ctgcttctca 60
tgctgctggt cagcagcctc tctccagtc aaggtgttct ggaggtctat tacacaagct 120
tgaggtgtag atgtgtccaa gagagctcag tctttatccc tagacgcttc attgatcgaa 180
ttcaaatctt gccccgtggg aatggttgct caagaaaaga aatcatagtc tggaagaaga 240
acaagtcaat tgtgtgtgtg gacctcaag ctgaatggat acaaagaatg atggaagtat 300
tgagaaaaag aagttcttca actctaccag ttccagtggt taagagaaag attccctgat 360
gctgatattt ccactaagaa cacctgcatt cttcccttat ccctgctctg gattttagtt 420
ttgngcttag ttaaatcttt tccaggaaaa agaacttccc catacaaata agcatgagac 480
tatgtaaaaa taaccttgca gaagctgatg gggcaaaact aagcttnttc actcac 536
```

<210> 222

<211> 565

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(565)

<223> n = A,T,C or G

<400> 222

```
ctcagagctc aagtctgaac tctacctcca gacagaatga agttcatctc gacatctctg 60
cttctcatgc tgctggtcag cagcctctct ccagtcceaag gtgttctgga ggtctattac 120
acaagcttga ggtgtagatg tgtccaagag agctcagctt ttatccctag acgcttcatt 180
gatcgaattc aaatcttgcc ccgtgggaat ggttgtccaa gaaaagaaat catagtcttg 240
aagaagaaca agtcaattgt gtgtgtggac cctcaagctg aatggataca aagaatgatg 300
gaagtattga gaaaaagaag ttcttcaact ctaccagttc cagtgtttaa gagaaagatt 360
ccctgatgct gatatttcca ctaagaacac ctgcattctt cccttatccc tgctctggat 420
tttagttttg tgcttagtta aatcttttcc aggaaaaaga acttcccat acaataaagc 480
atgagactat gtaaaaaata ccttgcnгаа gctgatggng caaactcaag cttcttcaact 540
cacagcacc tatatacact tggag 565
```

<210> 223

<211> 529

<212> DNA

<213> Homo sapiens

<400> 223

```
cgcggtgcga cgaaggagta ggtggtggga tctcacctg ggtccgatta gccttttctc 60
tgccttgctt gcttgagctt cagcgaatt cgaaatggct ggcggttaagg ctggaaagga 120
ctccggaaag gccaaagaaa aggcgggttt ccgctcgcag agagccggct tgcagttccc 180
agtgggccgt attcatcgac acctaaaatc taggacgacc agtcatggac gtgtgggcgc 240
gactgccgct gtgtacagcg cagccatcct ggagtacctc accgcagagg tacttgaact 300
```



```
ggcaggaaat gcatcaaaag acttaaaggt aaagcgtatt acccctcgtc acttgcaact 360
tgctattcgt ggagatgaag aattggattc tctcatcaag gctacaattg ctggtggtgg 420
tgtcattcca cacatccaca aatctctgat tgggaagaaa ggacaacaga agactgtcta 480
aaggatgcct ggattccttg ttatctcagg actctaaata ctctaacag 529
```

<210> 224

<211> 297

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(297)

<223> n = A,T,C or G

<400> 224

```
cctcccctgg acccaggcgc tcaggggtggg ggcgggtgaac accaacgggtg gaggtcccag 60
gtagtcccgg gagacagtca ggagtctggg gtgaggaggc ttcaagacct ctcaaggctt 120
tgcagggtatt taactgcatt cttcactctc ttgttggtgg ggtccgaaca gatggccctg 180
ccctgcacag ttacaaaaac gatggcntcc ctggagcagn cctnagatgn ctggnaccac 240
gtcttcagct ttctaanggg aatggctccc ttgaagtact ccaggcangc actcccg 297
```

<210> 225

<211> 253

<212> DNA

<213> Homo sapiens

<400> 225

```
cctcccctgg acccaggcgc tcaggggtggg ggcgggtgaac accaacgggtg gaggtcccag 60
gtagtcccgg gagacagtca ggagtctggg gtgaggaggc ttcaagacct ctcaaggctt 120
tgcagggtatt taactgcatt cttcactctc ttgttggtgg ggtccgaaca gatggccctg 180
ccctgcacag ttacaaaaac gatggcatcc ctggagcagt cctcagatgt ctggtaccac 240
gtcttcagct ttc 253
```

<210> 226

<211> 598

<212> DNA

<213> Homo sapiens

<400> 226

```
ccatctgatac tataaatgcg gtggcatcga caaaagaacc attgaaaaat ttgggaagga 60
ggctgctgag atgggaaaagg gctccttcaa gtatgcctgg gtcttgata aactgaaagc 120
tgagcgtgaa cgtggtatca ccattgatat ctccttgttg aaatttgaga ccagcaagta 180
ctatgtgact atcattgatg ccccaggaca cagagacttt atcaaaaaca tgattacagg 240
gacatctcag gctgactgtg ctgtcctgat tgttgctgct ggtgttggtg aatttgaagc 300
tggtatctcc aagaatgggc agacccgaga gcatgccctt ctggcttaca cactgggtgt 360
gaaacaacta attgtcgggtg ttaacaaaat ggattccact gagccaccct acagccagaa 420
gagatatgag gaaattgtta aggaagtcag cacttacatt aagaaaattg gctacaaccc 480
cgacacagta gcatttgtgc caatttctgg ttggaatggt gacaacatgc tggagccaag 540
tgctaacatg ccttgggttca agggatggaa agtcaccctg aaggatggca atgccagt 598
```

<210> 227

<211> 612

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(612)

<223> n = A,T,C or G

<400> 227

```
ctgttgactc agattcggca ttttaattac attgtttcca agtatgatat tctgagagtg 60
```

```
tctatagcac ttagtgctctg cttcatataa actaccagtt attatatatt tatgatgcaa 120
gtagttttcc aaatgtgggt aaagtctgag tctttttatc cccatgggta aaatctgaat 180
ctggctctct gtgtctctca gtgcttggtt attgctggtc agagagtaaa ttcttgataa 240
aagctgttga cttggctctc acagtttatg cagacattgg agagacaatt tggttatttc 300
aaacatcaca ggatttgagt aagaagacct ggttatgaaa caaggctctc ataattacta 360
gttatgactg ttgacaagtt accttttctt gtttacaagt tatttggcct ctttgaatta 420
cttgtaaaat agagataggg attcttttctt gatcatggaa catcaaataa agttatttga 480
tgaataactt tgatcatctg aaattataaa tataactaaa tgtaattat tatttggaaa 540
tttngggcac ctcatggngg catttttctat ggtcattttt tttcttttct cgcataatgg 600
ctaaaagtag gt                                     612
```

<210> 228
<211> 288
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)... (288)
<223> n = A,T,C or G

```
<400> 228
agccattggn ttagtcttta gctcagcgca aagaagagcg ccaggctcac ctcactaacc 60
agtatatgca gagaatggca agtgtagcag ctgttcccaa ccctgtaatc aacccttacc 120
agccagcacc tccttcaggt tacttcatgg cagctatccc acagactcag aaccgngctg 180
cactactatcc tcctagccaa attgctcaac taagaccaag tcctcgctgg actgctcagg 240
gtgccagacc tcattccattc caaaatatgc ccggtgctat ccgcccag 288
```

<210> 229
<211> 594
<212> DNA
<213> Homo sapiens

```
<400> 229
ctcagagctc aagtctgaac tctacctcca gacagaatga agttcatctc gacatctctg 60
cttctcatgc tgctggtcag cagcctctct ccagtccaag gtgttctgga ggtctattac 120
acaagcttgg ggtgtagatg tgtccaagag agctcagctt ttatccctag acgcttcatt 180
gatcgaattc aaatcttgcc ccgtgggaat ggttgtccaa gaaaagaaat catagtctgg 240
aagaagaaca agtcaattgt gtgtgtggac cctcaagctg aatggataca aagaatgatg 300
gaagtattga gaaaaagaag tttttcaact ctaccagttc cagtgtttaa gagaaagatt 360
ccctgatgct gatatttcca ctaagaacac ctgcattctt cccttatccc tgctctggat 420
tttagttttg tgcttagtta aatcttttcc aggaaaaaga acttccccat acaaataagc 480
atgagactat gtaaaaataa ccttgcaaaa gctgatgggg caaactcaag cttcttctact 540
cacagcacc cttatatacact tggagtttgc attcttattc atcagggagg aaag 594
```

<210> 230
<211> 571
<212> DNA
<213> Homo sapiens

```
<400> 230
ctccttctct cttacattga atgtagagaa ttagtccatt gtagcagctt gtgttgtcac 60
gcttcttctt ttgagcaact ttcttacact gaagaaaggc agaagtagtg cttcagaatg 120
tgatttccct ctaacctgtt ccttggtatg gctttttagt atagtatttt tttttgtcat 180
tttctccatc aacaaccagg gagactgcac ctgatggaaa agatatatga ctgcttcatg 240
acattcctaa actatctttt ttttattcca catctacgtt tttggtggag tcccttttgc 300
atcattgttt taaggatgat aaaaaaata acaactaggg acaatacaga acccattcca 360
tttatctttc tacagggctg acattgtggc acattcttag agttaccaca ccccatgagg 420
gaagctctaa atagccaaca cccatctgtt ttttgtaaaa acagcatagc ttatacatgg 480
acatgtctct gccttaactt ttcttaactc ccactctagg ctattgtttg catgtctacc 540
tacttttagc cattatgcga gaaaagaaaa a                                     571
```

<210> 231

<211> 584
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(584)
<223> n = A,T,C or G

<400> 231
aaacattagt gtccatagct tccaagagac atgctgactt tcatttcttg aggtactctg 60
cacatacgca ccacatctct atctggcctt tgcattggagt gaccatagct ccttctctct 120
tacattgaat gtagagaatg tagccattgt agcagcttgt gttgtcacgc ttcttctttt 180
gagcaacttt cttacactga agaaaggcag aatgagtgtg tcagaatgtg atttcctact 240
aaactgttcc ttggataggc ttttttagtat agtatttttt ttgttcattt tctccatcaa 300
caaccaggga gactgcacct gatggaaaag atatatgact gcttcattgac attcctaacc 360
tacctttttt tattccacat ctacgttttt ggtggagtcc cttttgcatc attgttttaa 420
ggatgataaa aaaaaataac aactagggac aatacagaac ccattccatt tatctttcta 480
cagggtgtgac attgtggcac attcttagag ttaccacacc ccattgaggga agctctaaat 540
agccaacacc catctgtttt ttgtaaaaac agcatanctt atac 584

<210> 232
<211> 457
<212> DNA
<213> Homo sapiens

<400> 232
ccacggctgc ttccagctcc tccctggaga agagctacga gctgcctgac ggccagggtca 60
tcaccattgg caatgagcgg ttccgctgcc ctgaggcact cttccagcct tccttccctgg 120
gcatggagtc ctgtggcatc cagcaacta ccttcaactc catcatgaag tgtgacgttg 180
acatccgcaa agacctgtac gccaacacag tgctgtctgg cggcaccacc atgtaccctg 240
gcattgccga caggatgcaa aaggagatca ctgccctggc acccagcaca atgaagatca 300
agatcattgc tcctcctgag cgcaagtact ccgtgtggat cggcggctcc atcctggcct 360
cgctgtccac cttccagcag atgtggatca gcaagcagga gtatgacgag tccggccctc 420
ccatcgtcca ccgcaaatgc ttctaggcgg actatga 457

<210> 233
<211> 256
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(256)
<223> n = A,T,C or G

<400> 233
cctcccctgg acccaggcgc tcagggtggg ggcggtgaac accaaccggtg gaggtcccag 60
gtagtcccgg gagacagtca ggagtctggg gtgaggaggc ttcaagacct ctcaaggctt 120
tgcaggattt taactgcatt cttcactctc ttgttgntgg ggtccgaaca gatggccctg 180
ccctgcncag ttacaaaaac gatggcatcc ctggagcagt cctcagatgt ctggtaccac 240
gtcttcagct ttctaa 256

<210> 234
<211> 571
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(571)
<223> n = A,T,C or G

<400> 234
cagagctcaa gtctgaactc tacctccaga cagaatgaag ttcattctcga catctctgct 60
tctcatgctg ctgggtcagca gcctctctcc agtccaaggt gttctggagg tctattacac 120
aagcttgagg tgtatgctg tccaagagag ctccagctctt atccctagac gcttcattga 180
tcgaattcaa atcttgcccc gtgggaatgg ttgtccaaga aaagaaatca tagtctggaa 240
gaagaacaag tcaattgtgt gtgtggaccc tcaagctgaa tggatacaaa gaatgatgga 300
agtattgaga aaaagaagtt cttcaactct accagttcca gtgtttaaga gaaagattcc 360
ctgatgctga tatttccact aagaacacct gcattcttcc ctatccctg ctctggattt 420
tagttttgtg cttagttaaa tcttttccag gaaaaagaac ttccccatac aaataagcat 480
ganactatgt aaaaataacc cttgcagaag ctgatggggc aaactcaagc ttcttcactc 540
acagcacctt atatacactt ggagtttgca t 571

<210> 235
<211> 489
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(489)
<223> n = A,T,C or G

<400> 235
ctgttgactc agattcggca ttttaattac attgtttcca agtatgatat tctgagagtg 60
tctatagcac ttagtgctctg cttcatataa actaccagtt attatatatt tatgatgcaa 120
gtagttttcc aaatgtgggt aaagtctgag tctttttatc cccatgggta aaatctgaat 180
ctggctctct gtgtctntca gtgcttgttt attgctggtc agagagtaaa ttcttgataa 240
aagctgttga cttggctctc acagtttatg canacattgg agagacaatt tggttatttc 300
aaacatcaca ggatnngagt aagaanacct ggttatgaaa caaggctctc ataattacta 360
gttatgactg ttgacaagtt accttntctt gnttacaagt tatttggcct ctttgaatta 420
cttgnaaat agagataggg attctttctt gatcatggaa catcnaatga agttattnga 480
tgaaatact 489

<210> 236
<211> 306
<212> DNA
<213> Homo sapiens

<400> 236
ctgctgcacc cagagctcct ttgggtctgc acatagctct gcctgagagc gcttgcgggg 60
caagaacagg atagctggga tggagcagcc caagcttgggt tcctgcttcc ggtagctgcg 120
gacaaccttg gcgggaatct tcctttgggt gtacttgagg caacagctcct gagccccctc 180
atcactgcct tgggtcctgg ggatgccaaa ggccagaacc aggataagga ggctcagagc 240
cagtgactga gccatgtctg tggtagaggg tgagtaagag gccagagctg agggtagagg 300
gggcag 306

<210> 237
<211> 560
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(560)
<223> n = A,T,C or G

<400> 237
ctcagagctc aagtctgaac tctacctcca gacagaatga agttcatctc gacatctctg 60
cttctcatgc tgctggtcag cagcctctct ccagtcctaag gtgttctgga ggtctattac 120
acaagcttga ggtgtagatg tgtccaagag agctcagctt ttatccctag acgcttcatt 180
gatcgaattc aaatcttggc cgtggggaat ggtgtgctca gaaaagaaat catagtctgg 240
aagaagaaca agtcaattgt gtgtgtggac cctcaagctg aatggatata aagaatgatg 300
gaagtattga gaaaaagaag ttcttcaact ctaccagttc cagtgtttaa gagaaagatt 360

```
ccctgatgct gatatttcca ctaagaacac ctgcattctt cccttatccc tgctctggat 420
tttagttttg tgcttagtta aatcttttcc agggaaaaaga ncttccccat acaataaagc 480
atgagactat gtaaaaaataa ccttgcagaa gctgatgggg caaactcaag cttcttcact 540
cacagcacc c tatatacact 560
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<210> 238

<211> 484

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (484)

<223> n = A,T,C or G

<400> 238

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aaaaaaggaa acagaaaaca gaagaaatca cttaaggaga gctgtcattt tctattggtg 60
aggatttcctg atcttgggga ggttcttgaa agttcgtctc tgtttcttct tcttctctt 120
cttgatttgg aataatttca atgtcttctt cattcttttg ttgggaagat gtttcagtta 180
gcccaccacac ttcttctttt atttcaatag tctgttcttt ttttcttctg ctgacaggag 240
aactatgtta gatttgggtc tggagcacgt tcttttccat tcattctcaa cgatgccagc 300
tattacaagt tcctggaaga aggcaaagat cagcatcact gacaaaatgc ccaagaacag 360
agattgtatg ctgtaacagt attgggtaga tggggagttt ttctcanagg gattagctgg 420
ttcatagtgt natatgttaa tatatggtgt gtgagctcta ataaaattca nactctccat 480
tttt 484
```

<210> 239

<211> 493

<212> DNA

<213> Homo sapiens

<400> 239

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ctgaacatgt tgggagagaa gcttcttggt cctaacgcca gccccgatgg tctcattccg 60
tggacgaggt tttgtaagga aaatataaat gataaaaatt ttcccttctg gctttggatt 120
gaaagcatcc tagaactcat taaaaaacac ctgctccctc tctggaatga tgggtgcac 180
atgggcttca tcagcaagga gcgagagcgt gccctgttga aggaccagca gccggggacc 240
ttcctgtctg ggttcagtga gagtccccgg gaaggggcca tcacattcac atgggtggag 300
cgttcccaga acggaggcga acctgacttc catgcggttg aacctacac gaagaaagaa 360
ctttctgctg ttactttccc tgacatcatt cgcaattaca aagtcattgc tgcctgagaat 420
attcctgaga atccctgaa gtatctgtat ccaaatattg acaaagacca tgcctttgga 480
aagtattact cca 493
```

<210> 240

<211> 439

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1) ... (439)

<223> n = A,T,C or G

<400> 240

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cagagctcaa gtctgaactc tacctccaga cagaatgaag ttcatctcga catctctgct 60
tctcatgctg ctggtcagca gcctctctcc agtccaaggt gttctggagg tctattacac 120
aagcttgagg tgtagatgtg tccaagagag ctcatctttt atccctagac gcttcattga 180
tcgaattcaa atcttgcccc gtgggaatgg ttgtccaaga aaagaaatca tagtctggaa 240
gaagaacaag tcaattgtgt gtgtggaccc tcaagctgaa tgaatacaaa gaatgatgga 300
agtattgaga aaaagaagtt cttcaactct accagttcca gtgtttaaga naagattcc 360
ctgatgctga tatttccact aagaacacct gcattcttcc cttatccctg ctctggattt 420
tagttttgng cttagttaa 439
```

<210> 241

<211> 529
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(529)
<223> n = A,T,C or G

<400> 241
tgtgtccaag agagctcagt ctttatccct agacgcttca ttgatcgaat tcaaatcttg 60
ccccgtggga atggttgtcc aagaaaagaa atcatagtct ggaagaagaa caagtcaatt 120
gtgtgtgtgg accctcaagc tgaatggata caaagaatga tggaagtatt gagaaaaaga 180
agttcttcaa ctctaccagt tccagtgttt aagagaaaaga ttccctgatg ctgatatttc 240
cactaagaac acctgcattc ttcccttatt cctgctctgg atttttagttt tgtgcttagt 300
taaatctttt ccaggaaaaa gaacttcccc atacaaataa gcatgagact atgtaaaaat 360
aaccttgca aagctgatgg ggcaaaactca agcttcttca ctacagcac cctatatata 420
cttgaggatt gcattcttat tcatcaggga ggaaagtctt ttgaaaata gttattcagt 480
tataagtaat acaggattat ttgattata tacttgntgn ttaatgttt 529

<210> 242
<211> 440
<212> DNA
<213> Homo sapiens

<400> 242
ctccctgagc agagggacct gcacacagag actccctcct gggctcctgg caccatggcc 60
ccactgaaga tgctggccct ggtcaccctc ctccctggggg cttctctgca gcacatccac 120
gcagctcgag ggacaaatgt gggccgggag tgctgcctgg agtacttcaa gggagccatt 180
ccccttagaa agctgaagac gtggtaccag acatctgagg actgctccag ggatgccatc 240
gtttttgtaa ctgtgcaggg cagggccatc tgctcgacc ccaacaacaa gagagtgaag 300
aatgcagtta aatacctgca aagccttgag aggtcttgaa gcctcctcac ccagactcc 360
tgactgtctc ccgggactac ctgggacctc caccgttggt gttcacgcc cccaccctga 420
ggcctgggt ccaggggagg 440

<210> 243
<211> 345
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(345)
<223> n = A,T,C or G

<400> 243
cctcccctgg acccaggcgc tcagggtggg ggcggtgaac accaacggtg gaggtcccag 60
gtagtcccgg gagacagtca ggagtctggg gtgaggaggc ttcaagacct ctcaaggctt 120
tgcaggatt taactgcatt cttcactctc ttgntgttgg ggtccgaaca gatggccctg 180
ccctgcacag ttacaaaaac gatggcatcc ctggagcagt cctcagatgt ctggtaccac 240
gtcttcagct ttctaagggg aatggctccc ttgaagtact ccaggcagca ctcccggccc 300
acattggtcc ctcgagctgc gtggatgtgc tgcananaan ccccc 345

<210> 244
<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(368)
<223> n = A,T,C or G

<400> 244
caagctttttt tttttttttt tttttttttt tttttatgan taatgggtcta tttatngatn 60
ccatttctatt ttaacaaana aaatntttca aattacaagg tntacaantc aatactgntt 120
tgaanngaaa aatnatttgc tttgaaagtg tntgcatgta tatatatatg ataaatgatt 180
ataacgtgtg tgctannngac aanatgtant ctttgggtgt tagttatata ctgnctacct 240
gtganangca aggtaagngg gtnacanact ntnaaattta tnaaacactt anatttttca 300
nggaagttac ntgaaggaac tagggagttt catgantana taaaangttc gggngggatc 360
tccaccgg 368

<210> 245
<211> 573
<212> DNA
<213> Homo sapiens

<400> 245
ccaaaagaag taagacagct tgctgaagat ttcttgaaag actatatattca tataaacatt 60
gggtgcacttg aactgagtgc aaaccacaac attcttcaga ttgtggatgt gtgtcatgac 120
gtagaaaagg atgaaaaact tattcgtcta atggaagaga tcatgagtga gaaggagaat 180
aaaaccattg tttttgtgga aaccaaaga agatgtgatg agcttaccag aaaaatgagg 240
agagatgggt gccctgccat ggggtatccat ggtgacaaga gtcaacaaga gcgtgactgg 300
gttctaaatg aattcaaaca tggaaaagct cctatttctga ttgttacaga tgtggcctcc 360
agagggctag atgtggaaga tgtgaaattt gtcatacaatt atgactaccc taactcctca 420
gaggattata ttcacggaat tggagaact gctcgagta ccaaacacagg cacagcatac 480
actttcttta cactaataa cataaagcaa gtgagcgacc ttatctctgt gcttcgtgaa 540
gctaatacaag caattaatcc caagttgctt cag 573

<210> 246
<211> 425
<212> DNA
<213> Homo sapiens

<400> 246
gacctgcaca cagagactcc ctctctgggct cctggcacca tggccctact gaagatgctg 60
gccctgggtca ccctcctcct gggggcttct ctgcagcaca tccacgcagc tcgagggacc 120
aatgtggggc gggagtgtct cctggagtac ttcaagggag ccattcccct tagaaagctg 180
aagacgtggg accagacatc tgaggactgc tccagggatg ccatacgtttt tgtaactgtg 240
cagggcaggg ccatactgtc ggacccaac aacaagagag tgaagaatgc agttaatac 300
ctgcaaagcc ttgagaggtc ttgaagcctc ctcacccag actcctgact gtctcccggt 360
actacctggg acctccaccg ttggtgttca ccgccccac cctgagcgcc tgggtccagg 420
ggagg 425

<210> 247
<211> 593
<212> DNA
<213> Homo sapiens

<400> 247
atctcgacat ctctgcttct catgctgctg gtcagcagcc tctctccagt ccaaggtgtt 60
ctggagggtct attcacaaag cttgaggtgt agatgtgtcc aagagagctc agtctttatc 120
cctagacgct tcattgatcg aattcaaatc ttgccccgtg ggaatggttg tccaagaaaa 180
gaaatcatag tctggaagaa gaacaagtca attgtgtgtg tggaccctca agctgaatgg 240
atacaaagaa tgatggaagt attgagaaaa agaagttctt caactctacc agttccagt 300
tttaagagaa agattcccctg atgctgatat ttccactaag aacacctgca ttcttccctt 360
atccctgctc tggatttttag ttttgtgctt agttaaatct tttccaggaa aaagaacttc 420
cccatacaaa taagcatgag actatgtaaa aataaccttg cagaagctga tgggggcaaac 480
tcaagcttct tcaactcacag caccctatat acacttgag tttgcattct tattcatcgg 540
ggaggaaagt ttctttgaaa atagttattc agttataagt aatacaggat tat 593

<210> 248
<211> 453
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(453)
<223> n = A,T,C or G

<400> 248
cagctcagtg gcacaagtga aagcaatgat cgagactaag acgggtataa tccctgagac 60
ccagattgtg acttgcaatg gaaagagact ggaagatggg aagatgatgg cagattacgg 120
catcagaaaag ggcaacttac tcttcctggc atcttattgt attggagggt gaccaccctg 180
ggcatgggggt gttggcaggg gtcaaaaagc ttatttcttt taatctctta ctcaacgaac 240
acatcttctg atgatttccc aaaattaatg agaatgagat gtagtagagta agatttgggt 300
gggatgggta ggatgaagta tattgcccac ctctatgttt ctttgattct aacacaatta 360
attaagtgc atgattttta ctaatgtatt actgagacta gtaaataaat ttttaagacn 420
aaaaaaaaa aaaaaaaaaa aaaaaaaagc ttg 453

<210> 249
<211> 608
<212> DNA
<213> Homo sapiens

<400> 249
ctcagagctc aagtctgaac tctacctcca gacagaatga agttcatctc gacatctctg 60
cttctcatgc tgcgtgtcag cagcctctct ccagtcacaag gtgttctgga ggtctattac 120
acaagcttga ggtgtagatg tgtccaagag agctcagctt ttatccctag acgcttcatt 180
gatcgaattc aaatcttggc ccgtgggaat ggtgtgccaa gaaaagaaat catagtctgg 240
aagaagaaca agtcaattgc gtgtgtggac cctcaagctg aatggataga aagaatgatg 300
gaagtattga gaaaaagaag ttcttcaact ccaccagttc cagtgtttaa gagaagatt 360
ccctgatgct gatatttcca ctaagaacac ctgcattctt cccttatccc tgctctggat 420
tttagttttg tgcttagtta aatcttttcc aggaaaaaga acttccccat acaataaagc 480
atgagactat gtaaaaaata ccttgcagaa gctgatgggg caaactcaag cttctttact 540
cacagcacc tatatacact tggagtttgc attcttattc atcaggaggg aaagtttctt 600
tgaaaaata 608

<210> 250
<211> 400
<212> DNA
<213> Homo sapiens

<400> 250
ccaggtacca atgggtgctg tgcaatccag acagtaattc tgcaaaactgc cttgaagaaa 60
aaggaccaat gttcgaacta cttccagggt aatccaacaa gatcccccg ctgaggactg 120
acctttttcc aaagacgaga atccaggact tgaatcgtat cttcccactt tctgaggact 180
actctggatc aggcctcggc tccggctccg gctctggatc aggatctggg agtggcttcc 240
taacggaaat ggaacaggat taccaactag tagacgaaag tgatgctttc catgacaacc 300
ttaggtctct tgacaggat ctgccctcag acagccagga cttgggtcaa catggattag 360
aagaggattt tatgttataa aagaggattt tcccaccttg 400

<210> 251
<211> 393
<212> DNA
<213> Homo sapiens

<400> 251
ctgctcatca gatggcgagg agatgaagac agatgggtgca gccacagttc gtttgatctc 60
taccttggtc cctccccga aagtgaagcga aggaggccac ttggcacgac cgtgacagta 120
ataaactgca aaatcttcag gctctaggct gctgacgggt agagtgaagt ctgtccaga 180
tccactgcca gtgaatctgg cggggatgcc agcgccctg taggatgtat cataaatgat 240
gatcctggga gcctggccag gtttctgttg ggaccagcct aagtaggtgg caacactctg 300
actggccctg caggagaggg tggctctctc ccctggagac aaagacaggg tggctggaga 360
ctgtgacaac acaagttctc cggtggagtc tgg 393

<210> 252
<211> 425

<212> DNA

<213> Homo sapiens

<400> 252

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cctgggtggaa agaaggctct agaacctgct tatagagcca caacagggtg cagacaactg 60
tgatgtcaac caatgtcact cgttcgccca ccagaaaagt cctcgtcttc aagtaagcat 120
ccagcagccc cagaattcgc ctcacttcct cctttgcatt ctcagtggcc tgtttggtgt 180
ggtgcatgat gcccgaagggt gggaacaccc aggtactggc tgggggacct atatcggaat 240
cagcaaaagct caccactgc accacctggg ctgctgcctc tggagtactt ccccgagct 300
cctcattgct cacatagtag gcaatggcgt tgctctcaaa cacacagaat ccatcatcac 360
cctcaaatgc tgggacctg ccggcaggaa atttgcggag aaattcaggg gtgcggttg 420
tttgg 425
```

<210> 253

<211> 603

<212> DNA

<213> Homo sapiens

<400> 253

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aaaaaaactt gtgcaattg caatcactga gtgattatgg aaaggcaaag tatatacagt 60
aatgtgagag aaactcaaac caagtaaggg taaaaatgaa atgattaaca ccaccagagg 120
aggaagctac tatcaaaata aaaccatact tcctaataaa ggtaaggcca tcataacccc 180
agaaaatgct tcatacttta gataattaaa aacacattat aacccaaaagc agatagtaac 240
attgagtatg ctgatttcaa aaagaagatg ggtctagata ccaggacagc tctttttagt 300
gccttcctta aaaagggcaa aactttttag agccatgtaa ttgtttatag ccatggcctg 360
gcttcaggca tctcataagt gaggcttcag aaagtccttg aagagtatat ggcatgaaa 420
ctgggctccc atctttacca taaagatgtt cttcttgaga ataagtgc ataggaagtg 480
atcgcttatg acatcatttc attgatcttg aggccatata aagagacttg ctgatattag 540
agcagtttct ttctaataca tattccgctg aattccaagc aatgaggcac acaccagttt 600
gtc 603
```

<210> 254

<211> 485

<212> DNA

<213> Homo sapiens

<400> 254

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aaaaaaggaa acagaaaaca gaagaaatca cttaaggaga gctgtcattt tctattggtg 60
aggattcctg atcttgggga ggttctggaa agttcgtctc tgtttcttct tcttctctt 120
cttggattgg aataatttca atgtcttctt cattctttgg ttgggaagat gtttcagtta 180
gcccacccac ttcttctttt atttcaatag tctgttcttt tttttcttct gctgacagga 240
gaactatgtt agatttgggt ctggagcacg ttcttttcca ttcattctca acgatgccag 300
ctattacaag ttcctggaag aaggcaaaaga tcagcatcac tgacaaaatg cccaagaaca 360
gagattgtat gctgtaacag tattgggtag atggggagtt tttctcagag ggattagctg 420
gttcacagtt gtatatgtta atatatggtg tgtgagctct aataaaattc agactctcca 480
ttttt 485
```

<210> 255

<211> 568

<212> DNA

<213> Homo sapiens

<400> 255

```
ctcagagctc aagtctgaac tctacctcca gacagaatga agttcatctc gacatctctg 60
cttctcatgc tgctggtcag cagctctctc ccagccaag gtgttctgga ggtctattac 120
acaagcttga ggtgtagatg tgtccaagag agctcagctt ttatccctag acgcttcatt 180
gatcgaattc aaatcttgcc ccgtgggaat ggttggtcaa gaaaagaaat catagtctgg 240
aagaagaaca agtcaattgt gtgtgtggac cctcaagctg aatggataca aagaatgatg 300
gaagtattga gaaaaagaag ttcttcaact ctaccagttc cagtgtttta gagaaagatt 360
ccctgatgct gatatttcca ctaagaacac ctgcattctt ccttatccc tgctctggat 420
tttagttttg tgcttagtta aatcttttcc aggaaaaaga acttccccat acaaataagc 480
atgagactat gtaaaaaata ccttgacaga gctgatgggg caaactcaag cttcttctact 540
cacagcacc tatatacact tggagtgtt 568
```

<210> 256
<211> 518
<212> DNA
<213> Homo sapiens

<400> 256
cctcccgcctt acgcagcttg tcatactggc gacaggttct ctcgaagagc gaggagatgc 60
tgggtgtggtt ggaaaaaagg aaacagaaaa cagaagaaat cacttaagga gagctgtcat 120
tttctattgg tgaggattcc tgatcttggg gaggttctgg aaagtctgtc tctgtttctt 180
cttcttctctc ttcttggatt ggaataattt caatgtcttc ttcatctttt ggttgggaag 240
atgtttcagt tagccaacc acttcttctt ttatttcaat agtctgttct ttttttctt 300
ctgtgtgacg gagaactatg ttagatttgg gtctggagca cgttcttttc cattcattct 360
caacgatgcc agctattaca agttcctgga agaaggcaaa gatcagcatc actgacaaaa 420
tgcccaagaa cagagattgt atgtctgtaac agtattgggt agatggggag tttttctcag 480
agggattagc tggttcacag ttgtatatgt taatatat 518

<210> 257
<211> 231
<212> DNA
<213> Homo sapiens

<400> 257
aaacttgatc caacctcttt gcatcttaca aggttaaaca gctaaaagaa gtaaaataag 60
aaggcaatgc ttgtggaatg tacagtgcac attggcggcg cagcctcat tacgattcgc 120
ctgcttgctt ctctgttcca atcgtttctt tggaaggcag tggatttttc tcttgcgtct 180
ctgtcttctt cagtttcgac ttatcgaatt tctcgatctc agccatatcg g 231

<210> 258
<211> 551
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(551)
<223> n = A,T,C or G

<400> 258
ctgaatatac taaacnttgc tctattatct gttgaattgc tgtatttcac tttttcagca 60
tttggggatc attattttaat tgaatttcta gagatcgatt ttccagacag gtctctgttc 120
ttcaatgaac aaatgataag aaacaatttg actccttata tgacaatgga attaaataaa 180
ttgacactca tctaggaata attctacaat catctccatc tctaagatta cctactgcaa 240
acaaagaatt gatctttctt tctcaaaaac cacatgggta agatgatcat tgtgactctg 300
aatgcaagaa taagtgaagt gaagctacaa ggggagatta tctgccaaca tagaaagaat 360
ctagaagaaa agattttatt acaggtaaca tgacatagct tggagccatc tttttggtct 420
cttgcataca ttttctctgc atgtctaagg aagaattcac aaggtagcaa gcaccaatc 480
tttctgcttt ggagtttcac aaattgaaaa tttgtccctc tcttgtaag tcaatcaaac 540
atctaccaat g 551

<210> 259
<211> 231
<212> DNA
<213> Homo sapiens

<400> 259
aaacttgatc caacctcttt gcatcttaca aagttaaaca gctaaaagaa gtaaaataag 60
aaggcaatgc ttgtggaatg tacagtgcac attggcggcg cagcctcat tacgattcgc 120
ctgcttgctt ctctgttcca atcgtttctt tggaaggcag tggatttttc tcttgcgtct 180
ctgtcttctt cagtttcgac ttatcgaatt tctcgatctc agccatatcg g 231

<210> 260
<211> 278

<212> DNA

<213> Homo sapiens

<400> 260

```
aaaatatccc tgaagtgaca cactcctttt ttgagaccga tactgggtatt cttttattat 60
agagactaaa aggtctgcct tactagactt cccacttttt gttctgaaag gaattaagga 120
ctgcagggtt ccagctctgt cttcccgagg ccattatgaa cagattaaat ggaaggacaa 180
attctaaata actgggcttt caacatgaaa agggaaaggc tgatggggag ttcagaacct 240
tgaatactgt aactgaacat ccctcaaggt taatgcag 278
```

<210> 261

<211> 272

<212> DNA

<213> Homo sapiens

<400> 261

```
ccaaaagaag taagacagct tgctgaagat ttctgaaag actatattca tataaacatt 60
ggtgcacttg aactgagtgc aaaccacaac attcttcaga ttgtggatgt gtgtcatgac 120
gtagaaaaag atgaaaaact tattcgtcta atggaagaga tcatgagtga gaaggagaat 180
aaaaccattg tttttgtgga aaccaaaga agatgtgatg agcttaccag aaaaatgagg 240
agagatgggt ggcctgccat gggatccat gg 272
```

<210> 262

<211> 500

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(500)

<223> n = A,T,C or G

<400> 262

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ccggcagttt gtcacagcca cagatgttgt ccgagggaaac cccaagttga acttggtttt 60
tattgccaac ctctttaaca gataccctgc cctgcacaaa ccagagaacc aggacattga 120
ctggggggct cttgaagggt agacgagaga agagcggaca tttaggaact ggatgaactc 180
cctgggtgtt aaccctcgag tcaatcattt gtacagtgc ttatcagatg ccctgggtcat 240
cttccagctc tatgaaaaga tcaaagttcc tgttgactgg aacagagtaa acaaaccgcc 300
atacccaaaa ctggggaggca atatgaagaa gcttgagaat tgtaactacg cggtagaatt 360
ggggaagaat caagcgaagt tctccctggt tggcatcggg ggacaagatc tcaatgaagg 420
aaaccgcact ctacactgg ccttgatttg gcagctaagt agaaggtata cactgaatat 480
cctcnaagaa attggtggtg 500
```

<210> 263

<211> 287

<212> DNA

<213> Homo sapiens

<400> 263

```
ctctggcctc ttactcacc cctaccacag acatgggtca gtcactggct ctgagcctcc 60
ttaccctggt tctggccttt ggcatcccca ggacccaagg cagtgatgga ggggctcagg 120
actgttgctt caagtacagc caaaggaaga ttcccgccaa gggtgtccgc agctaccgga 180
agcaggaacc aagcttaggc tgctccatcc cagctatcct gttcttgccc cgcaagcgct 240
ctcaggcaga gctatgtgca gacccaagg agctctgggt gcagcag 287
```

<210> 264

<211> 306

<212> DNA

<213> Homo sapiens

<400> 264

```
ctgccacct caccctcagc tctggcctct gactcacct ctaccacaga catggctcag 60
tactggctc tgagcctct tatcctggtt ctggcctttg gcatccccag gacccaaggc 120
```

agtgatggag gggctcagga ctgttgccctc aagtacagcc aaaggaagat tcccgccaaag 180
gttgtccgca gctaccggaa gcaggaacca agcttaggct gctccatccc agctatcctg 240
ttcttgcccc gcaagcgctc tcaggcagag ctatgtgcag acccaaaagga gctctgggtg 300
cagcag 306

<210> 265
<211> 242
<212> DNA
<213> Homo sapiens

<400> 265
ctgggagagc tagactaagt tgggtcatgat gcagaagcta ctcaaatgca gtcggcttgt 60
cctggctctt gccctcatcc tgggtctgga atcctcagtt caaggttatc ctacgcagag 120
agccaggtag caatgggtgc gctgcaatcc agacagtaat tctgcaaact gccttgaaga 180
aaaaggacca atgttcgaac tacttccagg tgaatccaac aagatcccc gtctgaggac 240
tg 242

<210> 266
<211> 132
<212> DNA
<213> Homo sapiens

<400> 266
ctgcttccat tgggtgggtca tttttgctgt caccagcaac gttgccacga cgaacatcct 60
tgacagacac attcttgaca ttgaagccca cattgtcccc aggaagagct tcaactcaaag 120
cttcatggtg ca 132

<210> 267
<211> 108
<212> DNA
<213> Homo sapiens

<400> 267
ccatgggaat ctaattaatt tcataatgat gttggttgaa catgatacca aaaaatgcag 60
gtattttcaa gaacaataag atagataaca gcattaaagc ataatcct 108

<210> 268
<211> 414
<212> DNA
<213> Homo sapiens

<400> 268
cctgacacaa tatccctgtt cactttgaag tgaattttga ctctatatcc agaacccttc 60
tttaacacaa tggtttcctt tttaggggt tccagatctc cagtaaggct catggtgatt 120
gggtccgggg cactctcaca aaccaggggt agccgggtga caacgacatt gggggctttc 180
ggatctgtca ccacaggacc atctcccagc agcgttttct tgtacttaat tagactctca 240
tcattctttgt ccatttctct cagctctttc agggacttct gtgggtggagg cttataattg 300
agcttgctgt ccagctcatc atcgtcatcc tcctccacat gtgggctctg gggctttttc 360
agtcattctg atctatttat tcagtgtctc acgtctctgt ccgggggtgcc tctg 414

<210> 269
<211> 461
<212> DNA
<213> Homo sapiens

<400> 269
cgcgtggagg gaatatgtgt tctggaagaa tagagatcaa attccaagga cggtggggaa 60
cagtgtgtga tgataacttc aacatagatc atgcatctgt catttgtaga caacttgaat 120
gtggaagtgc tgtcagtttc tctggttcat ctaattttgg agaaggctct ggaccaatct 180
ggtttgatga tcttatatgc aaccggaaat gagtcagctc tctggaactg caaacatcaa 240
ggatggggaa agcataactg tgatcatgct gaggatgctg gaggtagttg ctcaagggga 300
gcagatctga gcctgagact ggtagatgga gtcactgaat gttcagggaag attagaagtg 360
agattccaag gagaatgggg gacaatatgt gatgacggct gggacagtta cgatgctgct 420

gtggcatgca agcaactggg atgtccaact gccgtcccag c 461

<210> 270
<211> 206
<212> DNA
<213> Homo sapiens

<400> 270
gaatccaaca agatcccccg tctgaggact gacctttttc caaagacgag aatccaggac 60
ttgaatcgta tcttcccact ttctgaggac tactctggat caggcttcgg ctccggctcc 120
ggctctggat caggatctgg gagtggcttc ctaacggaaa tggacaagga ttccaactag 180
tagacgaaag tgatgctttc catgac 206

<210> 271
<211> 500
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(500)
<223> n = A,T,C or G

<400> 271
atgatgcaga agctactcaa atgcagtcgg gttgtcctgg ctcttgccct catcctgggt 60
ctggaatcct cagttcaagg ttatcctacg cagagagcca ggtaccaatg ggtgcgctgc 120
aatccagaca gtaattctgc aaactgcctt gaagaaaaag gaccaatgtt cnaactactt 180
ccagggtgaat ccaacaagat ccccggtctg aggactgacc tttttccaaa gaccagaatc 240
caggacttga atcgatatct cccnctttct gaggactact ctggatcagg ctccggctcc 300
ggctccggnt ctggatcagg atctgggagt ggcttcctaa cggaatgga acaggattac 360
caactagtag accaaagtga tgctttccat gacaacctta ggtctcttga caggaatctg 420
ccctcanaca gccnggactt gggccaacat ggattagaag aggattttat gttataaaag 480
aggattttcc ccccttgncn 500

<210> 272
<211> 511
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(511)
<223> n = A,T,C or G

<400> 272
ggtcatgatg cagaagctac tcaaatgcag tcggcttgtc ctggctcttg ccctcatcct 60
ggttctggaa tcctcagttc aaggttatcc tacgcagaga gccaggtagc aatgggtgcg 120
ctgcaatcca gacagtaatt ctgcaaatg ccttgaagaa aaaggaccaa tgttcgaact 180
acttccaggt gaatccaaca agatcccccg tctgaggact gacctttttc caaagacgag 240
aatccaggac ttgaatcgta tcttccnct ttctgaggac tactctggat caggcttcgg 300
ctcccgctcc ggctctggat caggatctgg gagtggcttc ctaacggaaa tggaaacnng 360
attaccaaac tagtagacga aagtgatgct ttccatgaca acccttaggt ctcttgacag 420
gaatctgccc tcacacngcc aggacttggg tcaacatgga ttagaagagg attttattgn 480
tataaaagag gattttcccc nccnttgacc c 511

<210> 273
<211> 101
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(101)

<223> n = A,T,C or G

<400> 273

gttngtaatn atgcanaagc tactcnaatg cagtcennct tttctggct cttgccctca 60
tcctggttct ngaatcctca cttcaagggt atcctacnca c 101

<210> 274

<211> 451

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(451)

<223> n = A,T,C or G

<400> 274

anctagacta nnntggtcat gatgcagaag ctactcaaat gcagtcggct tgtcctggct 60
cttgccctca tcctggttct ggaatcctca gttcaagggt atcctacgca gagagccagg 120
taccaatggg. tgcgctgcaa tccagacagt aattctgcaa actgccttga agaaaaagga 180
ccaatgttng aactacttnc aggtgaatnc aacangatcc cccgtctgag gactgacctt 240
tttccaaaga cgagaatcca ggacttgaat cgtatcttcc cactttctga ggactactct 300
ggatcaggct tgggctccgg ctccggctct ggatcaggat ctgggagtggt cttcctaacg 360
gaaatggaac aggattacca actantagac gaaagtgatg ctttccatga caaccttang 420
tcctcttgaca ggaatctgcc cncagacagc c 451

<210> 275

<211> 423

<212> DNA

<213> Homo sapiens

<400> 275

attgacactt cctggtggga tccgagtgag gcgacgggggt aggggttggc gctcaggcgg 60
cgaccatggc gtatcacggc ctactgtgct ctctcattgt gatgagcgtg ttctggggct 120
tcgtcggctt cttggtgcct tggttcatcc ctaagggtcc taaccgggga gttatcatta 180
ccatgttgggt gacctgttca gtttgcctgct atctcttttg gctgattgca attctggccc 240
aactcaaccc tctctttgga cgcgaattga aaaatgaaac catctgggtat ctgaagtatc 300
attggccttg aggaagaaga catgctctac agtgctcagt ctttgaggtc acgagaagag 360
aatgccttct agatgcaaaa tcacctcaa accagaccac ttttcttgac ttgcctggtt 420
tgg 423

<210> 276

<211> 433

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(433)

<223> n = A,T,C or G

<400> 276

tgnncatgat gcanaagcta ctcaaagtca gtcggcttgt cctggctctt gccctcatcc 60
tggttctgga atcctcagtt caaggttatc ctacgcagag agccagggtac caatgggtgc 120
gctgcaatcc agacagtaat tctgcaaaact gccttgaaga aaaaggacca atgttcgaac 180
tacttccang tgaatccaac aagatccccc gtctgaggac tgaccttttt ncaaagacga 240
gaatccagga cttgaatcgt atcttccac tttctgagga ctactctgga tcaggcttng 300
gntccggctc cggctctgga tcangatctg ggagtggctt cctaaccggaa atggaacagg 360
attaccaact agnngacgaa agtgatgctt tccatgacaa ctttaggtct cttgacagga 420
atctgccctc aga 433

<210> 277

<211> 478

<212> DNA

<213> Homo sapiens

<400> 277

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ctggctagggt gtgtgtgtat gtgagtaggg gtgctattga ttggcacata tttccccccc 60
tggagtttag ggggtggcaga aagcttttat agtaccaaaa aagtaaacat tgataaatatg 120
gcctgacaac aatcagatat gctaagctct agaagcaaaa gcaaggtagg attgcctcca 180
aatgttgaca ggtattagcc ataccacagt aactagatct aatgtgaggg ctaaatgcct 240
ggagaggcag aaccctaag gatgcttagt tatagctcca tgctgccgcc gagtggcttg 300
atgctccatt acaccctcct tggatccaac cttccattaa ggctgaaggc tctagagggc 360
agagtattca agatgttaga tctggtccaa gcccaaattc tagagttaaa agcagagggg 420
ttcttagtgg ctgaaaaaaa acaaaacctg atgacatttg ggactccagt tttgagga 478
```

<210> 278

<211> 208

<212> DNA

<213> Homo sapiens

<400> 278

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aagctactca aatgcagtcg gcttgcctg gctcttgccc tcactcctgg tctggaatcc 60
tcagtccaag gttatcctac gcagagagcc aggtaccaat ggggtgcgctg caatccagac 120
agtaattctg caaactgcct tgaagaaaaa ggaccaatgt tcgaactact tccagggtgaa 180
tccaacaaga tcccccgctc gaggactg 208
```

<210> 279

<211> 330

<212> DNA

<213> Homo sapiens

<400> 279

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ccacacagcc cctgtgctag acatcgctg gtgcccgcac aatgacaacg tcattgccag 60
tggctccgag gactgcacag tcatgtgtg ggagatcccg gatgggggcc tgatgctgcc 120
cctgcccag cccgtcgtca ccctggaggg ccacaccaag cgtgtgggca ttgtggcctg 180
gcacaccaca gcccagaacg tgctgctcag tgcaggttgt gacaactga tcatgggtgtg 240
ggacgtgggc actggggcgg ccatgctgac actggggcca gaggtgcacc cagacacgat 300
ctacagtgtg gactggagcc gagatggagg 330
```

<210> 280

<211> 294

<212> DNA

<213> Homo sapiens

<400> 280

```
ccaaactcct ccagatgcca gacggtctcc ttcttgtcca gatccacata gaacatctca 60
tcttcatcaa attcaaacat aaactcccct gttggtctat gcgtctgtac aaacgcggca 120
taagttagaca catggtccgc cttgatggcc ccagctcctc ggagactcag caggaaagcc 180
aaggagaggg ctctcaagat cacagctctg atatggaaca ttctgtcttc agggcgcatg 240
ttgtggggtc tataattgat gactgtgagc acaggaacag tgatgaggaa ctga 294
```

<210> 281

<211> 269

<212> DNA

<213> Homo sapiens

<400> 281

```
ccacaggcct ctaccccagc cacgtggagc tgagctgggt ggtgaatggg aaggaggtgc 60
acagtggggc cagcacagac ccgcagcccc tcaaggagca gcccgccctc aatgactcca 120
gatactgcct gagcagccgc ctgagggtct cggccacctt ctggcagaac ccccgcaacc 180
acttccgctg tcaagtccag ttctacgggc tctcggagaa tgacgagtgg acccaggata 240
gggccaaacc tgtcaccagc atcgtcagc 269
```

<210> 282

<211> 491
<212> DNA
<213> Homo sapiens

<400> 282
ccaggagtgt caaactctgt aagcacacgg ataccccgga gccgtgcgta ttcaatgacc 60
tccttcacat cctgtgctgt gtagatgtgg gtgacagggt tgtaggaccc ctttctcatg 120
agctctggaa aagtgaagct ctcatatggg aaggaaggat catctaccag atgccagtgg 180
aacacgttca atttattgta cgccatgaca tccagagtgt ccaggatgct agagagtggc 240
aggtaaatggc gagatgtatc caacagcaag ccccggtgag gaaagcgggg aaagtcctca 300
atctcagtct tgttgataaa gaactcggag agctccccag acagtctcag agaggagtaa 360
acactgggtca tcatttatgg tcagggtata attctccact gactccaaag taggaagctg 420
gttacatcca ggtgtgacta cagagacaac caacacattc ttctccagtg tatgcccggt 480
tccctaggtt g 491

<210> 283
<211> 472
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(472)
<223> n = A,T,C or G

<400> 283
cctcnnacng aaggctggtg accaggtccc aggcggggcaa gactcagcct tgggtggggcc 60
tgaggacaga ggaggcccag gagcatcggg gagagagggt gagggacacc gggagagcca 120
ggagcgtgga cacagccaga actcatcaca gaggctggcg tccagtcccc gggtcacgtgc 180
agcaggaaca agcagccact ctggggggcac cagggtggaga ggcaagacga caaagagggg 240
gcccggtgttc ttgcgaaagc ggggctgctg gccacgagtg ctggacagag gccccacgc 300
tctgcttgcc cccatcacgc cgttccgtga ctgtcacgca gaatctgcan acaggaaggg 360
agactctaag cgggagtgcg gccaaagcctg cctccgcccg tcaggaggga ctcccgggct 420
cactcnaagg aggtgccacc atttccgctt tggnnagctt ttctttttct tt 472

<210> 284
<211> 349
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(349)
<223> n = A,T,C or G

<400> 284
aaaaaattta ctcatcttcc ataaagcgac ttttaattgta tcaacactta aagatacaca 60
gtgacttaat gaaatatcag cacaactgca tagaattgag ctccagagaa ttatacactc 120
gagctgcttt cctgggctct ggtttataag ggtattggct tagagaccag cttggagtca 180
tttgccccta cccgggaaat gcaggccagg aaacttaaga ttttgcgggc cttttctgtt 240
tctaggtaaa atgcaggag ctccctgaag gncttgaaaa ccatcaacca ttcaaatatg 300
gtatcctggg gacctttcct cttgagttaa nggaagaaag gaggtttgg 349

<210> 285
<211> 179
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(179)
<223> n = A,T,C or G

<400> 285
aaagntggct caagactggc ccangcataa tactgtcaat ctaaaggtaa ccggcaacat 60
caaaaagtac atctcaaaag aatcaggctt aaagataaac aggagaactg gatatatcta 120
agagtaagaa gtgtaaacia tagaaaagag gtagggttta gggttctcat ctagggatt 179

<210> 286
<211> 462
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(462)
<223> n = A,T,C or G

<400> 286
ccagtacacc catgaatttg atggagatga gcagttctac gtggacctgg ggaggaagga 60
gactgtctgg tgtttgcctg ttctcagaca atttagattt gaccgcgaat ttgcaactgac 120
aaatatcgct gcctaaaaca taacttgaac agtctgatta aacgctccaa ctctaccgct 180
gtaccaatg aggntcctga ggtcacagtg ttttccaagt ctcccgtagac actgggtcag 240
cccaacatcc tcatctgtct tgtggacaac atctttcctc ctgtggnaaa catcacatgg 300
ctgagcaatg ggcactcagt cacagaangt gtttctgaga ccagcttctc ctccaagagt 360
gatcattcct tcttcaagat cagtacctca cctcctccc ttctggntga ggagagttat 420
gactgcaagg nggancactg gggactggga caagcctctt ct 462

<210> 287
<211> 388
<212> DNA
<213> Homo sapiens

<400> 287
ggacattcaa atgtctttat ccacattcct gaaggataat tgttatagat tccctacctc 60
cataggaatg cttataatgg attatctata caatctccac attcccacat tttgcattag 120
agaatggaat cagtcaaacc ctgttcccag agtttccctt agagtcttca cctgttgtct 180
tatatccatc taggaatccc catctctaata gtaagcttgg agatccgggc ccccggggga 240
caggtgactg aaggacaaaa actgacatctg ctctgctcag tggctggggg tacaggaaat 300
gtcacattct cctggtacag agaggccaca ggaaccagta tgggaaagaa aaccagcgt 360
tccctgtcag cagagctgga gatcccg 388

<210> 288
<211> 387
<212> DNA
<213> Homo sapiens

<400> 288
aaatttctca aataactaag tcttactaa ggcagcagtt caaaactggt ccaggaatta 60
aaatatattc ccatttgagg agtcttctt cacaccttca cctcctcagc ctttaagtata 120
tacacacaca cccaacaccc tcaatacttg actagcaaca ggctttacca tctttacctg 180
acaatgaccc cagggcggag atcgaaattc ttcttcaaa tctctaatag ctctctctca 240
ctcttctgag aggtaccata atggaaaatg gagatagata atggatgaga aactccaata 300
gcataagaga cctgaacaag aaccctccgg cacagacctc cttaacaag ggattttgcc 360
acccaacgag cagcataagc agacctg 387

<210> 289
<211> 279
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(279)
<223> n = A,T,C or G

<400> 289
ngnccacaag atatgttcta tagacgtcca tgagtcctct tgctgtgngg gagcgggtatc 60
cacagacttn tggaataatt ggcctgtgag gaagctcatc aaagctgcaa acagtacaan 120
tgaatgcaat aganagncac agggccttat tagcctttct gatggaggac ttganatttg 180
ttgnccagga anctattgtg tcataaactg aagagacatn ccactttgat ggattatttt 240
tcttttcaga aagacttggc ttccttgctc tttctactg 279

<210> 290
<211> 235
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(235)
<223> n = A,T,C or G

<400> 290
ngtccagtag ggctgagatg ttgggagcca tcaatcagga aagccgggtt agtaaagcag 60
ttgaagtgat gattcancac gttagaaaact tgaagaggat gtatgccaaa aagcaccgct 120
gaattagaag aactgaaaca gggtctttctg cagaatgaaa ggcctttcaa tntctttgaa 180
gatgatgatg actgccaaat taaaaaacgt tcagcttttc taaactccaa gccat 235

<210> 291
<211> 318
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(318)
<223> n = A,T,C or G

<400> 291
cctttccttg agctgcacgt gaacctgtgt gggcaggcag cgtttgcagg cgtgtttacg 60
ggcaggcagc gtttgcaggc gtgtttaccg gcaggcagcg tttgcaggcg tgtttacatg 120
caggcgtanc accatgtgag accactggtc cagggtttca gaggtcctgc tcaggtgaat 180
cggctgtgtt ctcacaagtt caccgagctg antgggtgtg caacatgaaa tactagtgtc 240
gtgagggaca gaagggacag aaagaggctn aagacatna tccagctata cctgtgcctc 300
ggcttttctc agacctcg 318

<210> 292
<211> 381
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(381)
<223> n = A,T,C or G

<400> 292
ccaagcctca tcaataactg tatccaaaag gagacgtgc ttgggggtgta cccagagaaa 60
acaccaagct ttcctggctt cccggccctc cctctcccca ttagtctttg ggggtgcatac 120
ataagtgttg tgtgaagtct cttgggggtt agaagatctt gcactcattg atggagaaga 180
gcctccttct gtttcgtctc ctggcctggt tgacggcagt tcggacgacg cactcaaaca 240
cctgctgtac tccccgattg ctaagggctg agcactccag gttagccctg gctctgacat 300
cctgggccag nttcttcctt tccatggcat tgacgcanga ggccctgttg ggccccatct 360
cccgtggtc agtctgggtg g 381

<210> 293
<211> 416
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(416)

<223> n = A,T,C or G

<400> 293

```
ccagtacacc catgaatttg atggagatga gcagttctac gtggacctgg ggaggaagga 60
gactgcctgg tgtttgcctg ttctcagaca atttagattt gacccgcaat ttgactgac 120
aaacatcgct gtcctaaaac ataacttgaa cagttctgatt aaacgctcca actctaccgc 180
tgctaccaat gaggttcctg aggtcacagt gttttccaag tctcccgta cactgggtca 240
gcccacatc ctcatctgtc ttgtggacaa catctttcct cctgtggna acatcacatg 300
gctgagcaat gggcactcag tcacanaang tgtttctgag accagcttcc tctccaagag 360
tgatcattnc ttcttcaana tcagntaccc caccctcctc cctcttctg aggaga 416
```

<210> 294

<211> 317

<212> DNA

<213> Homo sapiens

<400> 294

```
aaattatgac acaaaatttt attaacaagg aaatatccat taattgacta ctacagtaaa 60
aactttataa tgcttgatc atgaagaaag accttccttt tccttatata ttaattgaac 120
tacataggct tgctgtacat tttgttattc atgttataag aattctagat tccattgctt 180
ttgaaatag tttcttttta ggaactaaaa gtcaacttat agtttgattt ctgttttatt 240
tgtactgtgt ttctgatttt gtgggtttct aaataaaaag atcaaaccce ccactttcaa 300
tatactgttt tctattt 317
```

<210> 295

<211> 156

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(156)

<223> n = A,T,C or G

<400> 295

```
ccaaaagaag taagacagct tgctgaagat ttcctgaaag actatattca tataaacatt 60
ggtgcacttg aactgantgc aaaccacaac attcttcana ntgtggatgt gtgtcatgac 120
ntanaaaagg atgaaaaact tattcgtcta atggaa 156
```

<210> 296

<211> 533

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(533)

<223> n = A,T,C or G

<400> 296

```
cttgacctgct gctctggccc ctggtcctgt cctgttctcc agcatgggtgt gtctgaggct 60
ccctggaggc tcctgcatgg cagttctgac agtgacactg atggtgctga gctccccact 120
ggctttggct ggggacacca gaccacgttt cttggagtac tctacgtctg agtgatcatt 180
cttcaatggg acggagcggg tgcggttcct ggacagatac ttctataacc aagaggagta 240
cgtgcgcttc gacagcgacg tgggggagtt ccgggcggtg acggagctgg ggcggcctga 300
tgaggagtac tggaacagcc agaaggactt cctggaagac aggcgggccc cggtggacac 360
ctactgcaga cacaactacg gggttggtga gagcttcaca gtgcagcggc gagtccatcc 420
taagggtgact gtgtatcctt caaagacca cccctgcagc accacaacct cctgggtcgt 480
```

tctgngagtg gtttctatcc aggcagcatt gaatcangtg gttccggaat ggn 533

<210> 297

<211> 529

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(529)

<223> n = A,T,C or G

<400> 297

cctgtgaaa cgggccctc ccggagccca nggaaaagac tgcttctctc tcagcagccc 60
cattcctggt tattccaggg ctgaccaaca aggacatttc cacctcaca gctgctgctc 120
actgatgttc ccgtgggata agaggggaaa ttaagtgaca accgcagcag catccgctgg 180
gtctgtccct gtatcgcat ccagaggctt gcgcatacacc aagggtcggg cgtagctgtg 240
ctgccctgcg ttgtgtgcat agcctctctc tcctctgctt gcttaagtcc ttcttancca 300
ccctctccct tanggctcta ccaggatgc cacggggagc aggaatatta atcctagaat 360
cctgactctc agtggcaata cagagtgtac tccagggatg ctgggtgaaa cccggggaaat 420
tctactcacc attaaccttg ggagtaagag gccatacctc atctgaaact ttacctgccc 480
gggcggggcg ttcaaaaggc cnattccccc nccctttgcg ccnttatag 529

<210> 298

<211> 345

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(345)

<223> n = A,T,C or G

<400> 298

ccaatgtggt tggctctcan ctgtcantta gccaggttcc ataccttgac cagcttgtcc 60
cagccacagg agacgatgat agggttgctg ctgttgggag agaagcggac acaagacacc 120
cactctgagt ggctctcatc ctggacagtg tatttgcaca caccaggggt attccatagc 180
ttgatggttt tatctcgaga tccagagaca atctgccggt tgtcagagga gaaggccaca 240
ctcagcacat ccttggtatg gccacaaaat cgcctcgtgg tgggtgccgt tgtgagatcc 300
cagaggcgca gggttccatc ccaggagcct gagagggcaa actgg 345

<210> 299

<211> 182

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(182)

<223> n = A,T,C or G

<400> 299

ccacaagata tgttctagag acgtccatga gtcctcttgc tgtgtgggag cggnatccac 60
agacttctgg aataattggc ctgtgaggaa gccatcaaa gctgcaaaca gtacaatgaa 120
tgcaatagag agccagaggg ccttattagc cttntgatg gaggacttga gatttgttgc 180
cc 182

<210> 300

<211> 440

<212> DNA

<213> Homo sapiens

<400> 300

```
ctgcaaatgg ttctgctgaa acatctgcct tggacacagg gttctcgctc aacctttcag 60
agctgagaga atatacagag ggtctcacgg aagccaagga agacgatgat ggggaccaca 120
gttcccttca gtctggtcag tccgttatct cctgctgag ctcagaagaa ttaaaaaaac 180
tcatcgagga ggtgaagggt ctggatgaag caacattaaa gcaattagac ggcattccatg 240
tcaccatctt acacaaggag gaagggtgctg gtcttggggt cagcttggca ggaggagcag 300
atctagaaaa caagggtgatt acggttcaca gagtgtttcc aaatgggctg gcctcccagg 360
aagggactat tcagaagggc aatgaggttc tttcctcaac ggcaagtctc tcaaggggac 420
cacgcaccat gatgccttgg                                     440
```

<210> 301

<211> 396

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(396)

<223> n = A,T,C or G

<400> 301

```
cttgcgtccc cgcgtgtgtg cgcctaactc caggtgggtcc acccgagacc ccttgagcac 60
caaccctagt ccccgcgcg gccccttatt cgctccgaca agatgaaaga aacaatcatg 120
aaccaggaaa aactcgccaa actgcaggca caagtgcgca ttggtgggaa aggaactgct 180
cgagaaaaga agaagggtgt tcatagaaca gccacagcag atgacaaaaa acttcagtcc 240
tccttaaaga agttangggg aaacaatatc tctggtattg aagaggtgaa tatgtttaca 300
aaccaaggaa cagtgatcca cttaacaac cctaaagttc aggcattctc ggcagcgaac 360
actttcacca ttacaggcca tgctgagaca aagcag                                     396
```

<210> 302

<211> 548

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(548)

<223> n = A,T,C or G

<400> 302

```
ctgcgtgatt cccgtgattg cgttacaagc tttgtctcct tcgacttgga gtctttgtcc 60
aggacaatga gacactcaaa gagaacttat tgtcctgatt gggatgacaa ggattgggat 120
tatggaaaat ggaggagcag cagcagtcac aaaagaagga agagatcaca tagcagtgcc 180
caggagaaca agcgtgcaa atacaatcac tctaaaatgt gtgatagcca ttatctggaa 240
agcagggtcta taaatgagaa agattatcat agtcgacgct acattgatga gtacagaaat 300
gactacatc aaggatgtga acctggacat cgccaaagag accatgaaag ccggtatcag 360
aaccatagta gcaagtcttc tggtagaagt ggaagaagta gttataaaag caaacacagg 420
attcaccaca gtacttcaca tcgtcgttca catgggggtat gaaccgtttt tacctgcccg 480
ggcggggcgt aanggcgaat tccagcacac tnggcgccgt tctaggggat ccgagctcgg 540
tccanctt                                     548
```

<210> 303

<211> 232

<212> DNA

<213> Homo sapiens

<400> 303

```
ccagcgacag cctggcctgg gaatggactg gcagctcatc actaaaatga ctcctttcat 60
ggaatccact gctatgcagc cacactgacc acagagcaac tgaatagggt agcattggat 120
tgttgatgac aactcttcag cagaacaatt gtgtgtttga agggactgtt ttatgatgaa 180
ataactgtta tttcctggag ctaattgttg aatgacagtt tgtcaactgt tt                                     232
```

<210> 304

<211> 232

<212> DNA

<213> Homo sapiens

<400> 304

```
gctaaaccaa aagaagcctc cagacagccc tgagatcacc taaaaagctg ctaccaagac 60
agccacgaag atcctaccaa aatgaagcgc ttcctcttcc tcctactcac catcagcctc 120
ctggttatgg tacagataca aactggactc tcaggacaaa acgacaccag ccaaaccagc 180
agcccctcag catccagcag catgagcgga ggcattttcc ttttcttcgt gg 232
```

<210> 305

<211> 191

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(191)

<223> n = A,T,C or G

<400> 305

```
ccttgctca gatccaannt cactcgnaag aggccatgtc taccctnaat gacactcatg 60
gaggaaatgc tgagagaagc attcanatgc atgacacaag gtaagactgc caaaaatctt 120
gttcttgctc tcctcatctt gttatttggt ttatttttag gagttttgag agcaaatga 180
caacaccag a 191
```

<210> 306

<211> 342

<212> DNA

<213> Homo sapiens

<400> 306

```
aaacttttga gttgtagtca gaaactgttg ttggactgca tagttttcaa aagtttttgg 60
tacatttctg acttttagaaa tctggggttag gaatcccttt ccatatgcat atagactatt 120
ttctgagctt cttcaaaaca tgtttcagtg ggttcctgaa tgctcctgat gatagtctct 180
cttgtcgaaac tgtcaatggt aatctctcta ggggactgtg gctggatgta aatcttataa 240
agcttctttg ccctagaaat tctgctccac cgtgaggcaa ttttcttata ggtttcacat 300
gccatccaga attgaatatt ctcgtcactg tgctccattt tt 342
```

<210> 307

<211> 545

<212> DNA

<213> Homo sapiens

<400> 307

```
ccagtagggc tgagatgttg ggagccatca atcaggaaaag ccgggttagt aaagcagttg 60
aagtgatgat tcagcacgta gaaaacttga agaggatgta tgccaaagag cacgctgaat 120
tagaagaact gaaacagggt cttctgcaga atgaaaggtc tttcaatcct cttgaagatg 180
atgatgactg ccaaattaaa aaacgttcag cttctctaaa ctccaagcca tcttctctac 240
gaagagtgc tattgcctct ttaccagaa atattggaaa tgcaggaaatg gtggctggga 300
tggaataaa tgatcgattc agtagaaggt caagcagttg gcgtattttg gggcacaagc 360
agagtgaaca ccgtccctca ttacctcgat ttattagcac ctattcctgg gcagatgctg 420
aagaagaaaa atgtgaacta aaaactaaag atgactcaga gccatctgga gaagaaacag 480
tagaaaggac aaggaagcca agtctttctg aaaagaaaaa taatccatca aagtgggatg 540
tctct 545
```

<210> 308

<211> 330

<212> DNA

<213> Homo sapiens

<400> 308

```
cctccatctc ggctccagtc cacactgtag atcgtgtctg ggtgcacctc tgggccagtc 60
gtcagcatgg ccgcccagtc gccacgtcc cacaccatga tcacgttgctc acaacctgca 120
```

```
ctgagcagca cgttctgggc tgtggtgtgc caggccacaa tgcccacacg cttggtgtgg 180
ccctccaggg tgacgacggg ctcccgcagg ggcagcatca ggccccatc cgggatctcc 240
cacaccatga ctgtgcagtc ctccgagcca ctggcaatga cgttgtcatt gtgcgggcac 300
caggcgatgt ctacgcagg ggctgtgtgg 330
```

```
<210> 309
<211> 392
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(392)
<223> n = A,T,C or G
```

```
<400> 309
ngtcttgctt gctgctctgg cccctgggtc tgtcctgttc tccagcatgg tgtgtctgag 60
gctccctgga ggctcctgca tggcagttct gacagtgaca ctgatgggtc tgagctcccc 120
acttgctttg ggctggggac accagaccac gtttcttgga gtactctacg tctgagtgtc 180
atttcttcaa tgggacggag cgggtgcggt tcctggacag atacttctat aaccaagagg 240
agtacgtgcg ctccgacagc gacgtggggg agttccgggc ggtgacngag ctggggcggg 300
ctgatgagga gtactggaac agccannaag gacttcctgg aanacaggcg ggncgcgggtg 360
gacacctact gcanacacaa ctacgggggt gg 392
```

```
<210> 310
<211> 221
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(221)
<223> n = A,T,C or G
```

```
<400> 310
nccagggtca ggccctgggg tgaaaggaga cagggtgctgc caagaccata catcagtcac 60
ctggcagcag ctcgagaagc atgtcctcca cgccgtcaat cttgatgtgg tgcactaaag 120
cgccnagaaa acttgagtc tgaggatcgg tatcgtccat cagggtagag ctgccacatg 180
ataggcgaca ggcttggggc tatctgggtg ggggtcatag g 221
```

```
<210> 311
<211> 118
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(118)
<223> n = A,T,C or G
```

```
<400> 311
ncctcccaga gaaggctggt gaccaggtcc caggcgggca agactcagcc ttggtggggc 60
ctgaggacag aggaggccca ggagcatcgg ggagagaggt ggagggacac cnggaaaa 118
```

```
<210> 312
<211> 133
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(133)
<223> n = A,T,C or G
```

<400> 312
gccggncagg taaagaacta atttgtaaat tatgacacaa aattttatta acaaggaaat 60
atccattaat tgactactac agtaaaaact ttataatgct tgtatcatga agaaagacct 120
tccttttncc tat 133

<210> 313
<211> 274
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(274)
<223> n = A,T,C or G

<400> 313
ngtaaatgat tctttatttc aataaacttt aacaaacaat atataatatt tcttccttaa 60
aaagctcatt caagatcat aggcagactt cttccccatt gtattttagt tggggagata 120
aaggcaaaaa gaggaatgt aagctatctt acagtcattc tgagaacctc tggtttcattg 180
ctatactttc ccagctaaaa gttactaatt tacgaagttc agatctgaaa cttaaaaaatc 240
aanatccata tattagatg tcctgctgtc acac 274

<210> 314
<211> 268
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(268)
<223> n = A,T,C or G

<400> 314
gtgatctccc catttgaagg tcgactgatt agcaatctaa gttctgcccc gaactttaat 60
tcctcttttc caggtaatgc attcacagat cctggggact aggggtgtgga catctttggg 120
aggcattatt ctgcctgcca taatagaatt gttnggaaga ttaacaaca taatatacat 180
gacgtatgtt gangcacgct tggcacctgg gaaatactca ggatgtacta accattgctc 240
ctacacagnt cagctnctga aggagtcc 268

<210> 315
<211> 201
<212> DNA
<213> Homo sapiens

<400> 315
aaaatttcca acctgaagat gggtcataat tacacgttca ccgtccaagc aagatgcctt 60
tttggcaacc agatctgtgg ggagcctgcc atcctgctgt acgatgagct ggggtctggt 120
gcagatgcat ctgcaacgca ggctgccaga tctacggatg ttgctgctgt ggtggtgccc 180
atcttattcc tgatactgct g 201

<210> 316
<211> 202
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(202)
<223> n = A,T,C or G

<400> 316
cctcggatga tgaagacagt gccaccaca atgccacga ggccacaga caacccagg 60

gcgcagacca cagtctctgt gagctctgac ataggggctg gaatctcagg ctcccagtggt 120
ttcagaagag gcttgtccag tccccagtgcc tccaccttgc agtcatanct ctccctcanct 180
gaagggagga ggggtgaggna ac 202

<210> 317
<211> 182
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(182)
<223> n = A,T,C or G

<400> 317
accagcagtc ctgcggcacc tacctccgcy tgcgccagcc gccccccagg cccttcctgg 60
acatggggga gggcaccaag aaccgaatca tcacagccga ggggatcatc ctccctgttct 120
gcgcgggtgt gcctgggacg ctgctgctgt tnaggaaacg atggcaagaa cganaactcn 180
gg 182

<210> 318
<211> 149
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(149)
<223> n = A,T,C or G

<400> 318
ccagnacncc catgaanttgt atggaatga gcacttntac gtggacctgg ggaggaagga 60
gactgtctgg tgtttgcctg ttctcatata atttagattt gacccgcaat ttgncctgac 120
aaacactggc tgttctaaaa cataacttg 149

<210> 319
<211> 240
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(240)
<223> n = A,T,C or G

<400> 319
ccagcctaca atggggatgt tgtgtttctg ttcaccttcg tttactatgc ctgtgtcttc 60
tccaccacgc tggggtctgg gaggaatga cagacagagg atgagctcta cccagggcct 120
gcaggacctg cctgtagccc actctgctcg ccttagcact accactcctg ccaaggagga 180
ttccatttgg cagagcttct tccaggtgcc cagctatacc tgtgcctcgg ctttttcana 240

<210> 320
<211> 374
<212> DNA
<213> Homo sapiens

<400> 320
cctaggcatg acaatcggag gactcgaggg ggatggagga ctagtgatcg gctggctgct 60
tccagtcgat tagagaggtg aaaaagctga acgtgtgccca gtaatcttca aaaggcagaa 120
catatcacct ctgccccgta aactgttctc tccgagggaa aaaatggaag ttatcctcac 180
agttcactgc cgtgggtattt cttcttgtcc catcttttgc atgacttgcc atggtacagc 240
cttgtttcaa actgttcact gtgatctgtg ggtctttgag tttcagtgag tttgctgaaa 300
tgtcgaagaa gtagttccaa acttcaatgt tcaatgaaat tttgtttcaa gtttgaaatg 360

gagagagcag cttt

374

<210> 321

<211> 285

<212> DNA

<213> Homo sapiens

<400> 321

```
cctttccttg agctgcacgt gaacctgtgt gggcaggcag cgtttgcagg .cgtgtttacg 60
ggcaggcagc gtttgcaggc gtgtttaccg gcaggcagcg tttgcaggcg tgtttacatg 120
caggcgtagc accatgtgag accactggtc cagggtttca gagggtcctgc tcaggtgaat 180
cggctgtgtt ctcacaagtt cacggagctg agtgggtgtg caacatgaaa tactagtgtc 240
gtgagggaca gaagggacag aaagaggctg aagaccatca tccag 285
```

<210> 322

<211> 135

<212> DNA

<213> Homo sapiens

<400> 322

```
aaagagaact aatggaagtg gattgaatac agcagtctca actgggggca attttgcccc 60
ccagaggaca ttgggcaatg tttggagaca ttttgggtcat tatacttggg gggttggggg 120
atggtgggat gtgtg 135
```

<210> 323

<211> 297

<212> DNA

<213> Homo sapiens

<400> 323

```
ccattgcggg aacctcaag ttcaaccag agaccgacta cctgacgggc acggatggca 60
agaagttcag gctggaggct ccggatgcag atgagcttcc caaaggggag tttgaccag 120
ggcaggacac ctaccagcac ccaccaagg acagcagcgg gcagcatgtg gacgtgagcc 180
ccaccagcca gcgcctgcag ctccctggagc cttttgacaa gtgggatggc aaggacctgg 240
aggacctgca gatcctcatc aagggtcaaag ggaagtgtac cactgaccac atctcag 297
```

<210> 324

<211> 413

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(413)

<223> n = A,T,C or G

<400> 324

```
ccttgccctca natccnnggt cactcgyaag aggccatgtc taccctcaat gacactcatg 60
gaggaaatgc tgagagaagc attcagatgc atgacacaag agccaatgaa aggccctatt 120
gctatgcaat ctggtccaaa accactcttc aggaggatgt cttcactggt gggccccacg 180
caaagcttct tcatgagga atctaagact ttgggggctg tccagattat gaatgggctc 240
ttccacattg ccctgggggg tcttctgatg atcccagcaa gggatctatg caccatctg 300
tgtgactgtg tggtagcctc tctgggggag gcattatgta tattattttc cggatcactc 360
ctggcagnaa cggagaaaaa actccangaa gttgtttggt caaaggaaaa atg 413
```

<210> 325

<211> 340

<212> DNA

<213> Homo sapiens

<400> 325

```
ctgggggggc cgggaaagg gttgggcat gagccaggca gctccgaagc agtcaactgag 60
gccaggagc ctgcaccag gtcagtgggc gacctggctc tcaactcctgg cctgggtgct 120
```

```
cacctacaga ccacttcact tcccctgtcc gcagcgtcac tatgtcctca taggtggctg 180
tctgggtcaat gtccaggccc tcgtagggtg gatcttcctc catgccagcc ttgctgtcat 240
ccttgtccag cagcaggaag ataggcacga tgatgaagag gatgatcagc agcgtctgga 300
tcatgatgat accatccttc agcgtgttcc tctgcttcag 340
```

<210> 326
<211> 240
<212> DNA
<213> Homo sapiens

```
<400> 326
ccagcctaca atggggatgt tgtgtttctg ttcaccttcg tttactatgc ctgtgtcttc 60
tccaccacgc tggggtctgg gaggaatgga cagacagagg atgagctcta cccagggcct 120
gcaggacctg cctgtagccc actctgctcg ccttagcact accactcctg ccaaggagga 180
ttccatttgg cagagcttct tccaggtgcc cagctatacc tgtgcctcgg cttttctcag 240
```

<210> 327
<211> 353
<212> DNA
<213> Homo sapiens

```
<400> 327
aaaaaaacaa agaagaagaa gtcacaaagc aattgaaatg gagcatccgc ttggagaatt 60
aagacagggt gctcctgaga cagacttcca agacagcttc tttgaagtgc tgtgtggggg 120
taaatattct tcagcaaaga gggtcacagg taagggtccc gtgaaacagc agttctta 180
atcatcttta tcttccctta ggataatata ccccaaaata ctttgcattc ataagatgta 240
tacatcactg cagttcacga aacacagctc gctgcccaat acatatccat gttgcatggc 300
taatgaaatg tcaaacccta ctgggtacat ggcagtggag ctccacagca agg 353
```

<210> 328
<211> 267
<212> DNA
<213> Homo sapiens

```
<400> 328
cacagtcatc aattatagac cccacaacat gcgccctgaa gacagaatgt tccatatcag 60
agctgtgatc ttgagagccc tctccttggc tttcctgctg agtctccgag gagctggggc 120
catcaaggcg gacctgtgtt caacttatgc cgcgtttgta cagacgcata gaccaacagg 180
ggagtttatg tttgaatttg atgaagatga gatgttctat gtggatctgg acaagaagga 240
gaccgtctgg catctggagg agtttgg 267
```

<210> 329
<211> 228
<212> DNA
<213> Homo sapiens

```
<400> 329
cctccccagg acgacgtctt cccgacgcaa gagcaccctg aactgtaacc tatcctttat 60
ctcgtatggt aagggcagcc aggcgtgctg cttctcgtcc aaatacacga acttctccca 120
ggcccacagg cggtcgggtt ggctcgtgac tgctctcccg agtgtcgggc actcggccat 180
ggcgtcctcg ggccgcctaa gaagcaagag ccagagcctc tcaaggcc 228
```

<210> 330
<211> 580
<212> DNA
<213> Homo sapiens

```
<400> 330
ctgaaggatg aaagagattg gcaaggaagc aggaatgagt cagctttggg ggaatattac 60
ctggtggctc ccatcattta ttgcttagga catacccttt tacctacttg ctatcatgct 120
ggacctcagc atttcaggga ccagaaaaga tggggacacc aatgcaagcc caagactacc 180
atccagagga ccgttcctgc ccatgctgct tcctctagtt ttgctttcag agtgggtgtca 240
ccccattgc taactcaaga gtgcatcact aggccttcctg agcaggtttg atcgggattt 300
```

```
ggcctgggtc tgttggtcag ggaggcagag gtgtggggag aagggtgaaa ggtgactgag 360
ccagggttcc aggtctctca ctcacggggc tgaagctggg catcgtcagg ctgagagccc 420
ctcgacgtgc gccagcggta gcccttcttc ttgagcacgt gccagatcat gaagcctgcc 480
aggcccatga ggaagaagac cagcacaagc aggaagagca tatatagccc atgttggggc 540
ggttccaggt caggctgtgg ttccgacatg aggcctggg 580
```

```
<210> 331
<211> 542
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(542)
<223> n = A,T,C or G
```

```
<400> 331
aaactccaaa ttcctttatc gaagcagcta tctgctaata ttactgaatg acaagtcttt 60
ggaaatgata gttaaccgaa aatgcagaaa gaatcatagc aactaatgat aatgacgggt 120
aaaggataga aaataaaatt tttagccaca ggttggtggtt acagcatcca ggccatcacc 180
gacatctcgg cagggtatg ccgccacttc gtattaaacg tctactcctc cgagaatgcc 240
cttattaaat taagtgcata gtaaggcatc ccacccaga cagagggatc cacattcttt 300
aatcatgatg cgggccactg taacagggag atggatgcag gacgcagacg ggggtggggcg 360
cccaagcgac gcacttagac ggtgatctgt tggttttctc tgaaaaatga tctctggtgt 420
gaggcacaaa tatctggaaa catccggaag acctggctct gcggcggtc ctcgggggcc 480
tgcacacag anccggctcc acagctcttc ccagcctctt ctgccagttg ccggacatac 540
ag 542
```

```
<210> 332
<211> 345
<212> DNA
<213> Homo sapiens
```

```
<400> 332
ccaatgtggt tggctctcag cttgcagtta gccaggttcc atacctgac cagcttgtcc 60
cagccacggg agacgatgat agggttgctg ctgttggcg agaagcggac acaagacacc 120
cactctgagt ggctctcatc ctggacagtg tatttgcaca caccagggg attccatagc 180
ttgatggttt tatctcgaga tccagagaca atctgccggt tgtcagagga gaaggccaca 240
ctcagcacat ccttggtatg gccacaaaat cgctcgtgg tggtgcccgt tgtgagatcc 300
cagagggcga ggttccatc ccaggagcct gagagggcaa actgg 345
```

```
<210> 333
<211> 542
<212> DNA
<213> Homo sapiens
```

```
<400> 333
ctgtatgtcc ggcaactggc agaagaggct ggggaagagct gtggagccgg ctctgtgatg 60
caggcccccg aggagccgcc gccagaccag gtcttccgga tgtttccaga tacttggtcc 120
tcacaccaga gatcattttt cagagaaaac caacagatca ccgtctaagt gcgtcgcttg 180
ggcgccccac ccgctctgcg tccgtcatcc atctccctgt tacagtggcc cgcatcatga 240
ttaaagaatg tggatccctc tgtctggggg gggatgcctt actttgcact taatttaata 300
agggcattct cggaggagta gacgtttaat acgaagtggc ggcatagccc cgccgagatg 360
tcggtgatgg cctggatgct gtaaccacaa cctgtggcta aaaattttat tttctatcct 420
ttaccggtca ttatcattag ttgctatgat tctttctgca ttttcgggta actatcattt 480
ccaaagactt gtcattcagt aatattagca gatagctgct tcgataaagg aatttgagat 540
tt 542
```

```
<210> 334
<211> 618
<212> DNA
<213> Homo sapiens
```

<220>
<221> misc_feature
<222> (1)...(618)
<223> n = A,T,C or G

<400> 334
aaaaaaaaa taattaagat acagggtttca aaccatatta ccacgatttc aaaaattttg 60
tgaataaaaag aagacacacc gtatttataa agcttctagg ggctgtaata gatacataat 120
tttgggatgtg gtatagggttg gcctatataat acaaaaaatac gtcactaaaa ttaagtggag 180
tcacaataac tttttatgta actttgtttt agttctaatt tggtaacagt gactcaaaat 240
aaatagaatc atatttttagg tggaaactcg atgatccatg taagtagcgg ggctggagtt 300
ctgtgctgtc tgggcagaga aagcacttgg actgaaatgat gggcacagct ctctctgtga 360
agtcctgcag agtcactaac cttgagttca tgtgctctaa gcttctactgt ccctccaacc 420
caagatccca atttctttta ttccatcttg tttcctcttg taaacagaag agcacaatat 480
gacctgtttt caaaggagcc ggcaggaatc tggttctgat aacaaagtcc ctgtcactcc 540
tgtgtctatt agttctccta ggtagtttct tcagggtctgc gccaaactca cttcacagta 600
natgaaggaa tagtgcca 618

<210> 335
<211> 193
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(193)
<223> n = A,T,C or G

<400> 335
gaaccgnacc cgctccgtcc cattgaagaa atgacactca gacgtagagt actccaagaa 60
acgtgggncgt gtgtccccag ccaaagccag tggggagctc ancaccatca ntgtcactgn 120
cagaactgnc atgcaggaac ctccagggag cctnagacac accatgctgg anaacaggac 180
aggaccaggg gcc 193

<210> 336
<211> 421
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(421)
<223> n = A,T,C or G

<400> 336
ccaatcatag agatatctgc accagcctgc aaagcttcca tgaacgcttt ggtcccagac 60
ttggcgatag taccaagggtt attgatcaag tcagccttgg tcattccaat tccagtatcc 120
acaatagtga gagttcgatc ttgtttgttc ggtataaggt taatatgcag ctctttctca 180
gagtctaatt tactgggatc tgtcaagctt tcataccgga ttttgtccaa tgcatctgat 240
gaatttgaaa tgagctctct cagaaagatc tctttgttcg agtagaaagt attgatgatc 300
aatgacatca actgggcaat ttctgcctga aaggcgaacg tntnaacctc ctntcctccc 360
atcggttggg cttgggtctg ggtttcctca ngcatntgga acgacaccgc gccggtntac 420
c 421

<210> 337
<211> 481
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(481)
<223> n = A,T,C or G

<400> 337
ccttgccctca natccanggt cactcgggaag aggccatgtc taccctcaat gacactcatg 60
gaggaaatgc tganagaagc attcanatgc atgacacaag gtaagactgc caaaaatctt 120
gntcttgcgc tcctcatttt gttattngtt ttanttttag gagttntgag agcaaaatna 180
cancaccagc aaattcagta aatgggactt tcccggcaga nccaatgaaa ggccctattg 240
ctatgcaatc tgggtccaaaa ccaactcttca ggaggatgtn ttcactgggtg ggccccacgc 300
aaagcttctt catgagggaa tctaagactt tgggggctgt ccagattatg aatgggctct 360
tccacattgc cctggggggt cttctgatga tcccancagg gatctatgcn cccatctgtg 420
tgactgtgtg gtaccctctc tggggaggca ttatgtatat tatttccgga tcactcctgg 480
c 481

<210> 338
<211> 146
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(146)
<223> n = A,T,C or G

<400> 338
gtgtttgatg gtaaggtttn tcacanagcc gaaaatgtng ctgaanatca aaaaaatctc 60
acaagaaggg gagggagaag agattcgatt ctgagctctc tactcccggtg ttctgcgtag 120
agaagccgac tgntgctgga ggtcng 146

<210> 339
<211> 395
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(395)
<223> n = A,T,C or G

<400> 339
ctggaaaaag cnaaanagag ncttaagaac gtggatgaga acattcgcan gctcacnggg 60
cgggatccga atgacntgag gcccatccaa gccagattgc tggccctttc tggtcctggn 120
ggagggnagag gacgtggtag tntattactg aggcgtggat tctnanatag tgnaggagga 180
ccncagccn aacagagaga ccttgaaggg gcagtcanta ngctgggctg ggagcgtnng 240
accagaagag aatcacgcca ggaaagcgac ccggangatg atgatgttaa aaagccanca 300
ttgcagnctt cagttgtagc tacctncaaa gagcgcacac gtanagacnt tatccagnat 360
caaaaatattg atgaaaaggg aaagcaaagg aaccg 395

<210> 340
<211> 579
<212> DNA
<213> Homo sapiens

<400> 340
ctgccctact tttcaattca gatatactag taccttacct agaaataatg ttaacctag 60
gtgaagtcac tataatctgt agtctattat ttgggcattt gctacatgat gaggctgcc 120
agattgtggc aggtaaagag acaatgtaat ttgcactccc tatgatattt ctacattttt 180
agcgaccact agtggaagac attccccaaa attagaaaaa aaggagatag aagatttctg 240
tctatgtaaa gttctcaaaa tttgttctaa attaataaaa ctatctttgc gttcttttct 300
gcaacagatg attccaacat ggggtgttgt ctattcttct ttactcttga aacattagac 360
catgggaggc tcttacagcc ttgagttgat atttatacaa cccaaatcta ggcttgaacg 420
gtgaggtgtc aggtcatcaa atattcatgt ctatatagtc ttacacaggt tctcaaaaaa 480
aatgttcatg ggataggtca ttgataatgg attccttatt ctgagaactc cagacgactg 540
aaatatatga gagaaggaaa aggacatagt aggagcag 579

<210> 341
<211> 585
<212> DNA
<213> Homo sapiens

<400> 341
ccagtacacc catgaatttg atggagatga gcagttctac gtggacctgg ggaggaagga 60
gactgtcttg tgtttgccctg ttctcagaca atttagattt gacccgcaat ttgcactgac 120
aaacatcgct gtcctaaaac ataacttgaa cagtctgatt aaacgctcca actctaccgc 180
tgctaccaat gaggttcctg aggtcacagt gttttccaag tctcccgtga cactgggtca 240
gccaacatc ctcatctgtc ttgtggacaa catctttcct cctgtgggtca acatcacatg 300
gctgagcaat gggcactcag tcacagaagg tgtttctgag accagcttcc tctccaagag 360
tgatcattcc ttcttcaaga tcagttacct caccctcctc ccttctgctg aggaagagta 420
tgactgcaag gtggagcact ggggactgga caagcctctt ctgaaacact gggagcctga 480
gattccagcc cctatgtcag agctcacaga gactgtggtc tgcgccctgg gggtgtctgt 540
gggcctcgtg ggcattgtgg tgggcactgt cttcatcatc cgagg 585

<210> 342
<211> 295
<212> DNA
<213> Homo sapiens

<400> 342
aaaaagtctc taatattaaa gtcagaatat taatacaatt aatattaata ttaactacag 60
aaaagacaaa cagtagagaa cagcaaaaaa ataaaaagga tctccttttt tcccagccca 120
aattctcctc tctaaaagtg tccacaagaa ggggtgttta ttcttccaac acatttcact 180
tttctgtaaa tatacataaa cttaaaaaga aaacctcatg gagtcatctt gcacacactt 240
tcattgcagt ctctttgtag ctaacagtga agatttacct cgttctgctc agagg 295

<210> 343
<211> 534
<212> DNA
<213> Homo sapiens

<400> 343
aaatgtttca tttgcagagt tttatatcca ttaagtgcct ttgaaagttt ccagttgtgt 60
gggctgctgt ctcacctccc accaatttct cctttctcca tatggtgcta aaacctcaaa 120
gctgaggagg gctgcaggac ccttagcaga ttcaagtgtg cacccttgct ctgtgttcac 180
gccagggcct cctaaatgaa agacatcggt tacctgctta tgggaagggt agcagcaaaag 240
gaattgaagt tcgggacagg gtagaattat gggttttcat tgtgtttcat gccaaaccca 300
caaaatccaa aatagaattc aagttaaaca aacttctact acaaaatgga aggggaaaaa 360
ggctcaggaa ggtctatgag aatgagctga cttatctcgt taaatcttaa gataaatgag 420
ggtaacccaa ggctgcacct tgggttacca ccctgagtggt agttgagggt acttcatttg 480
attgcttcag gcgaactata taggtcaagt ccagattata aaaaaattat ctgc 534

<210> 344
<211> 464
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(464)
<223> n = A,T,C or G

<400> 344
caggcagagg ctctgggtca gtgcaggaag cagagtcaca gccagcgctt tgggggtggg 60
atgaaaggag atgacctggg ggctgctgta cagccactgt aggactctga tctcaggggg 120
acaggctgac acaggcagtt ggggaattctg ggcagggaca agcaggcggt acagaaaagt 180
gataaccaat cccagttaaa atagtctcag gagtgcagtc aggagccctt tctgactcct 240
gtgatggata ataaggccca ncccgaggaa gatgagcccc agcacgaagc ctccaatgcc 300
actcagcatc ttgctctggg cagattcaga ctgagcccc cactccacgg tgatgggggt 360
ctggaggctg ggggtgctcca cgtggcaggt gtagacgtct ccatgctggg gagtcatctt 420

cagcatcacc aggatctgga aggnccagtc accgnttcct aata 464

<210> 345

<211> 437

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(437)

<223> n = A,T,C or G

<400> 345

cctccgtggc agcagaagat cttttcgtcc actatggccg cgatgggcag gcagttgaag 60
cagtcagtga aggttttcca cagtttgatg ttgtagcgtc tcttgcactc atcgtagaaa 120
ccatagatgc ggttgatgct ggcacactcg tggttccac ggagcaggaa gaagttctcg 180
gggtacttga tcttataggc cagcagcagg cagatggtct ccaaggactg cttgcccctg 240
tccacatagt cccccagaaa gaggtagttg ctctcgggag ggaaccgcc atactcaaat 300
agtcgcagaa ggtcgtagta ctggccgtgt atgtcaccgc agatcttgag ggggtgcctcc 360
agctccanaa gaatgggctg gctcagaaaa atctcccggg atttcaggca cagaccgcgg 420
atctcgttct ctgtcag 437

<210> 346

<211> 562

<212> DNA

<213> Homo sapiens

<400> 346

ctgttgactc agattcggca ttttaattac attgtttcca agtatgatat tctgagagtg 60
tctatagcac ttagtgtctg cttcatataa actaccagtt attatatatt tatgatgcaa 120
gtagtgttcc aaatgtgggtg aaagtctgag tctttttatc cccatgggta aaatctgaat 180
ctggctctct gtgtctctca gtgcttgttt attgctggtc agagagtaaa ttcttgataa 240
aagctgttga cttggctctc acagtttatg cagacattgg agagacaatt tggttatttc 300
aaacatcaca ggatttgagt aagaagacct ggttatgaaa caaggctctc ataattacta 360
gttatgactg ttgacaagtt accttttctt gtttacaagt tatttggcct ctttgaatta 420
cttgtaaaaat agagataggg attctttctt gatcatgaaa catcaaatga agttatttga 480
tgaaatactt tgtcatctgg aaattataaa tataactaaa tgttaattat tatttgaat 540
ttgggcacct catggtggca tt 562

<210> 347

<211> 332

<212> DNA

<213> Homo sapiens

<400> 347

aaatattgta caggggaataa tcgagcatgc aaaattgaaa accccatgta aagacagcat 60
gataagctca ctggaaatth ttttaattaaa taagcttaaa aagacattgg actaaatgct 120
aatatatgga atataagatt tcccaatggt aatttagtta acaacttttt ttagtagtagca 180
tacacacaca taccaccttt atgtactatc tctagaagta aaatagtaaa ctatataaga 240
tagatatata tgagtagaac aaggaggaca tcttgaggtc atttcagaaa tgtacatgat 300
tttattgagt ctgcacacag tttatgattt tt 332

<210> 348

<211> 126

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(126)

<223> n = A,T,C or G

<400> 348


```
ggntgttgac tcanattcgg cattttaatt acattgtttc caagtatgat attctgagag 60
tgtctatagc acttagtgtc tgcttcatat aaactaccag ttattatata tttatgatgc 120
aagtag 126
```

<210> 349
<211> 294
<212> DNA
<213> Homo sapiens

```
<400> 349
ccacaaagcc attgtatgta gctttagctc agcgcaaaga agagcgccag gctcacctca 60
ctaaccagta tatgcagaga atggcaagtg tacgagctgt tccaaccct gtaatcaacc 120
cctaccagcc agcacctcct tcaggttact tcatggcagc tatcccacag actcagaacc 180
gtgctgcata ctatcctcct agccaaattg ctcaactaag accaagtcct cgctggactg 240
ctcagggtgc cagacctcat ccattccaaa atatgcccg tgctaaccgc ccag 294
```

<210> 350
<211> 237
<212> DNA
<213> Homo sapiens

```
<400> 350
ccagtattcc tggaggatat aacactgaca tcagcagggt tttcaatggc aacaattgca 60
cgagctgccg gcagaagctt ctcccaggtc ctcttgagat ttatgatata gatgccatca 120
cttttccttt tatagatgta ctgttccatc tggaagtcaa gattggtgcc acctaagtgg 180
gttcctgctg caaggaactt aaggacatcc tcctccttca ttgcaggac atcaagg 237
```

<210> 351
<211> 428
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(428)
<223> n = A,T,C or G

```
<400> 351
gtacaagctt tttttttttt tttttttttt ttttttttcc accaaagtgt atttntntga 60
aacaatcacc agttgctgtc ctntntggca cactganagc cccaggaggg tctttaactc 120
cnttcctcan attatattca tccccaaaat ntancctngg acaatanttt ggttacagca 180
tantcccagn aatgaggtcc cccaaatngc taagttttac ataggggana ctgggaaatt 240
caanaatng gatgganaaa ccataggatc caanataatg tcaggggggt naaaatnttg 300
ganaggcatg gtaccatcat tgagttngaa tctccttctc acttggagng gaagttgtag 360
gattctgcct ctaggaaatg ngccntccnt ntgaataatt ggncccagna anaggagngt 420
aactagag 428
```

<210> 352
<211> 563
<212> DNA
<213> Homo sapiens

```
<400> 352
aaaaaaaaact acatctcttt attgcagaat ttatacttgt ttgaaaaata caaatgtag 60
cgttgataag attgaagcat gttgaaaggt aagtacaggg aaaggtcctt tcagaatgac 120
tgcaacagtg cagcaaggat tcccattccc cgcctaaagg acaatacctt tttaatagaa 180
ataaatgagt tagttagtta gatttttatt acagattgaa ttaaacagtt agttacaaag 240
acattctctg atacattcat tcatagaggt cttaacgtat aaatacatag taaatatacct 300
ataaaatggg aggcaatctc atcgtgcatt atctttttgt gctcagactt gacttcacat 360
tcagtctcta catacagctt gattagaatc ataaaaacaa tatgaagacg attgcataaa 420
gggtagtatt gacaaagcat attcagatat tgtaacattt atgggtgggta aaaaatgtatc 480
ttttgaaaca atatattaga ctccattttt agctgaaatg aaatttactg attcaatctt 540
ttaagaatt tgtggatgtt tac 563
```

<210> 353
<211> 524
<212> DNA
<213> Homo sapiens

<400> 353
gctctggccc ctggtcctgt cctgttctcc agcatggtgt gtctgaggct ccctggaggc 60
tcctgcatgg cagttctgac agtgacactg atggtgctga gctccccact ggctttggct 120
ggggacacca gaccacgttt cttggagtac tctacgtctg agtgctattt cttcaatggg 180
acggagcggg tgcggttcct ggacagatac ttctataacc aagaggagta cgtgcgcttc 240
gacagcgacg tgggggagtt ccggggcggg acggagctgg ggccggcctga tgaggagtac 300
tggaacagcc agaaggactt cctggaagac aggcggggccg cgggtggacac ctactgcaga 360
cacaactacg gggttgtgga gagcttcaca gtgcagcggc gagtccatcc taaggtgact 420
gtgtatcctt caaagaccca gcccctgcag caccacaacc tcctggtctg ttctgtgagt 480
ggtttctatc caggcagcat tgaagtcagg tggttccgga atgg 524

<210> 354
<211> 340
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(340)
<223> n = A,T,C or G

<400> 354
ctgaagcaga ggaacacgct gaaggatggt atcatcatga tccanacgct gctgatcatc 60
ctnntcntca tcgtgcctat cttcctgctg ctggacaagg atgacagcaa ggctggcatg 120
gaggaagatc acacctacga gggcctggac attgaccaga cagccaccta tgaggacata 180
gtgacgctgc ggacagggga agtgaagtgg tctgtaggtg agcaccagg ccaggagtga 240
gagccaggtc gcccctatgc ctgggtgcag gctccctggc ctcagtgact gcttcggagc 300
tgcctggctc atggcccaac ccctttcccg gacccccag 340

<210> 355
<211> 556
<212> DNA
<213> Homo sapiens

<400> 355
cagagctcaa gtctgaactc tacctccaga cagaatgaag ttcatctcga catctctgct 60
tctcatgctg ctggtcagca gcctctctcc agtccaagggt gttctggagg tctattacac 120
aagcttgagg tgtagatgtg tccaagagag ctcagtcttt atccctagac gcttcattga 180
tcgaattcaa atcttgcccc gtgggaatgg ttgtccaaga aaagaaatca tagtctggaa 240
gaagaacaag tcaattgtgt gtgtggaccc tcaagctgaa tgatacaaa gaatgatgga 300
agtattgaga aaaagaagtt cttcaactct accagttcca gtgtttaaga gaaagattcc 360
ctgatgctga tatttccact aagaacacct gcattcttcc cttatccctg ctctggattt 420
tagttttgtg cttagttaaa tcttttccag gaaaaagaac ttccccatac aaataagcat 480
gagactatgt aaaaataacc ttgcagaagc tgatggggca aactcaagct tcttactca 540
caacacccta tataca 556

<210> 356
<211> 561
<212> DNA
<213> Homo sapiens

<400> 356
ccaagagggt gactcagagc cttccttgag ctaaactcgg ccaaccaagg cacgcagcat 60
gtccccctcag gtctccagtc agtccagggt gaccctcagt tctggacgtg tgtatatagc 120
tgtatttaat acctcaagggt cattgtggct ctggggatgc cggggcagga ggacgagggt 180
gcgctgtgga cacagcagtc cgcggaattc cgttctggga agccaatggt cgccggcacc 240
ccttgcttcc tccctctgtt gtctgcctgt gtgacacaca tcaatggcaa taacttcttc 300

```

caactcctcg cagaagtggg agaggccggc agcctgcacc gagaggggct ttcctctctc 360
ttgctccccg cttcgttctg ttttggtctg agagagtggg tcatccatac tctcattccc 420
tcgcctcccc ttgtggacgg gggctcttgc ttttcaattc ctgtgttttg gtgtcttccc 480
ttatctgcta ccctgaatca cctgccctgg tcttgcctgt tgatgggaac atgcttgtaa 540
actgcgtaac aaatctactt t                                     561

```

<210> 357

<211> 353

<212> DNA

<213> Homo sapiens

<400> 357

```

cgcagccatg gctcgtgggc ccaagaagca tctgaagcgg gtggcagctc caaagcattg 60
gatgctggat aaattgaccg gtgtgtttgc tcctcgtcca tccaccggtc cccacaagtt 120
gagagagtgt ctccccctca tcattttcct gaggaacaga cttaagtatg ccctgacagg 180
agatgaagta aagaagattt gcatgcagcg gttcattaaa atcgatggca aggtccgaac 240
tgatataacc tacctgtctg gattcatgga tgcctcagc attgacaaga cgggagagaa 300
tttcgctctg atctatgaca ccaagggtcg ctttgcgtga catcgtatta cac          353

```

<210> 358

<211> 202

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(202)

<223> n = A,T,C or G

<400> 358

```

ctgaagcaga ggaacacgct gaaggatggt atcatcatga tccanacgct gctgatcatc 60
ctattcatca tcgtgcctat cttcctgctg ctggacaagg atgacagcaa ggctggcatg 120
gaggaagatc acncctacga gggcctggac attgaccaga cagccaccta tgaggacata 180
gtgacgctgc ggacagggga ag                                     202

```

<210> 359

<211> 463

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(463)

<223> n = A,T,C or G

<400> 359

```

ctcctntgta tgactgcaag tcctccaaga tgccttctgc atntntnaat actacattca 60
cctgattata aatttccttc tcagactctg taggctgggc attttcanan tcaaggaaaa 120
aatttgccc ctgctcaagg tctgtgcatg tcaaaacttt aagaagattc cccatgttaa 180
ggtaccttca gccagtgtg gtgattctgt cctgttcctt ctatccttgg attggcggtc 240
cctctttcct agttcacttg ttccagtcct tcaacttctg tttcttgcta acaggtgtgc 300
aaatgaatta ccaactgggt aaccttgaat gagttaatca aattccaggc catcgtccac 360
gccaccaaca gtcaaaggcc aaggaagctg ttggctgaaa aggtggtcta tgttggcgtn 420
tggatccctg ccctcctgct gactattncc gacttcatct ttg          463

```

<210> 360

<211> 588

<212> DNA

<213> Homo sapiens

<400> 360

```

aaacattagt gtcatagct tccaagagac atgctgactt tcatttcttg aggtactctg 60
cacatacgca ccacatctct atctggcctt tgcattggagt gaccatagct ccttctctct 120

```

```

tacattgaat gtagagaatg tagccattgt agcagcttgt gttgtcacgc ttcttctttt 180
gagcaacttt cttacactga agaaaggcag aatgagtgct tcagaatgtg atttcctact 240
aacctgttcc ttggataggc ttttttagtat agtatattttt ttgtcatttt ctccatcaac 300
aaccagggag actgcacctg atggaaaaga tatatgactg cttcatgaca ttcctaaact 360
atcttttttt tattccacat ctacgttttt ggtggagtcc cttttgcac attgttttaa 420
ggatgataaa aaaaaataac aactagggac aatacagaac ccattccatt tatctttcta 480
cagggctgac attgtggcac attcttagag ttaccacacc ccatgagggg agctctaaat 540
agccaacacc catctgtttt ttgtaaaaac agcatagctt atacatgg 588

```

<210> 361

<211> 396

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(396)

<223> n = A,T,C or G

<400> 361

```

ctgttgactc agattcggca ttttaattac attgtttcca agtatgatat tctgagagtg 60
tctatagcac ttagtgtctg cttcatataa actaccagtt attatatatt tatgatgcaa 120
gtagttttcc aaatgtggtg aaagtctgag tctttttatc cccatgggta aaatctgaat 180
ctggctctct gtgtctctca gtgcttggtt attgctggtc agagagttaa ttcttgataa 240
aagctgtntg anttggctct cacagtttat gcagacattg gagagacaat ttggttatgt 300
caaacatcac aggatttgag taagaagacc tggttatgaa acaaggctct cataataact 360
agttatgact gttgacaagg ttaccttttc ttgttt 396

```

<210> 362

<211> 253

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(253)

<223> n = A,T,C or G

<400> 362

```

gaaggatggt atcatcatga tccagacgct gctgatcatc ctcttcatca tcgtgcctat 60
cttctgctg ctggacaagg atgacagcaa ggctggcatg gaggaagatc acacctacga 120
gggcctggac attgaccaga cagccaccta tgaggacata gtgacgctgc ggacagggga 180
agtgaagtgg ttctgtaggt gangcacca gccaggagt gagagccagg tcgccccatg 240
acctgggtgc agg 253

```

<210> 363

<211> 571

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(571)

<223> n = A,T,C or G

<400> 363

```

ccttgcctca gatccaaggt cactcggaag aggccatgtc taccctcaat gacactcatg 60
gaggaatgct tgagagaagc attcagatgc atgacacaag gtaagactgc caaaaatctt 120
gttcttgctc tcctcatttt gttatttggt ttatttttag gatttttgag agcaaaatga 180
caacacccag aaattcagta aatgggactt tcccggcaga gccaatgaaa ggccctattg 240
ctatgcaatc tggtcacaaa ccactcttca ggaggatgtc ttcactggtg ggccccgcgc 300
aaagcttctt catgagggaa tctaagactt tgggggctgt ccagattatg aatgggctct 360
tccacattgc cctggggggt cttctgatga ttccagcagg gatctatgca cccatctgtg 420

```

tgactgtgtg gtaccctctc tggggaggca ttatgtatat tatttccgga tcaactcctgg 480
cagcaacgga gaaaaactcc aggaagtgtt gggtaaagg aaaaatgata atgaattcat 540
tgancctntt tgctgccatt tctggaatga t 571

<210> 364
<211> 420
<212> DNA
<213> Homo sapiens

<400> 364
ctgtagcctc tgcaagtga aatccaggcc gacttgcaat cattggactg atgtccaagt 60
gcaatcacca tacagcagct acaggcagg ctggctgata gggagtatgg gagaaggaca 120
cgctcagatg aaaaactgca tgcaacgatt ttcaccactg aacacactgt tttctgtgat 180
agaaactgtc ggccctgctg ggggacaaga tattcacggc ctcactagcc agtgagatgc 240
caccagggcg gcctgcccc t gatgctcctt tgttacctgc taaagaagga ccataaggta 300
aaaggcacct taccttatgg agtgagccca gaccccaggg aaaagcttgg gtagaacaat 360
ccaaggggca gcctgggtgt gagaatccag cccaagctag ctgctctaga agcctggagg 420

<210> 365
<211> 374
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(374)
<223> n = A,T,C or G

<400> 365
agccacttgt ttctcatttg gtcgaaacag cctgcccaca gggatcacca ctggctcata 60
tagcttctgc ttccagacac actccatcgc cttgtcgatt ttggaatgtc tgggctcaga 120
cttcattgctc gtgggtgtaa tacgatgtac agcaaagcga cccttggtgt catagatcag 180
acggaaattc tctcccgtct tgncaatgct gatgacatcc atgaatccag cagnggtagg 240
tnatattcagt tcggaccttg ccactnattt taatgaaccg ctgcatgcaa atcttcttta 300
cttcactcnc tgnccaggca tacttaagtc tgttcctcag gaaaatgatg agggggagac 360
actctctnna ctgt 374

<210> 366
<211> 431
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(431)
<223> n = A,T,C or G

<400> 366
tcaagtctga actctacctc cagacagaat gaagttcatc tcgacatctc tgcttctcat 60
gctgctggtc agcagcctct ctccagtcca aggtgttctg gaggtctatt acacaagctt 120
gaggtgtaga tgtgtccaan agagctcagt ctttatccct anacgcttca ttgatcgaat 180
tcaaatcttg ccccgtggga atggttgtcc aagaaaagaa atcatagtct ggaagaagaa 240
caagtcaatt gtgtgtgtgg accctcaagc tgaatggata caaagaatga tggaagtatt 300
gagaaaaaga agttcttcaa ctctaccagt tcagtggtt aagagaaaga ttccctgatg 360
ctgatatttc cactaagaac acctgcattc ttcccttacc cctgctctgg atttttagttt 420
tgngcttagt t 431

<210> 367
<211> 286
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (1)...(286)
<223> n = A,T,C or G

<400> 367
ctgtctcaca ctttacaagc tgtgagagac acatcagagc cctgggcact gtcactgctt 60
gcagccctgag tgtaactccc tccttttcta tctgagctct tcctcctcca catcacggca 120
gcgaccacag ctccagtgat cacagctcca aggagaacca ggccagcaat gatccccacg 180
atggggatgg tgggctggga agacagctcc catctcangg tgaggggctt gggcagaccc 240
tcattgctga catggcaggt gtatctctgc tcctctccag aaggca 286

<210> 368
<211> 536
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(536)
<223> n = A,T,C or G

<400> 368
ctcaagcttg aactctacct ccagacagaa tgaagttcat ctgcacatct ctgcttctca 60
tgctgctggt cagcagcctc tcctcagtc aaggtgttct ggaggtctat tacacaagct 120
tgaggtgtag atgtgtccaa gagagctcag tccttatccc tagacgcttc attgatcgaa 180
ttcaaatctt gccccgtggg aatggtgtgc caagaaaaga aatcatagtc tggaagaaga 240
acaagtcaat tgtgtgtgtg gacctcaag ctgaatggat acaaagaatg atggaagtat 300
tgagaaaaag aagttcttca actctaccag ttccagtggt taagagaaag attccctgat 360
gctgatattt cactaagaa cacctgcatt cttcccttat ccctgctctg gattttagtt 420
ttgngcttag ttaaatcttt tcacagaaaa agaacttccc catacaaata agcatgagac 480
tatgtaaaaa taaccttgca gaagctgatg gggcaaacct aagcttnttc actcac 536

<210> 369
<211> 565
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(565)
<223> n = A,T,C or G

<400> 369
ctcagagctc aagtctgaac tctacctcca gacagaatga agttcatctc gacatctctg 60
cttctcatgc tgctgggtcag cagcctctct ccagtcacaag gtgttctgga ggtctattac 120
acaagcttga ggtgtagatg tgtccaagag agctcagctt ttatccctag acgcttcatt 180
gatcgaaattc aaatcttgcc ccgtgggaat ggttggtccaa gaaaagaaat catagtctgg 240
aagaagaaca agtcaattgt gtgtgtggac cctcaagctg aatggatata aagaatgatg 300
gaagtattga gaaaagaag ttcttcaact ctaccagttc cagtgtttta gagaaagatt 360
ccctgatgct gatatttcca ctaagaacac ctgcattctt cccttatccc tgctctggat 420
tttagttttg tgcttagtta aatcttttcc aggaaaaaga acttcccat acaataaagc 480
atgagactat gtaaaaaata ccttgcnгаа gctgatggng caaactcaag cttcttcact 540
cacagcacc tatatacact tggag 565

<210> 370
<211> 402
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(402)
<223> n = A,T,C or G

<400> 370
ctgttgactc anattcggca ttttaattac attgtttcca agtatgat tctgagagt 60
tctatagcac ttagtgtctg cttcatataa actaccagtt attatatatt tatgatgcaa 120
gtanttttcc aaatgtggng aaagtctgag tctttttatc cccatgggta aaatctgaat 180
ctggctctct gtgtctctca gtgcttgttt attgctggtc agagagtaaa ttcttgataa 240
aanctgttga cttggctctc acagtttatg cagacattgg agagacaatt tggttatttc 300
aaacatcaca ggatttgagt aagaagacct ggttatgaaa caaggctctc ataattacta 360
gttatgactg ttgacaagnt accttttctt gtttacaant ta 402

<210> 371
<211> 346
<212> DNA
<213> Homo sapiens

<400> 371
ctgcccact tttcaattca gatatactag taccttacct agaaataatg ttaacctagg 60
gtgaagtcac tataatctgt agtctattat ttgggcatth gctacatgat gagtgtgtcc 120
agatttgtgc aggtaaagag acaatgtaat ttgcaactccc tatgatattt ctacattttt 180
agcgaccact agtgggaagac attcccccata attagaaaaa aaggagatag aagatttctg 240
tctatgtaaa gttctcaaaa tttgttctaa attaataaaa ctatcttggg gttcttttct 300
gcaacagatg attcaaaaaa aaaaaaaaaa aaaaaaaaaa agcttg 346

<210> 372
<211> 348
<212> DNA
<213> Homo sapiens

<400> 372
cctacgacga ggaccggctt ttcttcttcg acttttccca gaacactcgg gtgccttgcc 60
tgcccgaatt tgctgactgg gctcaggaac agggagatgc tcctgccatt ttatttgaca 120
aagagttctg cgagtggatg atccagcaaa tagggccaaa acttgatggg aaaatcccg 180
tgtccagagg gtttctctatc gctgaagtgt tcacgctgaa gcccctggag tttggcaagc 240
ccaacacttt ggtctgtttt gtcagtaatc tcttcccacc catgctgaca gtgaactggc 300
agcatcattc cgtccctgtg gaaggatttg ggcctacttt tgtctcag 348

<210> 373
<211> 598
<212> DNA
<213> Homo sapiens

<400> 373
ccatctgatc tataaatgag gtggcatcga caaaagaacc attgaaaaat ttgggaagga 60
ggctgtctgag atgggaaagg gctccttcaa gtatgcctgg gtcttgataa aactgaaagc 120
tgagcgtgaa cgtggtatca ccattgatat ctccctgttg aaatttgaga ccagcaagta 180
ctatgtgact atcattgatg ccccaggaca cagagacttt atcaaaaaca tgattacagg 240
gacatctcag gctgactgtg ctgtcctgat tgttgcctgt ggtgttggtg aatttgaagc 300
tggtatctcc aagaatgggc agacccgaga gcatgccctt ctggcttaca cactgggtgt 360
gaaacaacta attgtcgggt ttaacaaaat ggattccact gagccaccct acagccagaa 420
gagatatgag gaaattgtta aggaagtcag cacttacatt aagaaaattg gctacaacct 480
cgacacagta gcatttgtgc caatttctgg ttggaatggt gacaacatgc tggagccaag 540
tgctaactg ccttgggtca agggatggaa agtcaccctg aaggatggca atgccagt 598

<210> 374
<211> 381
<212> DNA
<213> Homo sapiens

<400> 374
cctgacacaa tatccctgtt cactttgaag tgaattttga ctctatattc agaaccottcc 60
tttaacacaa tggtttcctt tttgagggtc tccagatctc cagtaagggtc catgggtgatt 120
gggtccgggg cactctcaca aaccagggtg agcgggtgta caacgacatt gggggctttc 180
ggatctgtca ccacaggacc atctcccagc agcgttttct tgtacttaat tagactctca 240

```
tcattctttgt ccatttcctg cagctctttc agggacttct gtgggtggagg cttataattg 300
agcttgctgt ccagctcatc atcgtcatcc tcctccacat gtggctctgg ggctttttca 360
gtcattctga tctatttatt c 381
```

```
<210> 375
<211> 573
<212> DNA
<213> Homo sapiens
```

```
<400> 375
ccaaaagaag taagacagct tgctgaagat ttcttgaag actatattca tataaacatt 60
ggtgcacttg aactgagtgc aaaccacaac attcttcaga ttgtggatgt gtgtcatgac 120
gtagaaaaag atgaaaaact tattcgtcta atggaagaga tcatgagtga gaaggagaat 180
aaaaccattg tttttgtgga aaccaaaaga agatgtgatg agcttaccag aaaaatgagg 240
agagatgggt ggccctgccat gggatatccat ggtgacaaga gtcaacaaga gcgtgactgg 300
gttctaaatg aattcaaaca tggaaaagct cctattctga ttgctacaga tgtggcctcc 360
agagggctag atgtggaaga tgtgaaattt gtcatacaatt atgactaccc taactcctca 420
gaggattata ttcatcgaat tggaagaact gctcgagta ccaaaacagg cacagcatatc 480
actttcttta cacctaataa cataaagcaa gtgagcgacc ttatctctgt gcttcgtgaa 540
gctaatacaag caattaatcc caagttgctt cag 573
```

```
<210> 376
<211> 612
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(612)
<223> n = A,T,C or G
```

```
<400> 376
ctgttgactc agattcggca ttttaattac attgtttcca agtatgatat tctgagagtg 60
tctatagcac ttagtgtctg ctccatataa actaccagtt attatatatt tatgatgcaa 120
gtagttttcc aaatgtggtg aaagtctgag tctttttatc cccatgggta aaatctgaat 180
ctggctctct gtgtctctca gtgcttgttt attgctggtc agagagtaaa ttcttgataa 240
aagctgttga cttggctctc acagtttatg cagacattgg agagacaatt tggttatttc 300
aaacatcaca ggatttgagt aagaagacct ggttatgaaa caaggctctc ataattacta 360
gttatgactg ttgacaagtt acccttttctt gtttacaagt tatttggcct ctttgaatta 420
cttgtaaaat agagataggg attcttttctt gatcatggaa catcaaatga agttatttga 480
tgaaataact tgatcatctg aaattataaa tataactaaa tgttaattat tatttggaaa 540
tttngggcac ctcatggngg cattttctat ggtcattttt tttcttttct cgcataatgg 600
ctaaaagtag gt 612
```

```
<210> 377
<211> 288
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(288)
<223> n = A,T,C or G
```

```
<400> 377
agccattgnn tgtagcttta gctcagcgca aagaagagcg ccaggctcac ctactaacc 60
agtatatgca gagaatggca agtgtacgag ctgttcccaa ccctgtaatc aaccctacc 120
agccagcacc tccttcaggt tacttcatgg cagctatccc acagactcag aaccngctg 180
catactatcc tcctagccaa attgtccaac taagaccaag tcctcgctgg actgctcagg 240
gtgccagacc tcatccattc caaaatatgc ccggtgctat ccgcccag 288
```

```
<210> 378
<211> 584
```


<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(584)
<223> n = A,T,C or G

<400> 378
aaacattagt gttcatagct tccaagagac atgctgactt tcatttcttg aggtactctg 60
cacatacgca ccacatctct atctggcctt tgcatggagt gaccatagct ccttctctct 120
tacattgaat gtagagaatg tagccattgt agcagcttgt gttgtcacgc ttcttctttt 180
gagcaacttt cttacactga agaaaggcag aatgagtgtc tcagaatgtg atttctact 240
aacctgttcc ttggataggc tttttagtat agtatTTTTT ttgtcattt tctccatcaa 300
caaccaggga gactgcacct gatggaaaag atatatgact gcttcatgac attcctaaac 360
tacctttttt tattccacat ctacgttttt ggtggagtcc cttttgcac attgttttaa 420
ggatgataaa aaaaaataac aactagggac aatacagaac ccattccatt tatctttcta 480
cagggctgac attgtggcac attcttagag ttaccacacc ccatgaggga agctctaaat 540
agccaacacc catctgtttt ttgtaaaaac agcatanctt atac 584

<210> 379
<211> 457
<212> DNA
<213> Homo sapiens

<400> 379
ccacggctgc ttccagctcc tccctggaga agagctaega gctgcctgac ggccagggtca 60
tcaccattgg caatgagcgg ttccgctgcc ctgaggcact cttccagcct tccttctctg 120
gcatggagtc ctgtggcatc cacgaaacta ccttcaactc catcatgaag tgtgacgtgg 180
acatcgcaaa agacctgtac gccaacacag tgctgtctgg cggcaccac atgtaccctg 240
gcattgccga caggatgcaa aaggagatca ctgccctggc acccagcaca atgaagatca 300
agatcattgc tcctcctgag cgcaagtact ccgtgtggat cggcggctcc atcctggcct 360
cgctgtccac cttccagcag atgtggatca gcaagcagga gtatgacgag tccggccctc 420
ccatcgtcca ccgcaaatgc ttctaggcgg actatga 457

<210> 380
<211> 574
<212> DNA
<213> Homo sapiens

<400> 380
ctgctgtaac caggtttccc cttgtgggaa gtgttgtttc ttgctgggca gttgggaagg 60
gaatggagaa cagagaagag agtggaaatc acatgctcac ttgaactttc ctggggaacg 120
tctcctcaca gcgtacacaa gagcctccct ttagaaatgg agtgttcatt ttatcatggg 180
aaaagaatct gagtgggaca tgattcagaa caggaccggc ccaaggaaat gcaggggctg 240
tggagtggga tggagacaag ctctgaaagg acacatggga gatctagatg tagaaggtag 300
acaagtagta ggataactca caggatggat ccactggagg ttaagacatg tggtaagaca 360
gtgtaatagg aagctgctca gttggagaaa gtaagggaagc aaacattgtt accgtggggg 420
caatggagag gacagtggag agccctttat cctgataagg gtggctttga ggtaaaggaa 480
ggaaagagga tgccttgaga gggccactg tattagagag gacctggaag ccaggatgct 540
aattctgggg agatggattc cccaggctta ctct 574

<210> 381
<211> 571
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(571)
<223> n = A,T,C or G

<400> 381

```
cagagctcaa gtctgaactc tacctccaga cagaatgaag ttcattctga catctctgct 60
tctcatgctg ctggtcagca gcctctctcc agtccaaggt gttctggagg tctattacac 120
aagcttgagg ttagatgtg tccaagagag ctccagtctt atccctagac gcttcattga 180
tcgaattcaa atcttgcccc gtgggaatgg ttgtccaaga aaagaaatca tagtctggaa 240
gaagaacaag tcaattgtgt gtgtggaccc tcaagctgaa tggatacaaa gaatgatgga 300
agtattgaga aaaagaagtt cttcaactct accagttcca gtgtttaaga gaaagattcc 360
ctgatgtgta tatttccact aagaacacct gcattcttcc cttatccctg ctctggattt 420
tagttttgtg cttagttaaa tcttttccag gaaaaagaac ttccccatac aaataagcat 480
ganactatgt aaaaataacc cttgcagaag ctgatggggc aaactcaagc ttcttcactc 540
acagcaccct atatacactt ggagtttgca t 571
```

```
<210> 382
<211> 471
<212> DNA
<213> Homo sapiens
```

```
<400> 382
ccaccaccaa tttcttcgag gatattcagt gtataccttc tcattagctg ccaaatcaag 60
gccagtgtga gagtgcggtt tccttcattg agatcttgtc caccgatgcc aaccagggag 120
aacttcgctt gattcttccc caattctacc gcgtagttag aattctcaag cttcttcata 180
ttgcctccca gtttggggta tggcggtttg tttactctgt tccagtcaac aggaactttg 240
atcttttcat agagctggaa gatgaccagg gcattctgata agtcactgta caaatgattg 300
actcgagggg taacacccag ggagttcctc cagttcctaa atgtccgctc ttctctcgtc 360
tcaccttcaa gagcccccca gtcaatgtcc tggttctctg gtttgtgcag ggcaggggat 420
ctgttaaaga ggttggcaat aaaagccaag ttcaacttgg ggttccctcg g 471
```

```
<210> 383
<211> 489
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(489)
<223> n = A,T,C or G
```

```
<400> 383
ctgttgactc agattcggca ttttaattac attgtttcca agtatgat tctgagagtg 60
tctatagcac ttagtgtctg cttcatataa actaccagtt attatatatt tatgatgcaa 120
gtagttttcc aaatgtgtg aaagtctgag tctttttatc cccatgggta aaatctgaat 180
ctggctctct gtgtctntca gtgcttgttt attgctggtc agagagtaaa ttcttgataa 240
aagctgttga cttggctctc acagtttatg canacattgg agagacaatt tggttatttc 300
aaacatcaca ggatnngagt aagaanacct gggtatgaaa caaggctctc ataattacta 360
gttatgactg ttgacaagtt accttntctt gnttacaagt tatttggcct ctttgaatta 420
cttgnaaaat agagataggg attctttctt gatcatggaa catcnaatga agttattnga 480
tgaaatact 489
```

```
<210> 384
<211> 306
<212> DNA
<213> Homo sapiens
```

```
<400> 384
ctgctgcacc cagagctcct ttgggtctgc acatagctct gcctgagagc gcttgccggg 60
caagaacagg atagctggga tggagcagcc caagcttggg tcctgcttcc ggtagctgcy 120
gacaaccttg gcgggaatct tcctttgggt gtacttgagg caacagtcct gagccccctc 180
atcactgcct tgggtcctgg ggaatgcaaa ggccagaacc aggataagga ggctcagagc 240
cagtgaactg gccatgtctg tggtagaggg tgagtaagag gccagagctg agggtagggt 300
gggcag 306
```

```
<210> 385
<211> 560
<212> DNA
```

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(560)

<223> n = A,T,C or G

<400> 385

```
ctcagagctc aagtctgaac tctacctcca gacagaatga agttcatctc gacatctctg 60
cttctcatgc tgctggtcag cagcctctct ccagtccaag gtgttctgga ggtctattac 120
acaagcttga ggtgtagatg tgtccaagag agctcagctc ttatccctag acgcttcatt 180
gatcgaattc aaatcttgcc ccgtgggaat ggtgttccaa gaaaagaaat catagtctgg 240
aagaagaaca agtcaattgt gtgtgtggac cctcaagctg aatggataca aagaatgatg 300
gaagtattga gaaaaagaag ttcttcaact ctaccagttc cagtgtttaa gagaagatt 360
ccctgatgct gatatttcca ctaagaacac ctgcattctt cccttatccc tgctctggat 420
tttagttttg tgcttagtta aatcttttcc aggaaaaaga ncttcccat acaaataaagc 480
atgagactat gtaaaaataa ccttgcagaa gctgatgggg caaactcaag cttcttccact 540
cacagcacc tatatacact 560
```

<210> 386

<211> 186

<212> DNA

<213> Homo sapiens

<400> 386

```
ctgtgccaa gtgctgaatc ccatgactcg cagctctgtg ccgcagccct ggtagacctc 60
cgagggtgtg ttgcacttct gctggcagaa gtagatgcc a ttgtcctcaa accggatgcc 120
ttggatggtg aggggtggcg gagattcgtt ctgggactct tccatgcggc ccttttccag 180
cttcag 186
```

<210> 387

<211> 439

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(439)

<223> n = A,T,C or G

<400> 387

```
cagagctcaa gtctgaactc tacctccaga cagaatgaag ttcattctga catctctgct 60
tctcatgctg ctggtcagca gcctctctcc agtccaaggt gttctggagg tctattacac 120
aagcttgagg tgtagatgtg tccaagagag ctacgtcttt atccctagac gcttcattga 180
tcgaattcaa atcttgcccc gtgggaatgg ttgtccaaga aaagaataca tagtctggaa 240
gaagaacaag tcaattgtgt gtgtggaccc tcaagctgaa tgaatacaaa gaatgatgga 300
agtattgaga aaaagaagtt cttcaactct accagttcca gtgtttaaga naaagattcc 360
ctgatgctga tatttccact aagaacacct gcattcttcc cttatccctg ctctggattt 420
tagttttgng cttagttaa 439
```

<210> 388

<211> 320

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(320)

<223> n = A,T,C or G

<400> 388

```
ccacacagac tcaccaagcc acagacttgt cttccacaag caggttctta cctcagccac 60
gaagggaacca agccacagct actaaaggtt gaactcaaa atatgtacag ggtattaaac 120
```

```
aaatnccaag gggaacagnt aacttgaata caaggtcaaa atcagcaaca agntctacaa 180
tccagtgctg atatcaata caagcttcaa ggacaatttc ttttcgaagg cttattccan 240
tttcgngagg ctagcatgag gtgtgngcat ttgccagggg caaatttcta ttctcaatta 300
acctatgcag naaatgctac                                     320
```

<210> 389
<211> 331
<212> DNA
<213> Homo sapiens

```
<400> 389
ctgccctact tttcaattca gatatactag taccttacct agaaataatg ttaacctagg 60
gtgaagtcac tataatctgt agtctattat ttgggcattt gctacatgat gagtgcctgcc 120
agattgtggc aggtaaagag acaatgtaat ttgcactccc tatgatattt ctacattttt 180
agcgaccact agtgggaagac attccccaaa attagaaaaa aaggagatag aagatttctg 240
tctatgtaaa gttctcaaaa tttgttctaa attaataaaa ctatctttgt gttcttttct 300
acaaaaaaaa aaaaaaaaaa aaaaaaaaaa g                                     331
```

<210> 390
<211> 391
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(391)
<223> n = A,T,C or G

```
<400> 390
cttttttttt tttttttttt ttttttngag ttttnattat ttgngnggct aaaaanaagg 60
gaacatggtt ggaggcccgag tgaganaaac agtgnnttga atcaaagagc anaatgatag 120
aaactgactt canagcaact tnttggcagc agtatccaat ttggaagtgg aaggtctgtc 180
ctggagccag atgctaacga aacacagcaa atgcttttcc taaggcacaa tagtcttttc 240
agnagactca ggaaccctgt ttatgcanat cctcgnngaa ctttcttgct cctcctgtgc 300
atgaagatgc ccactccaca natgatgagc cccagcacna agcccccagc tcccgtaaat 360
gtcttactcc gggcanaatc agactgngcc t                                     391
```

<210> 391
<211> 462
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(462)
<223> n = A,T,C or G

```
<400> 391
ccttgcctca natccaaggt cactcgggaag aggccatgtc taccctcaat gacactcatg 60
gaggaaatgc tganagangc attcagatgc atgacacaag gtaagactgc caaaaatctt 120
gttcttgctc tcctcatttt gttatttgtt ttatttttag gagtttngag agcaaatga 180
cnacaccag aaattcagta aatgggactt tcccggcaga accaatgaaa ggccctattg 240
ctatgcaatc tggtncaaaa ccactcttna ngaggatgtc ttactgggtg ggccccacnc 300
aaagcttctt cntgagggaa tctaanactt tgggggctgn ccagattatn aatgggctct 360
tccacattgc cctgggggggt cttntgatga tcccancngg gatctatgca cccatctgtg 420
tgactgtgtg gtnccctctc tggggaggca ttatgtatat ta                                     462
```

<210> 392
<211> 554
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (1)...(554)
<223> n = A,T,C or G

<400> 392

```
aaagcgaatt catactataa cagcagaaac aaaacttcag atttcagaat ttgttattgg 60
caaaatttat tctcattata cctgcttcac atgggtatat tactattaaa acagaatacc 120
atagagtaat tgcattatctt gaaaattctn tcattttaca atgcacttca ccaatgaaac 180
agntaatttc cattttgaaa attaaaagaa aacagcacag agaagttaaa tgcggtgtag 240
caaagttatg gggctctgctt gagggcacta acctcaacag attattcctc ctctccttag 300
aataaccatg aaaatacaaa tttacttagc acatttttgc tttttaagta gctgggtcat 360
tttctgaatt tcccacattc agagtccag tcattattgt tacatcatgt ttgcagaaac 420
cttgtcttat ttagtgtcta tttgcatata accctgaaa cattattatt tgaaaacttt 480
tctatatctc aaattaatat acattttcat aacctacctt tgnattaaga cttgcaattt 540
tatcaattcta ttat 554
```

<210> 393

<211> 555

<212> DNA

<213> Homo sapiens

<400> 393

```
ctgttgactc agattcggca ttttaattac attgtttcca agtatgatat tctgagagtg 60
tctatagcac ttagtgtctg cttcatataa actaccagtt attatatatt tatgatgcaa 120
gtagttttcc aaatgtggtg aaagtctgag tctttttatc cccatgggta aaatctgaat 180
ctggctctct gtgtctctca gtgcttggtt attgctggtc agagagtaaa ttcttgataa 240
aagctgttga cttggctccc acagtttatg cagacattgg agagacaatt tggttatttc 300
aaacatcaca ggatttgagt aagaagacct ggttatgaaa caaggctctc ataattacta 360
gttatgactg ttgacaagtt accttttctt gtttacaagt tatttggcct ctttgaatta 420
cttgtaaaat agagataggg attctttctt gatcatggaa catcaaatga agttatttga 480
tgaaatactt tgtcatctgg aaattataaa tataactaaa tgttaattat tatttgaat 540
ttgggcacct catgg 555
```

<210> 394

<211> 340

<212> DNA

<213> Homo sapiens

<400> 394

```
ctgggggggtc cgggaaaggg gttggggccat gagccaggca gctccgaagc agtcactgag 60
gccaggggagc ctgcacccag gtcatggggc gacctggctc tcaactcctg cctgggtgct 120
cacctacaga ccacttcact tcccctgtcc gcagcgctac tatgtcctca taggtggctg 180
tctgggtcaat gtccaggccc tcgtagggtg gatcttcctc catgccagcc ttgctgtcat 240
cctgtgccag cagcaggaag ataggcacga tgatgaagag gatgatcagc agcgtctgga 300
tcgatgatgat accatccttc agcgtgttcc tctgcttcag 340
```

<210> 395

<211> 482

<212> DNA

<213> Homo sapiens

<400> 395

```
aaaaaaacag aacatttaca agacaccagt tattttgtgc cccatagtgc attaaaaaag 60
tttactttac ctttattatt atttccctag gctagtcaag cagcaaacca ttaatcgggtc 120
ggagaaacct tcatgacata tgcccgaactg gctcttcgcc acccacttga aggacactac 180
ccaatcgatg gaagccttta atcgcacagc cctccctatt agcggactat tggcggatgc 240
agacatgttc tactcgagca gttaccaagg accactttac tgcgatcagg attccaacga 300
ccacctaat tctgtatctt caactctttt cgaccggacc tcttattcgg aagcgttaca 360
ggaagacagg tctcaactta gggatcagat caggttatca acgctctggg atcgctgcaa 420
cctggcactt caaggaaagt caccgataac gtctagaccg gcaaacacag atctagaggt 480
gg 482
```

<210> 396

<211> 448
<212> DNA
<213> Homo sapiens

<400> 396
gaaagaatcc ctatctctat tttacaagta attcaaagag gccaaataac ttgtaaacaa 60
gaaaaggtaa cttgtcaaca gtcataacta gtaattatga gagccttggt tcataaccag 120
gtcttcttac tcaaatcctg tgatgtttga aataaccaa ttgtctctcc aatgtctgca 180
taaaactgtga gagccaagtc aacagctttt atcaagaatt tactctctga ccagcaataa 240
acaagcactg agagacacag agagccagat tcagatttta cccatgggga taaaaagact 300
cagactttca ccacatttgg aaaactactt gcatcataaa tatataataa ctggtagttt 360
atatgaagca gacactaagt gctatagaca ctctcagaat atcatacttg gaaacaatgt 420
aattaaaatg ccgaatctga gtcaacag 448

<210> 397
<211> 573
<212> DNA
<213> Homo sapiens

<400> 397
ccaaaagaag taagacagct tgctgaagat ttcctgaaag actatattca tataaacatt 60
ggtgcacttg aactgagtg aaaccacaac attcttcaga ttgtggatgt gtgtcatgac 120
gtagaaaagg atgaaaaact tattcgtcta atggaagaga tcatgagtga gaaggagaat 180
aaaaccattg tttttgtgga aaccaaaga agatgtgatg agcttaccag aaaaatgagg 240
agagatgggt ggcctgccat gggatatccat ggtgacaaga gtcaacaaga gcgtgactgg 300
gtttctaaatg aattcaaaca tggaaaagct cctattctga ttgctacaga tgtggcctcc 360
agagggctag atgtggaaga tgtgaaattt gtcacaaatt atgactaccc taactcctca 420
gaggattata ttcacgaat tggagaact gctcgcagta ccaaacagg cacagcatac 480
actttcttta cacctaataa cataaagcaa gtgagcgacc ttatctctgt gcttcgtgaa 540
gctaatacaag caattaatcc caagtgtctt cag 573

<210> 398
<211> 340
<212> DNA
<213> Homo sapiens

<400> 398
ctgggggggtc cgggaaagggt gttgggcat gagccaggca gctccgaagc agtcactgag 60
gccagggagc ctgcaccag gtcattgggc gacctggctc tcactcctgg cctgggtgct 120
cacctacaga ccacttcact tccctgttcc gcagcgtcac tatgtcctca taggtggctg 180
tctgttcaat gtccaggccc tcttagtgtt gatcttccct catgccagcc ttgctgtcat 240
ccttggtccag cagcaggaag ataggcacga tgatgaagag gatgatcagc agcgtctgga 300
tcatgatgat accatccttc agcgtgttcc tctgcttcag 340

<210> 399
<211> 593
<212> DNA
<213> Homo sapiens

<400> 399
atctcgacat ctctgcttct catgctgctg gtcagcagcc tctctccagt ccaaggtggt 60
ctggagggtct attacacaag cttgaggtgt agatgtgtcc aagagagctc agtctttatc 120
cctagacgct tcattgatcg aattcaaact ttgccccgtg ggaatggttg tccaagaaaa 180
gaaatcatag tctggaagaa gaacaagtca attgtgtgtg tggaccctca agctgaatgg 240
atacaaagaa tgatggaagt attgagaaaa agaagttctt caactctacc agttccagt 300
tttaagagaa agattccctg atgctgatat ttccactaag aacacctgca ttcttccctt 360
atcccctgctc tggatttttag ttttgtgctt agttaaatct tttccaggaa aaagaacttc 420
cccatacaaa taagcatgag actatgtaaa aataaccttg cagaagctga tggggcaaac 480
tcaagcttct tcaacacag caccctatat acacttgag tttgcattct tattcatcgg 540
ggaggaaagt ttctttgaaa atagttattc agttataagt aatacaggat tat 593

<210> 400
<211> 504

<212> DNA

<213> Homo sapiens

<400> 400

```
aaatcctgag tcaagccaaa aaaaaaaaaa aaaacccaaa caaaacaaaa aaaacaaata 60
aagccatgcc aatctcatct tgttttctgc gcaagttagg ttttgtcaag aaaggggtga 120
acgcaactaa gtcatagtcc gcctagaagc atttgcggtg gacgatggag gggccggact 180
cgtcatactc ctgcttgctg atcacatctg ctggaagggtg gacagcgagg ccaggatgga 240
gccgccgatc cacacggagt acttgcgctc aggaggagca atgatcttga tcttcattgt 300
gctgggtgcc agggcagtga tctccttctg catcctgtcg gcaatgccag ggtacatggt 360
ggtgccgcca gacagcactg tgttggcgta caggtctttg cggatgtcca cgtcacactt 420
catgatggag ttgaaggtag tttcgtggat gccacaggac tccatgcccc ggaaggaagg 480
ctggaagagt gcctcagggc agcg
```

<210> 401

<211> 608

<212> DNA

<213> Homo sapiens

<400> 401

```
ctcagagctc aagtctgaac tctacctcca gacagaatga agttcatctc gacatctctg 60
cttctcatgc tgctggtcag cagcctctct ccagtcctga gtgttctgga ggtctattac 120
acaagcttga ggtgtagatg tgtccaagag agctcagtct ttatccctag acgcttcatt 180
gatcgaattc aaatcttgcc ccgtgggaat ggtgtgcca gaaaagaaat catagtcttg 240
aagaagaaca agtcaattgc gtgtgtggac cctcaagctg aatggataca aagaatgatg 300
gaagtattga gaaaaagaag ttcttcaact ccaccagttc cagtgtttaa gagaagatt 360
ccctgatgct gatatttcca ctaagaacac ctgcattctt cccttatccc tgctctggat 420
tttagttttg tgcttagtta aatcttttcc aggaataaga acttcccat acaataaagc 480
atgagactat gtaaaaataa ccttgcagaa gctgatgggg caaactcaag cttctttact 540
cacagcacc tatatacact tggagtttgc attcttattc atcaggaggg aaagtctctt 600
tgaaaaata
```

<210> 402

<211> 588

<212> DNA

<213> Homo sapiens

<400> 402

```
ctggggccagg agctgtgccc agtgccctgca gccttcataa gcacacacgt ccattcccta 60
ctaaggccca gacctcctgg tatctgcccc gggctccctc atcccacctc catccggagt 120
tgcccaagat gcatgtccag cataggcagg attgctcggt ggtgagaagg ttaggtccgg 180
ctcagactga ataagaagag ataaaaattg ccttaaaact tacctggcag tggctttgct 240
gcacggctctg aaaccacctg ttcccaccct cttgaccgaa atttcttctg gacacagaga 300
agggcaaaagg tctgagccca gagttgacgg agggagtatt tcagggttca cttcaggggc 360
tcccaaaagcg acaagatcgt tagggagaga ggcccagggt ggggactggg aatttaagga 420
gagctgggaa cggatccctt aggttcagga agcttctgtg caagctgcga ggtatggctt 480
ggccgaaggg ttgctctgcc cgccgcgcta gctgtgagct gagcaagcc ctgggctcac 540
agcaccccaa aagcctgtgg cttcagtcct gcgtctgcac cacacatt
```

<210> 403

<211> 425

<212> DNA

<213> Homo sapiens

<400> 403

```
cctggtggaa agaaggctct agaacctgct tatagagcca caacagggtg cagacaactg 60
tgatgtcaac caatgtcact cgttcgcccc ccagaaaagt cctcgtcttc aagtaagcat 120
ccagcagccc cagaattcgc ctcaacttct cctttgcatt ctcaagtggc tgtttgttgt 180
ggtgcatgat gccaagggtg gggaaacccc aggtactggc tgggggactc atatcggaat 240
cagcaaaagt caccactgct accacctggg ctgctgcctc tggagtactt ccccgagct 300
cctcattgct cacatagtag gcaatggcgt tgctctcaaa cacacagaat ccatcatcac 360
cctcaaatgc tgggaccttg ccggcaggaa atttgcggag aaattcaggg gtgctgttgt 420
tttgg
```

<210> 404
<211> 603
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(603)
<223> n = A,T,C or G

<400> 404
ctggtggtta acaagtggat cgtcatgttc agtagtttat acattatgtg agaagtaacg 60
ttctgattct ttttcttaca cagaattggc agaggggggc gatttgggag gaaaggtgtg 120
gctataaact ttgttactga agaagacaag aggattcttc gtgacattga gactttctac 180
aatactacag tggaggagat gcccataaat gtggctgacc ttatttaatt cctgggatga 240
gagtttttga tgacgtgctc gctgttgctg aataggcgat cacaacgtgc attgtgcttc 300
tttctttggg aatatttgaa tcttgtctca atgctcataa cggatcagaa atacagattt 360
tgatagcaaa gcgacgttag tcgtgagctc ttgtgaggaa agtcattggc tttatcctct 420
ttagagttag actgttgggg tgggtataaa agatgggggc tgtaaaatct ttctttctta 480
gaaattttatt tcctagtctt gtagaaatgg ntgnattaga tgttctctat catttaataa 540
tatacttgn gactaaaaga tataagtgtc gnataaaatc agccaattat gttaaaactag 600
cat 603

<210> 405
<211> 603
<212> DNA
<213> Homo sapiens

<400> 405
aaaaaaactt gtgcaaattg caatcactga gtgattatgg aaaggcaaag tatatacagt 60
aatgtgagag aaactcaaac caagtaaggg taaaaatgaa atgattaaca ccaccagagg 120
aggaaagctac tatcaaaata aaaccatact tcctaataaa ggtaaggcca tcataacccc 180
agaaaatgct tcatacttta gataattaaa aacacattat aaccaaagc agatagtaac 240
attgagtatg ctgatttcaa aaagaagatg ggtctagata ccaggacagc tctttttagt 300
gccttcctta aaaagggcaa aacttttttag agccatgtaa ttgtttatag ccatggcctg 360
gcttcaggca tctcataagt gaggcttcag aaagtccttg aagagtatat ggcagtga 420
ctgggctccc atctttacca taaagatgtt cttcttgaga ataagtgc ataggaagt 480
atcgcttatg acatcatttc attgatcttg aggccatata aagagacttg ctgatattag 540
agcagtttct ttctaataca tattccgctg aattccaagc aatgaggcac acaccagttt 600
gtc 603

<210> 406
<211> 578
<212> DNA
<213> Homo sapiens

<400> 406
ctgctgtgga agggctcctt caagcccagc gagcatgtga aaccaggggc cccaggaaac 60
ctgacagtgc acaccaatgt ctccgacact ctgctgtgta cctggagcaa cccgtatccc 120
cctgacaatt acctgtataa tcacttcacc tatgcagtca acatttggag tgaaaacgac 180
ccggcagatt tcagaatcta taacgtgacc tacctagaac cctccctccg catcgagcc 240
agcaccctga agtctgggat ttctacagg gcacgggtga gggcctgggc tcagtgtctat 300
aacaccacct ggagtgtgtg gagccccagc accaagtggc acaactccta cagggaagcc 360
ttcgagcagc acctcctgct gggcgctcag gcttctgca ttgtcatcct ggccgtctgc 420
ctgttgtgct atgtcagcat caccaagatt aagaaagaat ggtgggatca gattcccaac 480
ccagcccga gccgcctcgt ggctataata atccaggatg ctcagggggc acagtgggag 540
aagcgggtccc gaggccagga accagccaag tgcccaca 578

<210> 407
<211> 568
<212> DNA
<213> Homo sapiens

<400> 407

```
ctcagagctc aagtctgaac tctacctcca gacagaatga agttcatctc gacatctctg 60
cttctcatgc tgctggtcag cagcctctct ccagccaag gtgttctgga ggtctattac 120
acaagcttga ggtgtagatg tgtccaagag agctcagtct ttatccctag acgcttcatt 180
gatcgaattc aaatcttgcc ccgtgggaat ggttgtccaa gaaaagaaat catagtctgg 240
aagaagaaca agtcaattgt gtgtgtggac cctcaagctg aatggataca aagaatgatg 300
gaagtattga gaaaaagaag ttcttcaact ctaccagttc cagtgtttaa gagaaagatt 360
ccctgatgct gatatttcca ctaagaacac ctgcattctt cccttatccc tgctctggat 420
tttagttttg tgcttagtta aatcttttcc aggaaaaaga acttccccat acaaataagc 480
atgagactat gtaaaaataa ccttgcagaa gctgatgggg caaactcaag cttcttctact 540
cacagcacc tatatacaact tggagttt 568
```

<210> 408

<211> 125

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(125)

<223> n = A,T,C or G

<400> 408

```
ctgggggggtc caggaaaggg gttggggccat gagccaggca gctccgaagc agtcactgag 60
gccagggaagc ctgcacccag nncatgggnc gaccnggctc tcactcctgy cctggggtgct 120
cacct 125
```

<210> 409

<211> 291

<212> DNA

<213> Homo sapiens

<400> 409

```
ccagtgccta gacaaatttg gggttggggg gaacactttg gtttgaaagc acagagcagt 60
ttgccatggt tcttctgtgc ctaccattct cccttgccct caacttctgt aagatggggg 120
ggggacaaaa agagaagtaa agttaagaag aaagtggaaa attaaaaaaa agatgtcaaa 180
gtttttacat gcataatatt cagcttatgc tgaagaccta cctgtatggt gcacattgaa 240
tcatactttc agaacccttc agaaaccatc cctctctccc taaagaattt t 291
```

<210> 410

<211> 231

<212> DNA

<213> Homo sapiens

<400> 410

```
aaacttgatc caacctcttt gcatcttaca aagttaaaca gctaaaagaa gtaaaataag 60
aaggcaatgc ttgtggaatg tacagtgcac attggcggcg cagccctcat tacgattcgc 120
ctgcttgctt ctctgttca atcgtttctt tggaaggcag tggatttttc tcttgcgtct 180
ctgtcttctt cagtttcgac ttatcgaatt tctcgatctc agccatatcg g 231
```

<210> 411

<211> 406

<212> DNA

<213> Homo sapiens

<400> 411

```
cctaagaact gagacttggt acacaaggcc aacgacctaa gattagccca gggttgtagc 60
tggaagacct acaaccacaag gatggaaggc ccctgtcaca aagcctacct agatggatag 120
aggacccaag cgaaaaaggt atctcaagac taacggccgg aatctggagg cccatgaccc 180
agaaccagg aaggatagaa gcttgaagac ctggggaaat cccaagatga gaaccctaaa 240
ccctacctct tttctattgt ttacacttct tactcttaga tatttccagt tctcctgttt 300
atctttaagc ctgattcttt tgagatgtac tttttgatgt tgccggttac ctttagattg 360
```

acagtattat gcctgggcca gtcttgagcc agctttacct cggccg 406

<210> 412
<211> 278
<212> DNA
<213> Homo sapiens

<400> 412
aaaatatccc tgaagtgaca cactcctttt ttgagaccga tactggtatt cttttattat 60
agagactaaa aggtctgcct tactagactt cccacttttt gttctgaaag gaattaagga 120
ctgcagggtt ccagctctgt cttcccgagg ccattatgaa cagattaaat ggaaggacaa 180
attctaaata actgggcttt caacatgaaa agggaaaagg tgatggggag ttcagaacct 240
tgaatactgt aactgaacat ccctcaaggt taatgcag 278

<210> 413
<211> 284
<212> DNA
<213> Homo sapiens

<400> 413
ccgggcagggt ctggaagcct tgttggtccc taagcctttg tttcatgcta cagtactgag 60
gggtatgtgt cccaatgca cagccacccg cacacaactc aatgagcttc ctgggaaaca 120
ctattccccc acctccacct taggtggctg cctcagtttt ccaaccactg gaatcagtcc 180
ctcagctcct gcctctagtc tccaccccaa aagttcagtc gtctctgtct tggagggcac 240
tgtcggcccc ctcaggttga agttcaacac tcctcaatga gcag 284

<210> 414
<211> 288
<212> DNA
<213> Homo sapiens

<400> 414
aaaaatacac cttttattct gagacattga ccttcactag agtgggacct gtggccccag 60
cctggcttga gaagcagtc agggcctgag tgacaccatt tccctttcct gaaataggaa 120
caagtatttc caaaggagaa aggagagccc agagagatct gtacaggacc tctcttgac 180
atggtgactg gaggcagagg gtggggagct ggagaggagt ccagtccttc caacaaatat 240
tgagggcttc aaagagctct tcctggacgt ttctcttaat ctggattt 288

<210> 415
<211> 348
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(348)
<223> n = A,T,C or G

<400> 415
ccaaaagaag taagacagct tgctgaagat ttcctgaaag actatattca tataaacatt 60
ggtgcacttg aactgagtgc aaaccacaac attcttcaga ttgtggatgt gtgtcatgac 120
ntanaaaagg atgaaaaact tattngtcta atggaagaga tcatgagtga gaaggagaat 180
aaaaccattg tttttgtgga aaccaaaaga agatgtgatg agcttaccag aaaaatgagg 240
agagatgggt ggctgccat gggatccat ggngacaaga gtcaacaaga gcgtgactgg 300
gctctaaatg aatccaaaca tggaaaagct cctattctga ttntaca 348

<210> 416
<211> 284
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (1)...(284)

<223> n = A,T,C or G

<400> 416

```
ggcggcaaga tggcagtga aatatccaag aagaggaagt ttgtcgtga tggcatcttc 60
aaagctgaac tgaatgagtt tcttactcgg gagctggctg aagatggcta ctctggagtt 120
gaggggtgcga gttacaccaa ccaggacaga aatcattatc ttanccacca gaacacanaa 180
tgttcttggt gagaagggcc ggcggattcg ggaactgact gctgtagttc agaagaggtt 240
tggctttcca gagggcagtg tagagcttta tgctnaaaag gtgg 284
```

<210> 417

<211> 212

<212> DNA

<213> Homo sapiens

<400> 417

```
ccaatgtggt tggctctcag cttgcagtta gccaggttcc atacctgac cagcttgctc 60
cagccacagg agacgatgat aggggttgctg ctgttgggcg agaagcggac acaagacacc 120
cactctgagt ggctctcatc ctggacagtg tatttgcaca caccaggggt attccatagc 180
ttgatgggtt tatctcgaga tccaaaaaca at 212
```

<210> 418

<211> 285

<212> DNA

<213> Homo sapiens

<400> 418

```
cctttccttg agctgcacgt gaacctgtgt gggcaggcag cgtttgcagg cgtgtttacg 60
ggcaggcagc gtttgcaggc gtgtttaccg gcaggcagcg tttgcaggcg tgtttacatg 120
caggcgtagc accatgtgag accactggtc caggggttca gaggtcctgc tcaggtgaat 180
cggctgtgtt ctcaacaagt caccgagctg agtgggtgtg caacatgaaa tactagtgtc 240
gtgagggaca gaaaggacag aaagaggctg aagaccatca tccag 285
```

<210> 419

<211> 271

<212> DNA

<213> Homo sapiens

<400> 419

```
ggtggcaaca aacctgacca catgattaag cctgttgaag tcactgagtc agcataaata 60
aagactgcac aggagaatta cccctatacc tgagcctcaa ccttctgggg gaaaggggaa 120
tagataacat acttcttact tgtctgtaca gtaccttggt gcagatgggt gatataaat 180
ggtaaatagaa tagcacagcc agacttgctt cctgcatggt agggagagac acaaaaagtg 240
ggaaactgct tttccacaag gaatctccgt a 271
```

<210> 420

<211> 287

<212> DNA

<213> Homo sapiens

<400> 420

```
ctctggcctc ttactcacc cttaccacag acatggctca gtcactggct ctgagcctcc 60
ttaccctggt tctggccttt ggcaccccca ggacccaagg cagtgatgga ggggctcagg 120
actgttgctt caagtacagc caaaggaaga ttcccgccaa ggttgctccg agctaccgga 180
agcaggaacc aagcttaggc tgctccatcc cagctatcct gttcttgccc cgcaagcgct 240
ctcaggcaga gctatgtgca gacccaaagg agctctgggt gcagcag 287
```

<210> 421

<211> 286

<212> DNA

<213> Homo sapiens

<400> 421

```
ccagagcggg gagtcccacc acctcgaact ctgggaattc gagccacagc tctgccagta 60
ccccaagact cagcactagt ctgatgacct gctaattcac tgacagcata gggctgtctg 120
ttgtttttgc gcaagttggt gtgaacaaag ttcacaatat ctggtcgaat aggagccttg 180
aatacagcag gcaaagtgac atttttgcca gatgactccc ccttttcgga gtacaccgat 240
atcagtgggc gagcacacgc catggcggag agaggagaca gccacg 286
```

<210> 422

<211> 306

<212> DNA

<213> Homo sapiens

<400> 422

```
ctgcccacct caccctcagc tctggcctct gactcaccct ctaccacaga catggctcag 60
tacttggtctc tgagcctcct tacccttggt ctggcctttg gcatccccag gaccaaggc 120
agtgtatggag gggctcagga ctgttgcttc aagtacagcc aaagggaagat tcccccaag 180
gttgtccgca gctaccgaa gcaggaacca agcttaggct gctccatccc agctatcctg 240
ttcttgcccc gcaagcgctc tcaggcagag ctatgtgcag acccaaagga gctctggggtg 300
cagcag 306
```

<210> 423

<211> 242

<212> DNA

<213> Homo sapiens

<400> 423

```
ctgggagagc tagactaagt tggtcatgat gcagaagcta ctcaaagca gtcggcttgt 60
cctggctctt gccctcatcc tggttctgga atcctcagtt caaggttatc ctacgcagag 120
agccaggtac caatgggtgc gctgcaatcc agacagtaat tctgcaaact gccttgaaga 180
aaaaggacca atgttcgaac tacttccagg tgaatccaac aagatcccc gtctgaggac 240
tg 242
```

<210> 424

<211> 132

<212> DNA

<213> Homo sapiens

<400> 424

```
ctgcttccat tgggtgggtca tttttgctgt caccagcaac gttgccacga cgaacatcct 60
tgacagacac attcttgaca ttgaagccca cattgtcccc aggaagagct tcaactcaaag 120
cttcatgggtg ca 132
```

<210> 425

<211> 414

<212> DNA

<213> Homo sapiens

<400> 425

```
cctgacacaa tatccctggt cactttgaag tgaattttga ctctatatcc agaacccttc 60
tttaacacaa tggtttcctt tttagaggct tccagatctc cagtaaggct catggtgatt 120
gggtcccggy cactctcaca aaccagggtg agccgggtga caacgacatt gggggctttc 180
ggatctgtca ccacaggacc atctcccagc agcgttttct tgtacttaat tagactctca 240
tcacttttgt ccatttcctg cagctctttc agggacttct gtgggtggagg cttataattg 300
agcttgctgt ccagctcatc atcgctatcc tcctccacat gtgggctctg gggctttttc 360
agtcattctg atctatttat tcagtgtctc acgtctctgt ccgggggtgcc tctg 414
```

<210> 426

<211> 101

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(101)

<223> n = A,T,C or G

<400> 426

ctgtgattct ccaactgaaat ttttttttta agggagctca aggtcacaag aagaaatgaa 60
aggaacaatc agcagccctg ttcanaaggn ggtttgaaga c 101

<210> 427

<211> 353

<212> DNA

<213> Homo sapiens

<400> 427

gtttcagccg aaggactctt ctattcggaa gtacaccctc actattagga agattcttag 60
gggtaatttt tctgaggaag gaggactagc caacttaaga attacaggaa gaaagtgggt 120
tggaagacag ccaaagaaat aaaagcagat taaactgtat caggtagatt ccagcctgtt 180
ggcaactcca taaaaacatt tcagatttta atccgaattt agctaataag actggatttt 240
tggtttttat gttgtgtgtc acagagctaa aaactcagtt cccaaatccc cagtttatgc 300
agccgccatc aggtatttta agctaaactt cttcacccct gagagcatgt cag 353

<210> 428

<211> 104

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(104)

<223> n = A,T,C or G

<400> 428

tatttaaaaa ctcaacagga cctacactac ntgttcaaat ctgtaatctt tcacaccnca 60
ctaacaaagt tnttaggaaa acaggactac ccaaanatgt tacc 104

<210> 429

<211> 471

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(471)

<223> n = A,T,C or G

<400> 429

ccaaaaaann tcaagattnn ntttttttat ttgtactgaa aaactaatca taactgttaa 60
ttctcagcca tctttgaagc ttgaaagaag agtctttggt attttgtaaa cgtagcaga 120
ctttcctgcc agtgtcagaa aatcctattt atgaatcctg tcggtagtcc ttggtatctg 180
aaaaaaatc caaatagtac catacatgag ttatttctaa gtttgaaaag taaaaagaaa 240
ttgcatcaca ctaattacaa aatacaagtt ctggaaaaaa tatttttctt cattttaaaa 300
cttttttaac taataatggc tttgaaagaa gaggcctaat ttgggggtgg taactaaaa 360
caaaagaaat gattgacttg aggggtctctg tttggtaaaa atacatcatt agcttaata 420
agcagcagaa ggtagtattt aattatgtan cttctgtnaa tattaagtgt t 471

<210> 430

<211> 395

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(395)

<223> n = A,T,C or G

<400> 430
aggcgacnng gtaggggnng gcgctcaggg ggcgaccatg gcgtatcacg gcctcactgt 60
gcctctcatt gtgatgagcg tgttctgggg cttcgtcggc ttcttggtgc cttgggttcac 120
ccctaagggt cctaaccggg gagttatcat taccatgttg gtgacctgtt cagtttgctg 180
ctatctcttt tggctgattg caattctggc ccaactcaac cctctctttg gaccgcaatt 240
gaaaaatgaa accatctggt atctgaagta tcattggcct tgaggaagaa gacatgctct 300
acagtgtcga gtctttgagg tcacgagaag agaatgcctt ctatagcaaa aatcacctcc 360
aaaccagacc acttttcttg acttgccctg tttgg 395

<210> 431
<211> 303
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(303)
<223> n = A,T,C or G

<400> 431
caggcatgaa aaaatgacaa gaattttaaa acaagggcat catttgatct ttaaatatga 60
ctatttttct taaaaacgat ggattttgac caacctagat gtacaccata gtttatagat 120
caaataaaag ctattaaaaa tatcttaact tnttacaat gttagcagtc tttgtgtgca 180
gtattagaga tcagagttgt gattgtttct gagcatgtct tgtgggttat aactatgttt 240
tcaattaaaa ttataagatt gagatacttt ctggaagatg tatagaaaat gttgntatat 300
tca 303

<210> 432
<211> 477
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(477)
<223> n = A,T,C or G

<400> 432
tttttttnnt ttttttnnt aaaanaagga ttttaggttt ntttgngaa acaaaagcag 60
atataaaaag ttacaaagat ttanatttt cattcacaaa aaaagtcatt cacattttac 120
actatacacg ttatgatata aatacaggaa agtattatgt gcattgtaaa gagaaaggaa 180
aaatagaac ctactagatc aacacagngt tgttctgtgc tctaaaaac cttaaaggngg 240
attacattta atgcaacaac caagggaacc tgcttaaaac tactgngtat tattgtagct 300
agagtcatc cttctaagcc aaaggagggt ttataaaaaa naatcaatat tgggccaatc 360
cctttgngcc ctttttctct ttttctatgn gcattttatt ttttgntac tcttcttcaa 420
gttgctctaa actgaaatta gggaaggagt ctcactttcc nttanagggt tttcttt 477

<210> 433
<211> 566
<212> DNA
<213> Homo sapiens

<400> 433
ccaggtttta gatattaacc tggctgcaga gccaaaagt aaccgaggaa aagcaggtgt 60
gaaacgatct gcagcggaga tgtacgggtc agtaacagaa cacccttctc cgtccctct 120
actcagctcc tcttttgact tggactatga cttcaacgg gactattatg ataggatgta 180
cagttaccca gcacgtgtac ctcctcctcc tcctattgct cgggctgtag tgccctcgaa 240
acgtcagcgt gtatcaggaa acacttcacg aaggggcaaa agtggcttca attctaagag 300
tggacagcgg ggatcttcca agtctggaaa gttgaaagga gatgacctc aggccattaa 360
gaaggagctg acccagataa aacaaaaagt ggattctctc ctggaaaacc tggaaaaaat 420
tgaaaaggaa cagagcaaac aagcagtaga gatgaagaat gataagtcag aagaggagca 480
gagcagcagc tccgtgaaga aagatgagac taatgtgaag atggagtctg aggggggtgc 540
agatgactct gctgaggagg gggacc 566

<210> 434
<211> 384
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(384)
<223> n = A,T,C or G

<400> 434
ccacagggga aggcaagagg cgatagctgg gggtcacttg tctactagatg gaagctcctt 60
gggtccacaca gtcccaaaga aagggtctgcc tttggggccca cgaaacccat cccagccctc 120
acaggctgaa cctcaccctg ggttttccca gagaggtgcc caagaagacc caagctgccc 180
caagtcagag gagcagcagg aaacagcctc agaagtccgt cactcttcag tactcctccc 240
ttagaatgtc cacttcctgt ttggtgacca tggcaaccaa aagacaatgg cagtgcagtg 300
cgtgtgggat gggggagctc catcttcctt gggtagatgg ggaggagact ccagtgacca 360
ngagaagcgg ggagagccat ggga 384

<210> 435
<211> 468
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(468)
<223> n = A,T,C or G

<400> 435
ctgtggctgt ctgtcagaga agcacatttt tctgcagata attagaatgg cttcccccat 60
ctctcacgga ctgtcccaag tctagaaaag aattgagttc ctcttctatt agtcaaataa 120
aagggaagag aatgtttgtc ttcctttcct ttctgtagt ttaagaaaat aaacgaactt 180
aatgattcta aattatcagt gagcttaaca ctgtactata gaccaaagat taccttttca 240
aaaagtcctt tgaggtgaaa tattttgtat acgtaataca tagatgcaca tataaacaca 300
cacatataga atctcaatat tttaacactt ctttgggtag ttgtactaac tactaacc 360
tgaggaaaaa gttaagaaat tgaaagtgtt ttcttcanaa gttgagattt aacaataaaa 420
ggtgttactt tgataactaa aagggaacttt attatcctct tcctaaaa 468

<210> 436
<211> 124
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(124)
<223> n = A,T,C or G

<400> 436
gtaggggtgc cagatgcnnt acaanatttc tgggttaaatt tgaatttcag taaacaatga 60
atagtttttc attgtaccat gaaatatcca aaacatactt atatgtnaag tattatttat 120
ttgn 124

<210> 437
<211> 126
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(126)

<223> n = A,T,C or G

<400> 437

```
ggntgttgac tcanattcgg cattttaatt acattgtttc caagtatgat attctgagag 60
tgtctatagc acttagtgct tgcttcatat aaactaccag ttattatata tttatgatgc 120
aagtag                                           126
```

<210> 438

<211> 612

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(612)

<223> n = A,T,C or G

<400> 438

```
ctgttgactc agattcggca ttttaattac attgtttcca agtatgatat tctgagagtg 60
tctatagcac ttagtgctctg ctctcatataa actaccagtt attatatatt tatgatgcaa 120
gtagttttcc aaatgtggtg aaagtctgag tctttttatc cccatgggta aaatctgaat 180
ctggctctct gtgtctctca gtgcttggtt attgctggtc agagagtaaa ttcttgataa 240
aagctgttga cttggctctc acagtttatg cagacattgg agagacaatt tggttatttc 300
aaacatcaca ggatttgagt aagaagacct ggttatgaaa caaggctctc ataattacta 360
gttatgactg ttgacaagtt accttttctt gtttacaagt tatttggcct ctttgaatta 420
cttgtaaaat agagataggg attctttctt gatcatggaa catcaaatga agttatttga 480
tgaaatactt tgcacatctg aaattataaa tataactaaa tgtaattat tatttggaaa 540
tttngggcac ctcatggngg cattttctat ggtcattttt tttcttttct cgcataatgg 600
ctaaaagtag gt                                           612
```

<210> 439

<211> 330

<212> DNA

<213> Homo sapiens

<400> 439

```
ccacacagcc cctgtgctag acatcgctg gtgcccgcac aatgacaacg tcattgccag 60
tggctccgag gactgcacag tcatggtgtg ggagatcccg gatggggggc tgatgctgcc 120
cctgctggag cccgtcgtca ccttgaggag ccacaccaag cgtgtgggca ttgtggcctg 180
gcacaccaca gcccagaaacg tgctgctcag tgcaggttgt gacaacgtga tcatggtgtg 240
ggacgtgggc actggggcgg ccatgctgac actggggcca gaggtgcacc cagacacgat 300
ctacagtgtg gactggagcc gagatggagg                                           330
```

<210> 440

<211> 472

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(472)

<223> n = A,T,C or G

<400> 440

```
cctcnnacng aaggctggtg accaggtccc aggcggggcaa gactcagcct tgggtggggc 60
tgaggacaga ggaggcccag gagcatcggg gagagaggtg gagggacacc gggagagcca 120
ggagcgtgga cacagccaga actcatcaca gaggtggcg tccagtcccg ggtcacgtgc 180
agcagggaaca agcagccact ctggggggcac caggtggaga ggcaagacga caaagagggt 240
gcccgtgttc ttgcgaaagc ggggctgctg gccacgagtg ctggacagag gccccacgc 300
tctgcttgcc cccatcacgc cgttccgtga ctgtcacgca gaatctgcan acaggaaggg 360
agactctaag cgggagtgcg gccaaagcctg cctccgcccg tcagggagga ctcccgggct 420
cactcnaagg aggtgccacc atttccgctt tggnnagctt ttctttttct tt                                           472
```


<210> 441
<211> 349
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(349)
<223> n = A,T,C or G

<400> 441
aaaaaattta ctcatcttcc ataaagcgac ttttaattga tcaacactta aagatacaca 60
gtgactttaat gaaatatcag cacaactgca tagaattgag ctccagagaa ttatacactc 120
gagctgcttt cctgggctct gggtttataag ggtattggct tagagaccag cttggagtca 180
tttggcccta cccgggaaat gcaggccagg aaacttaaga ttttgcgggc cttttctgtt 240
tctaggtaaa atgcagggag ctccctgaag gncttgaaaa ccatcaacca ttcaaatatg 300
gtatcctggg gacctttcct cttgagttaa nggaagaaag gaggttttg 349

<210> 442
<211> 179
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(179)
<223> n = A,T,C or G

<400> 442
aaagntggct caagactggc ccangcataa tactgtcaat ctaaaggtaa ccggcaacat 60
caaaaagtac atctcaaaag aatcaggctt aaagataaac aggagaactg gatatatcta 120
agagtaagaa gtgtaaacaa tagaaaagag gtagggttta gggttctcat ctagggatt 179

<210> 443
<211> 170
<212> DNA
<213> Homo sapiens

<400> 443
ccgccgcggg tccgtgcgcc cagcgtccca gggcccaggc cgagcagaca aagatcattc 60
cactcagcct gggacgatgg ggaggaaaaa aatccagatc tcccgcattc tggaccaaag 120
gaatcggcag gtgacgttca ccaagcggaa gttcgggctg atgaagaagg 170

<210> 444
<211> 342
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(342)
<223> n = A,T,C or G

<400> 444
ngtctcacag gtagtctcct gagtagttga cggctagcgg ggagctagtt ccgccgcata 60
gttatagtgt tgatgtgtga acgctgacct gtcctgtgtg ctaagagcta tgcagcttag 120
ctgaggcgcc tagattacta gatgtgctgt atcacgggga atgaggtggg ggtgcttatt 180
ttttaatgaa ctaatcagag cctcttgaga aattgttact cattgaactg gagcatcaag 240
acatctcatg gaagtggata cggagtgatt tgggtgccat gcttttcacc ctnaggacat 300
ttaatcngag aacctcctgt ngaattttgt gggagacact tg 342

<210> 445
<211> 387

<212> DNA

<213> Homo sapiens

<400> 445

```
aaatttctca aataactaag tcttactaa ggcagcagtt caaaactgtt ccaggaatta 60
aaatatattc ccatttgagg agtcttcctt cacaccttca cctcctcagc cttaagtata 120
tacacacaca cccaacaccc tcaatacttg actagcaaca ggctttacca tctttacctg 180
acaatgaccc cagggcggag atcgaaatc ttcttcacaa tctctaatag ctctctctca 240
ctcttctgag aggtaccata atggaaaatg gagatagata atggatgaga aactccaata 300
gcataagaga cctgaacaag aacctctcgg cacagacctc cttaacaag ggattttgcc 360
acccaacgag cagcataagc agacctg 387
```

<210> 446

<211> 279

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(279)

<223> n = A,T,C or G

<400> 446

```
ngnccacaag atatgttcta tagacgtcca tgagtcctct tgctgtgngg gagcggatc 60
cacagacttn tggaataatt ggcctgtgag gaagctcatc aaagctgcaa acagtacaan 120
tgaatgcaat aganagncac agggccttat tagcctttct gatggaggac ttganatttg 180
ttgnccagga anctattgtg tcataaactg aagagacatn ccactttgat ggattatttt 240
tcttttcaga aagacttggc ttccttgctc tttctactg 279
```

<210> 447

<211> 235

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(235)

<223> n = A,T,C or G

<400> 447

```
ngtccagtag ggctgagatg ttgggagcca tcaatcagga aagccgggtt agtaaagcag 60
ttgaagtgat gattcancac gtagaaaact tgaagaggat gtatgccaaa aagcaccgct 120
gaattagaag aactgaaaca ggttcttctg cagaatgaaa ggcctttcaa tncctttgaa 180
gatgatgatg actgccaaat taaaaaacgt tcagcttttc taaactccaa gccat 235
```

<210> 448

<211> 292

<212> DNA

<213> Homo sapiens

<400> 448

```
ccatgtcccc agaattgaag ccagagaatc gctcagatat ccctgagggc cggctcgttat 60
caaaaagagat gattaggaca ggggcctggc ctggcttctg gtaataccag tgtacattgt 120
tactcccaat attgtttccc ccacaggtaa tcttgcccggt ctttctctggg gccactgaca 180
ctgaggggtgt ctgagtcaac acataggagg tcacagagtc tgtgcagtga gagaggaggc 240
cgaggaggag aacggtccag gccatggctg aggcaccacc agtgctgctt cc 292
```

<210> 449

<211> 318

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature
<222> (1)...(318)
<223> n = A,T,C or G

<400> 449
cctttccttg agctgcacgt gaacctgtgt gggcaggcag cgtttgcagg cgtgtttacg 60
ggcaggcagc gtttgcaggc gtgtttaccg gcaggcagcg tttgcaggcg tgtttacatg 120
caggcgtanc accatgtgag accactggtc cagggtttca gaggtcctgc tcagggtgaat 180
cggctgtgtt ctcacaagtt cacggagctg antgggtgtg caacatgaaa tactagtgt 240
gtgagggaca gaagggacag aaaggaggctn aagaccatna tccagctata cctgtgcctc 300
ggcttttctc agacctcg 318

<210> 450
<211> 317
<212> DNA
<213> Homo sapiens

<400> 450
aaattatgac acaaaatttt attaacaagg aaatatccat taattgacta ctacagtaaa 60
aactttataa tgcttgtatc atgaagaaag accttccttt tccttatata ttaattgaac 120
tacataggct tgctgtacat tttgttatc atgttataag aattctagat tccattgctt 180
ttgaaatag tttcttttta ggaactaaaa gtcaacttat agtttgattt ctgttttatt 240
tgtactgtgt ttctgatttt gtgggtttct aaataaaaag atcaaaccga ccactttcaa 300
tatactgttt tctattt 317

<210> 451
<211> 156
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(156)
<223> n = A,T,C or G

<400> 451
ccaaaagaag taagacagct tgctgaagat ttcctgaaag actatattca tataaacatt 60
ggtgcacttg aactgantgc aaaccacaac attcttcana ntgtggatgt gtgtcatgac 120
ntanaaaagg atgaaaaact tattcgtcta atggaa 156

<210> 452
<211> 345
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(345)
<223> n = A,T,C or G

<400> 452
ccaatgtggt tggctctcan cttgcantta gccaggttcc ataccttgac cagcttgtcc 60
cagccacagg agacgatgat agggttgctg ctgttgggcg agaagcggac acaagacacc 120
cactctgagt ggctctcatc ctggacagtg tatttgcaca caccagggt attccatagc 180
ttgatggttt tatctcgaga tccagagaca atctgccggt tgtcagagga gaaggccaca 240
ctcagcacat ccttggtatg gccacaaat cgctcgttg tggtgcccgt tgtgagatcc 300
cagaggcgca gggttccatc ccaggagcct gagagggcaa actgg 345

<210> 453
<211> 182
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(182)
<223> n = A,T,C or G

<400> 453
ccacaagata tgttctagag acgtccatga gtcctcttgc tgtgtgggag cggnatccac 60
agacttctgg aataattggc ctgtgaggaa gcccatcaaa gctgcaaaca gtacaatgaa 120
tgcaatagag agccagaggg ccttattagc cttntgatg gaggacttga gatttgttgc 180
cc 182

<210> 454
<211> 440
<212> DNA
<213> Homo sapiens

<400> 454
ctgcaaatgg ttctgctgaa acatctgcct tggacacagg gttctcgctc aacctttcag 60
agctgagaga atatacagag ggtctcacgg aagccaagga agacgatgat ggggaccaca 120
gttcctctca gtctggtcag tccgttatct cctgctgag ctcaagaaga ttaaaaaaac 180
tcctcgagga ggtgaaggtt ctggatgaag caacattaaa gcaattagac ggcatccatg 240
tcaccatctt acacaaggag gaaggtgctg gtcttgggtt cagcttggca ggaggagcag 300
atctgaaaaa caaggtgatt acggttcaca gagtgtttcc aaatgggctg gcctcccagg 360
aagggactat tcagaagggc aatgaggttc tttcctcaac ggcaagtctc tcaaggggac 420
cacgcacat gatgccttgg 440

<210> 455
<211> 396
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(396)
<223> n = A,T,C or G

<400> 455
cttgcgtccc cgcgtgtgtg cgcctaactct caggtgggtcc acccgagacc ccttgagcac 60
caaccctagt ccccgcgcg gcccttatt cgctccgaca agatgaaaga aacaatcatg 120
aaccagga aaactcgcaa actgcaggca caagtgcgca ttggtgggaa aggaactgct 180
cgcagaaaga agaagggtgt tcatagaaca gccacagcag atgacaaaaa acttcagttc 240
tccttaaaaga agttanggtt aaacaatatc tctggtattg aagaggtgaa tatgtttaca 300
aaccaaggaa cagtgatcca cttaacaac cctaaagtcc aggcattctt ggcagcgaac 360
actttcacca ttacaggcca tgctgagaca aagcag 396

<210> 456
<211> 232
<212> DNA
<213> Homo sapiens

<400> 456
ccagcgacag cctggcctgg gaatggactg gcagctcatc actaaaatga ctcctttcat 60
ggaatccact gctatgcagc cacactgacc acagagcaac tgaatagggtg agcattggat 120
tgttgatgac aactcttcag cagaacaatt gtgtgtttga agggactgtt ttatgatgaa 180
ataactgtta tttcctggag ctaattgttg aatgacagtt tgtcaactgt tt 232

<210> 457
<211> 232
<212> DNA
<213> Homo sapiens

<400> 457
gctaaaccaa aagaagctc cagacagccc tgagatcacc taaaagctg ctaccaagac 60

```
agccacgaag atcctaccaa aatgaagcgc ttcctcttcc tctactcac catcagcctc 120
ctgggttatgg tacagataca aactggactc tcaggacaaa acgacaccag ccaaaccagc 180
agccctcag catccagcag catgagcgga ggcatcttcc tttctctcgt gg 232
```

<210> 458

<211> 342

<212> DNA

<213> Homo sapiens

<400> 458

```
aaacttttga gttgtagtca gaaactgttg ttggactgca tagttttcaa aagtttttgg 60
tacattttctg acttttagaaa tctggggttag gaatcccttt ccatatgcat atagactatt 120
ttctgagctt cttcaaaaaca tgtttcagtg ggttcctgaa tgttcctgat gatagtctct 180
cttgtcgaaac tgtcaatggt aatctctcta ggggactgtg gctggatgta aatcttataa 240
agcttctttg ccctagaaat tctgtccac cgtgaggcaa ttttcttata ggtttcacat 300
gccatccaga attgaatatt ctgctcactg tgctccattt tt 342
```

<210> 459

<211> 545

<212> DNA

<213> Homo sapiens

<400> 459

```
ccagtagggc tgagatgttg ggagccatca atcaggaaaag ccgggttagt aaagcagttg 60
aagtgatgat tcagcacgta gaaaacttga agaggatgta tgccaaagag cacgctgaat 120
tagaagaact gaaacaggtt cttctgcaga atgaaaggtc tttcaatcct cttgaagatg 180
atgatgactg ccaaattaaa aaacgttcag cttctctaaa ctccaagcca tcttctctac 240
gaagagtgcac tattgcctct ttaccagaa atattggaaa tgcaggaatg gtggctggga 300
tggaataaa tgatcgattc agtagaaggc caagcagttg gcgtattttg ggggtcaaac 360
agagtgaaca ccgtccctca ttacctgat ttattagcac ctattcctgg gcagatgctg 420
aagaagaaaa atgtgaacta aaaactaaag atgactcaga gccatctgga gaagaaacag 480
tagaaggac aaggaagcca agtctttctg aaaagaaaaa taatccatca aagtgggatg 540
tctct 545
```

<210> 460

<211> 330

<212> DNA

<213> Homo sapiens

<400> 460

```
cctccatctc ggctccagtc cacactgtag atcgtgtctg ggtgcacctc tgggcccagt 60
gtcagcatgg ccgcccagtc gccacgtcc cacaccatga tcacgttgtc acaacctgca 120
ctgagcagca cgttctgggc tgtggtgtgc caggccacaa tgccacacg cttggtgtgg 180
ccctccaggg tgacgacggg ctcccgcagg ggcagcatca ggccccatc cgggatctcc 240
cacaccatga ctgtgcagtc ctcggagcca ctggcaatga cgttgtcatt gtgcgggcac 300
caggcgatgt ctacgcagg ggtgtgtgg 330
```

<210> 461

<211> 118

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(118)

<223> n = A,T,C or G

<400> 461

```
ncctccaga gaaggctggt gaccaggtcc caggcgggca agactcagcc ttggtggggc 60
ctgaggacag aggaggccca ggagcatcgg ggagagaggt ggagggacac cnggaaaa 118
```

<210> 462

<211> 310

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(310)
<223> n = A,T,C or G

<400> 462
atgttgggag ccatcaatca ggaaagccgg gttagtaaag cagttgaagt gatgattcag 60
cacgtanaaa acttgaagag gatgtatgcc aaanagcacg ctggaattag aagaactgaa 120
acaggttctt ctgcataatg aaaggtcttt caatcctctt gaagatgatg atgactgcca 180
aattaaaaaa cgtccagctt ctctaaactc caagccatct tctctacgaa gagtgactat 240
tgcctcttta ccanaaata ttggaaatgc aggaatggtg gctgggatgg aaaataatga 300
tccgattcnn 310

<210> 463
<211> 133
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(133)
<223> n = A,T,C or G

<400> 463
gccggncagg taaagaacta atttgtaaat tatgacacaa aattttatta acaaggaaat 60
atccattaat tgactactac agtaaaaact ttataatgct tgtatcatga agaaagacct 120
tccttttncc tat 133

<210> 464
<211> 182
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(182)
<223> n = A,T,C or G

<400> 464
accagcagtc ctgcggcacc tacctccgcy tgcgccagcc gccccccagg cccttcctgg 60
acatggggga gggcaccaag aaccgaatca tcacagccga ggggatcatc ctctgttct 120
gcgcggtggt gcctgggacg ctgctgctgt tnaggaaacg atggcaagaa cganaactcn 180
gg 182

<210> 465
<211> 149
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(149)
<223> n = A,T,C or G

<400> 465
ccagnacncc catgaanttg atgganatga gcactntnac gtggacctgg ggaggaagga 60
gactgtctgg tgtttgcctg ttctcatata atttagattt gacccgcaat ttgncctgac 120
aaacactggc tgttctaaaa cataacttg 149

<210> 466

<211> 374
<212> DNA
<213> Homo sapiens

<400> 466
cctagggcatg acaatcggag gactcgaggg ggatggagga ctagtgatcg gctggctgct 60
tccagtcgat tagagaggtg aaaaagctga acgtgtgccca gtaatcttca aaaggcagaa 120
catatcacct ctgccccgta aactgttctc tccgaggga aaaatggaag ttatcctcac 180
agttcactgc cgtgggtatctt cttctgtgcc catcttttgc atgacttgcc atggtacagc 240
cttgtttcaa actgttctact gtgatctgtg ggtctttgag tttagtgag tttgctgaaa 300
tgtcgaagaa gtagttccaa acttcaatgt tcaatgaaat tttgttcaa gtttgaaatg 360
gagagagcag cttt 374

<210> 467
<211> 545
<212> DNA
<213> Homo sapiens

<400> 467
ccagtagggc tgagatgttg ggagccatca atcaggaaag ccgggttagt aaagcagttg 60
aagtgatgat tcagcacgta gaaaacttga agaggatgta tgccaaagag cacgctgaat 120
tagaagaact gaaacagggtt cttctgcaga atgaaaggtc tttcaatcct cttgaagatg 180
atgatgactg ccaaattaaa aaacgttcag cttctctaaa ctccaagcca tcttctctac 240
gaagagtgc tattgcctct ttaccagaa atattggaaa tgcaggaatg gtggctggga 300
tggaataa tgatcgattc agtagaaggt caagcagttg gcgtattttg gggtaaacg 360
agagtgaaca ccgtccctca ttacctcgat ttattagcac ctattcctgg gcagatgctg 420
aagaagaaaa atgtgaacta aaaactaaag atgactcaga gccatctgga gaagaacag 480
tagaaaggac aaggaagcca agtctttctg aaaagaaaa taatccatca aagtgggatg 540
tctct 545

<210> 468
<211> 285
<212> DNA
<213> Homo sapiens

<400> 468
cctttccttg agctgcacgt gaacctgtgt gggcaggcag cgtttgcagg cgtgtttacg 60
ggcaggcagc gtttgcaggc gtgtttaccg gcaggcagcg tttgcaggcg tgtttacatg 120
caggcgtagc accatgtgag accactgggc cagggtttca gaggtcctgc tcaggatgaat 180
cggctgtgtt ctacaagtt caccgagctg agtgggtgtg caacatgaaa tactagtgtc 240
gtgagggaca gaagggacag aaagaggctg aagaccatca tccag 285

<210> 469
<211> 135
<212> DNA
<213> Homo sapiens

<400> 469
aaagagaact aatggaagtg gattgaatac agcagttctca actgggggca attttgcccc 60
ccagaggaca ttgggcaatg tttggagaca ttttgggtcat tatacttggg ggggtggggg 120
atggtgggat gtgtg 135

<210> 470
<211> 511
<212> DNA
<213> Homo sapiens

<400> 470
ccagtagggc tgagatgttg ggagccatca atcaggaaag ccgggttagt aaagcagttg 60
aagtgatgat tcagcacgta gaaaacttga agaggatgta tgccaaagag cacgctgaat 120
tagaagaact gaaacagggtt cttctgcaga atgaaaggtc tttcaatcct cttgaagatg 180
atgatgactg ccaaattaaa aaacgttcag cttctctaaa ctccaagcca tcttctctac 240
gaagagtgc tattgcctct ttaccagaa atattggaaa tgcaggaatg gtggctggga 300

```
tggaaaataa tgatcgattc agtagaaggt caagcagttg gcgtattttg gggtaaagc 360
agagtgaaca ccgtccctca ttacctgat ttattagcac ctattcctgg gcagatgctg 420
aagaagaaaa atgtgaacta aaaactaaag atgactcaga gccatctgga gaagaaacag 480
tagaaaggac aaggaaagcca agtcttttctg a 511
```

```
<210> 471
<211> 562
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(562)
<223> n = A,T,C or G
```

```
<400> 471
ctgagacaaa agtaggcccc aatccttcca cagggatgga atgatgctgc cagttcactg 60
tcagcatggg tgggaagaga ttactgacaa aacagaccaa agtgttgggc ttgccaaact 120
ccaggggctt cagcgtgaac acttcagcga taggaaaccc tgggtggggg attgaagtgt 180
agggggaaaa agagactagt ttatagtgta tctctgtgtt tggaggggccc atggcatatg 240
gaggggaggg cagagaagaa cacagtgggt caggccttgg gagacagaga tgagcgagga 300
gctgggctct gaaggagagt cttcttccag gcaaggactg canctagacg tagaagcaga 360
gccagatcca ggctactctg gacccctcca ccatgacttc cttcagcact tcctgtctag 420
agctcacatt gatgtctaac catgactgtt cttctcacta agacatagtc acgtcatcag 480
atatttcac tcttccatc catcttctg ggcatagtag cacaagtgtt aatattcagt 540
angtatcagt tggtagctgt tg 562
```

```
<210> 472
<211> 487
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(487)
<223> n = A,T,C or G
```

```
<400> 472
aaaaatggag agtctgaatt ttattagagc tcacacacca tatattaaca tatacaactg 60
tgaaccagct aatccctctg agaaaaactc cccatctacc caatactgtt acagcatata 120
atctctgttc ttgggcattt tgtcagtgat gctgatcttt gccttcttcc aggaacttgt 180
aatagctggc atcgttgaga atgaatggaa aagaacgtgc tccagaccca aatctaacat 240
agttctctctg tcagcagaag aaaaaaaga acagactatt gaaataaaag aagaagtgtt 300
tgggctaact gaaacatctt cccaacccaa gaatgaagaa gacattgaaa ttattccaat 360
ccaagaagag gaagaagaag aaacagagac gaactttcca gaacctcccc aagatcagga 420
atcctcacna atagaaaatg acagctcttc ttaagtgtt tcttctgttt tctgtttttc 480
ctttttt 487
```

```
<210> 473
<211> 340
<212> DNA
<213> Homo sapiens
```

```
<400> 473
ctgggggggc cggaagagg gttgggcat gagccaggca gctccgaagc agtcactgag 60
gccagggagc ctgcacccag gtcattgggc gacctggctc tcaactctgg cctgggtgct 120
cacctacaga ccacttcaat tcccctgtcc gcagcgtcac tatgtcctca taggtggctg 180
tctggtcaat gtccaggccc tcgtaggtgt gatcttctc catgccagcc ttgctgtcat 240
cctgtccag cagcaggag ataggcacga tgatgaagag gatgatcagc agcgtctgga 300
tcatgatgat accatccttc agcgtgttcc tctgcttcag 340
```

```
<210> 474
<211> 542
```


<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(542)
<223> n = A,T,C or G

<400> 474
aaactccaaa ttcctttatc gaagcagcta tctgctaata ttactgaatg acaagtcttt 60
ggaatgata gtttaaccgaa aatgcagaaa gaatcatagc aactaatgat aatgacgggt 120
aaaggataga aaataaaatt tttagccaca ggttgtgggt acagcatcca ggccatcacc 180
gacatctcgg cagggtatg ccgccacttc gtattaaacg tctactcctc cgagaatgcc 240
cttattaaat taagtgc aaa gtaaggcatc ccacccaga cagagggatc cacattcttt 300
aatcatgatg cggggccactg taacagggag atggatgcag gacgcagacg ggggtggggcg 360
cccaagcgac gcacttagac ggtgatotgt tggttttctc tgaaaaatga tctctgggtg 420
gaggcacaaa tatctggaaa catccggaag acctggctg gcggcggctc ctcggggggc 480
tgcatacag anccggctcc acagctcttc ccagcctctt ctgccagttg ccggacatac 540
ag 542

<210> 475
<211> 342
<212> DNA
<213> Homo sapiens

<400> 475
aaacttttga gttgtagtca gaaactggtg ttggactgca tagttttcaa aagtttttgg 60
tacatttctg acttttagaaa tctggggtag gaatcccttt ccataatgcat atagactatt 120
ttctgagctt cttcaaaaca tgtttcagtg ggttcctgaa tgttcctgat gatagtctct 180
cttgcgaac tgtcaatggt aatctctcta ggggactgtg gctggatgta aatcttataa 240
agcttctttg ccctagaaat tctgctccac cgtgaggcaa ttttcttata ggtttcacat 300
gccatccaga attgaatatt ctctcactg tgctccattt tt 342

<210> 476
<211> 421
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(421)
<223> n = A,T,C or G

<400> 476
ccaatcatag agatatctgc accagcctgc aaagcttcca tgaacgcttt ggtcccagac 60
ttggcgatag taccaaggtt attgatcaag tcagccttgg tcattccaat tccagtatcc 120
acaatagtga gagttcgatc ttgtttgttc ggtataaggt taatatgcag ctctttctca 180
gagtctaatt tactggatc tgtcaagctt tcataccgga ttttgtccaa tgcatactgat 240
gaatttgaaa tgagctctct cagaaagatc tctttgttcg agtagaaagt attgatgatc 300
aatgacatca actgggcaat ttctgcctga aaggcgaacg tntnaacctc ctntcctcc 360
atcggttggc cttgggtctg ggtttcctca ngcatntgga acgacaccgc gccggtntac 420
c 421

<210> 477
<211> 562
<212> DNA
<213> Homo sapiens

<400> 477
ctgttgactc agattcggca ttttaattac attgtttcca agtatgatat tctgagagtg 60
tctatagcac ttagtgtctg cttcatataa actaccagt attatatatt tatgatgcaa 120
gtagttttcc aaatgtggtg aaagtctgag tctttttatc cccatgggta aaatctgaat 180
ctggctctct gtgtctctca gtgcttgggt attgctggtc agagagtaaa ttcttgataa 240


```
aagctgttga cttggctctc acagtttatg cagacattgg agagacaatt tggttatttc 300
aaacatcaca ggatttgagt aagaagacct ggttatgaaa caaggctctc ataattacta 360
gttatgactg ttgacaagtt accttttctt gtttacaagt tatttggcct ctttgaatta 420
cttgtaaaat agagataggg attccttctt gatcatgaaa catcaaatga agttatttga 480
tgaaatactt tgtcatctgg aaattataaa tataactaaa tgtaattat tatttgaaat 540
ttgggcacct catggttgca tt 562
```

<210> 478
<211> 294
<212> DNA
<213> Homo sapiens

```
<400> 478
ccacaaagcc attgtatgta gcttttagtc agcgcaaaga agagcgccag gctcacctca 60
ctaaccagta tatgcagaga atggcaagtg tacgagctgt tcccaacctt gtaattcaacc 120
cctaccagcc agcacctcct tcagggttact tcatggcagc tatcccacag actcagaacc 180
gtgctgcata ctatcctcct agccaaattg ctcaactaag accaagtcct cgctggactg 240
ctcagggtgc cagacctcat ccattccaaa atatgcccgg tgctatccgc ccag 294
```

<210> 479
<211> 237
<212> DNA
<213> Homo sapiens

```
<400> 479
ccagttattcc tggaggatat aacactgaca tcagcagggt tttcaatggc aacaattgca 60
cgagctgccca gcagaagctt ctcccagggt ctcttgagat ttatgatata gatgccatca 120
cttttccttt tatagatgta ctgttccatc tggaagtcaa gattggtgcc acctaaagtg 180
gttctctgctg caaggaactt aaggacatcc tcctccttca tttgcaggac atcaagg 237
```

<210> 480
<211> 563
<212> DNA
<213> Homo sapiens

```
<400> 480
aaaaaaaaact acatctcttt attgcagaat ttatacttgt ttgaaaaata caaaatgtag 60
cgttgataag attgaagcat gttgaaaggt aagtacaggg aaaggctcct tcagaatgac 120
tgcaacagtg cagcaaggat tcccattccc cgcctaaagg acaatacctt tttaatagaa 180
ataaatgagt tagttagtta gatttttatt acagattgaa ttaaaccagtt agttacaaag 240
acattctctg atacattcat tcatagaggt cttaacgtat aaatacatag taaatatcct 300
ataaaatggt aggcaatctc atcgtgcatt atctttttgt gctcagactt gacttcacat 360
tcagtctcta catacagctt gattagaatc ataaaaaca tatgaagacg attgcataaa 420
gggatagttt gacaaagcat attcagatat tgtaacattt atgggtgggt aaaaatgtatc 480
ttttgaaaca atatattaga ctccattttt agctgaaatg aaatttactg attcaatcct 540
tttaagaatt tgtggatgtt tac 563
```

<210> 481
<211> 340
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(340)
<223> n = A,T,C or G

```
<400> 481
ctgaagcgaga ggaacacgct gaaggatggt atcatcatga tccanacgct gctgatcatc 60
ctnntentca tcgtgcctat cttcctgctg ctggacaagg atgacagcaa ggctggcatg 120
gaggaagatc acacctacga gggcctggac attgaccaga cagccaccta tgaggacata 180
gtgacgctgc ggacagggga agtgaagtgg tctgtaggtg agcaccagc ccaggagtga 240
gagccaggtc gccccatgac ctgggtgcag gctccctggc ctcagtgaact gcttcggagc 300
```

tgcttggtc atggccaac cctttcccg gacccccag 340

<210> 482
<211> 353
<212> DNA
<213> Homo sapiens

<400> 482
cgagccatg gctcgtggtc ccaagaagca tctgaagcgg gtggcagctc caaagcattg 60
gatgctggat aaattgaccg gtgtgtttgc tcctcgtcca tccaccggtc cccacaagtt 120
gagagagtgt cccccctca tcattttcct gaggaacaga ctttaagtatg ccctgacagg 180
agatgaagta aagaagattt gcatgcagcg gttcattaaa atcgatggca aggtccgaac 240
tgatataacc taccctgctg gattcatgga tgtcatcagc attgacaaga cgggagagaa 300
tttccgtctg atctatgaca ccaagggctg ctttgctgta catcgtatta cac 353

<210> 483
<211> 202
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(202)
<223> n = A,T,C or G

<400> 483
ctgaagcaga ggaacacgct gaaggatggt atcatcatga tccanacgct gctgatcatc 60
ctattcatca tcgtgcctat cttcctgctg ctggacaagg atgacagcaa ggctggcatg 120
gaggaagatc acncctacga gggcctggac attgaccaga cagccaccta tgaggacata 180
gtgacgctgc ggacaggga ag 202

<210> 484
<211> 306
<212> DNA
<213> Homo sapiens

<400> 484
aaaaacaatc tacaggcagt tctttacaag tctcatatct acagatagca caagctatgg 60
catggcgtat ggccctccctc cttaaatatac gattcttttg catattggaa ttggtcagcc 120
tcaaagaccg gctggctaca tcgtcgacag agacagtccc gcttattcct ctgcacggac 180
tcggagacgg tcctcagcgg gagagctca ggtctccctg ggccagacac gtgccccaga 240
gagtccccag aagcatggac agttctgctc tgtttccatc gctcaggcag gggagagagt 300
ccgtgg 306

<210> 485
<211> 396
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(396)
<223> n = A,T,C or G

<400> 485
ctgttgactc agattcggca ttttaattac attgtttcca agtatgatat tctgagagtg 60
tctatagcac ttagtgtctg cttcatataa actaccagtt attatatatt tatgatgcaa 120
gtagttttcc aaatgtggtg aaagtctgag tctttttatc cccatgggta aaatctgaat 180
ctggctctct gtgtctctca gtgcttggtt attgctggtc agagagtaaa ttcttgataa 240
aagctgtntg anttggctct cacagtttat gcagacattg gagagacaat ttggttattt 300
caaacatcac aggatttgag taagaagacc tggttatgaa acaaggctct cataattact 360
agttatgact gttgacaagg ttaccttttc ttgttt 396

<210> 486
<211> 253
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(253)
<223> n = A,T,C or G

<400> 486
gaaggatggt atcatcatga tccagacgct gctgatcadc ctcttcatca tcgtgcctat 60
cttctctgctg ctggacaagg atgacagcaa ggctggcatg gaggaagatc acacctacga 120
gggcctggac attgaccaga cagccaccta tgaggacata gtgacgctgc ggacagggga 180
agtgaagtgg ttctgtaggt gangcaccca ggccaggagt gagagccagg tcgccccatg 240
acctgggtgc agg 253

<210> 487
<211> 374
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(374)
<223> n = A,T,C or G

<400> 487
agccacttgt ttctcatttg gtcgaaacag cctgcccaca gggatcacca ctgggtcata 60
tagcttctgc ttccagacac actccatcgc cttgtcgatt ttggaatgtc tgggctcaga 120
cttcatgctc gtgggtgtaa tacgatgtac agcaaagcga cccttggtgt catagatcag 180
acggaaattc tctcccgctc tgncaatgct gatgacatcc atgaatccag cagnggtagg 240
tnatatcagt tcggaccttg ccatcnattt taatgaaccg ctgcatgcaa atcttcttta 300
cttcatctnc tgncagggca tacttaagtc tgttcctcag gaaaatgatg agggggagac 360
actctctnna cttg 374

<210> 488
<211> 529
<212> DNA
<213> Homo sapiens

<400> 488
cgcggtgcga cgaaggagta ggtggtggga tctcaccgtg ggtccgatta gccttttctc 60
tgccttgctt gcttgagctt cagcggaatt cgaaatggct ggcggtaagg ctggaaaagga 120
ctccggaaaag gccaaagaaa aggcgggttc ccgctcgcag agagcccgct tgcagttccc 180
agtgggccgt attcatcgac acctaaaatc taggacgacc agtcatggac gtgtggggcg 240
gactgccgct gtgtacagcg cagccatcct ggagtacctc accgcagagg tacttgaact 300
ggcaggaaat gcatcaaaaag acttaaagggt aaagcgtatt acccctcgtc acttgcaact 360
tgctattcgt ggagatgaag aattggattc tctcatcaag gctacaattg ctggtggtgg 420
tgtcattcca cacatccaca aatctctgat tgggaagaaa ggacaacaga agactgtcta 480
aaggatgcct ggatttcctg ttatctcagg actctaaata ctctaacag 529

<210> 489
<211> 402
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(402)
<223> n = A,T,C or G

<400> 489

```
ctgttgactc anattcggca ttttaattac attgtttcca agtatgatat tctgagagtg 60
tctatagcac ttagtgctctg cttcatataa actaccagtt attatatatt tatgatgcaa 120
gtanttttcc aaatgtggng aaagtctgag tctttttatc cccatgggta aaatctgaat 180
ctggctctct gtgtctctca gtgcttgttt attgctgggc agagagtaaa ttcttgataa 240
aanctgttga cttggctctc acagtttatg cagacattgg agagacaatt tggttatttc 300
aaacatcaca ggatttgagt aagaagacct ggttatgaaa caaggctctc ataattacta 360
gttatgactg ttgacaagnt accttttctt gtttacaant ta 402
```

<210> 490

<211> 556

<212> DNA

<213> Homo sapiens

<400> 490

```
gtttgatgac cgtcgcggac gccagtgagg atttcccatg cggggaagag gtggttttga 60
cagaatgcct cctggtcggg gtgggcgtcc catgcctcca tctagaagag attatgatga 120
tatgagccct cgtcaggagc cacctccccc tcttcccgga cgaggcggcc ggggtggtag 180
cagagctcgg aatcttcctc ttcctccacc accaccacct agagggggag acctcatggc 240
ctatgacaga agaggagacg ctggagaccg ttacgacggc atgggttggt tcaagtgcga 300
tgaaacttgg gactctgcaa tagatacatg gagcccatca gaatggcaga tggcttatga 360
accacagggg ggctccggat atgattattc ctatgcaggg ggtcgtggct catatgggtga 420
tcttggttga cctattatta ctacacaagt aactattccc aaagatttgg ctggatctat 480
tattggcaaa ggtggtcagc ggattaaaca aatccgtcat gagtcgggag cttcgcataa 540
aattgatgag ccttta 556
```

<210> 491

<211> 381

<212> DNA

<213> Homo sapiens

<400> 491

```
cctgacacaa tatccctggt cactttgaag tgaattttga ctctatattc agaaccttcc 60
tttaacacaa tggtttcctt tttgagggtc tccagatctc cagtaaggtc catggtgatt 120
gggtccgggg cactctcaca aaccagggtg agccgggtga caacgacatt gggggcttcc 180
ggatctgtca ccacaggacc atctcccagc agcgttttct tgtacttaat tagactctca 240
tcattcttct ccatttcctg cagctcttcc agggacttct gtgggtggagg cttataattg 300
agcttgctgt ccagctcatc atcgtcatcc tcctccacat gtggctcttg ggctttttca 360
gtcattctga tctatttatt c 381
```

<210> 492

<211> 573

<212> DNA

<213> Homo sapiens

<400> 492

```
ccaaaagaag taagacagct tgctgaagat ttcctgaaag actatattca tataaacatt 60
ggtgcacttg aactgagtg aaaccacaac attcttcaga ttgtggatgt gtgtcatgac 120
gtagaaaagg atgaaaaact tattcgtcta atggaagaga tcatgagtga gaaggagaat 180
aaaaccattg tttttgtgga aaccaaaaga agatgtgatg agcttaccag aaaaatgagg 240
agagatgggt ggcctgccat gggatatccat ggtgacaaga gtcaacaaga gcgtgactgg 300
gttctaatag aattcaaaca tggaaaagct cctattctga ttgctacaga tgtggcctcc 360
agagggctag atgtggaaga tgtgaaattt gtcatacaat atgactaccc taactcctca 420
gaggattata ttcatcgaat tggaaagaact gctcgcagta ccaaaacagg cacagcatatc 480
actttcttta cacctaataa cataaagcaa gtgagcgacc ttatctctgt gcttcgtgaa 540
gctaatacag caattaatcc caagttgctt cag 573
```

<210> 493

<211> 288

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(288)

<223> n = A,T,C or G

<400> 493

```
agccattggn tgtagcttta gctcagcgca aagaagagcg ccaggctcac ctactaacc 60
agtatatgca gagaatggca agtgtacgag ctgttcccaa ccctgtaatc aaccctacc 120
agccagcacc tccttcaggt tacttcatgg cagctatccc acagactcag aaccgngctg 180
catactatcc tcctagccaa attgctcaac taagaccaag tcctcgctgg actgctcagg 240
gtgccagacc tcattccattc caaaatatgc ccggtgctat ccgccag 288
```

<210> 494

<211> 574

<212> DNA

<213> Homo sapiens

<400> 494

```
ctgctgtaac caggtttccc cttgtgggaa gtgtgtgttc ttgctgggca gttgggaagg 60
gaatggagaa cagagaagag agtggaaatc acatgctcac ttgaactttc ctggggaacg 120
tctcctcaca gcgtacacaa gagcctccct ttagaaatgg agtgttcatt ttatcatggg 180
aaaagaatct gagtgggaca tgattcagaa caggaccggc ccaaggaagt gcaggggctg 240
tggaagtggga tggagacaag ctctgaaagg acacatggga gatctagatg tagaagggtac 300
acaagtagta ggataactca caggatggat ccactggagg ttaagacatg tggtaagaca 360
gtgtaaatagg aagctgctca gttggagaaa gtaagggaagc aaacattgtt accgtggggg 420
caatggagag gacagtggag agccctttat cctgataagg gtggctttga ggtaaaggaa 480
ggaaagagga tgcttgaga ggccccactg tattagagag gacctggaag ccaggatgct 540
aattctgggg agatggattc cccaggctta ctct 574
```

<210> 495

<211> 471

<212> DNA

<213> Homo sapiens

<400> 495

```
ccaccacca tttcttcgag gatattcagt gtataccttc tcattagctg ccaaatcaag 60
gccagtgtga gagtgcggtt tccttcattg agatcttgtc caccgatgcc aaccagggag 120
aacttcgctt gattcttccc caattctacc gcgtagttac aattctcaag cttcttcata 180
ttgcctccca gtttggggta tggcggtttg tttactctgt tccagtcaac aggaactttg 240
atcttttcat agagctggaa gatgaccagg gcatctgata agtcactgta caaatgattg 300
actcgagggt taacacccag ggagttcatc cagttcctaa atgtccgctc ttctctcgtc 360
tcaccttcaa gagcccccca gtcaatgtcc tggttctctg gtttgtgcag ggcagggtat 420
ctgttaaaga ggttggaat aaaagccaag ttcaacttgg ggttccctcg g 471
```

<210> 496

<211> 489

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(489)

<223> n = A,T,C or G

<400> 496

```
ctgttgactc agattcggca ttttaattac attgtttcca agtatgatat tctgagagtg 60
tctatagcac ttagtgtctg cttcatataa actaccagtt attatatatt tatgatgcaa 120
gtagttttcc aaatgtggtg aaagtctgag tctttttatc cccatgggta aaatctgaat 180
ctggctctct gtgtctntca gtgcttgttt attgctggtc agagagtaaa ttcttgataa 240
aagctgttga cttggctctc acagttttatg canacattgg agagacaatt tggttatttc 300
aaacatcaca ggatnngagt aagaanacct ggttatgaaa caaggctctc ataattacta 360
gttatgactg ttgacaagtt accttntctt gnttacaagt tatttggcct ctttgaatta 420
cttgnaaaat agagataggg attctttctt gatcatggaa catcnaatga agttatnnga 480
tgaaatact 489
```

<210> 497
<211> 306
<212> DNA
<213> Homo sapiens

<400> 497
ctgctgcacc cagagctcct ttgggtctgc acatagctct gcctgagagc gcttgccggg 60
caagaacagg atagctggga tggagcagcc caagcttggt tcctgcttcc ggtagctgcg 120
gacaaccttg gcgggaatct tcctttggct gtacttgagg caacagtcct gagccccctcc 180
atcactgcct tgggtcctgg ggatgccaaa ggccagaacc aggataagga ggctcagagc 240
cagtactga gccatgtctg tggtagaggg tgagtaagag gccagagctg agggtagaggt 300
gggcag 306

<210> 498
<211> 345
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(345)
<223> n = A,T,C or G

<400> 498
ccaatgtggt tggctctcag cttgcagtta gccagggttc ataccttgac cagcttgtcc 60
cagccacagg agacgatgat aggggttgctg ctgttgggag agaagcggac acaagacacc 120
cactctgagt ggctctcatc ctggacagtg tatttgaca caccagggt attccatagc 180
ttgatggttt tatctcgaga tccanagaca atctgccggt tgtcagagga gaaggccaca 240
ctcancacat ccttggcatg gccacaaaat cgnctnctgg tggtgcccgt tgtgagatcc 300
cagagggcga gggttccatc ccaggagcct gagagggcaa actgg 345

<210> 499
<211> 555
<212> DNA
<213> Homo sapiens

<400> 499
ctgttgactc agattcggca ttttaattac attgtttcca agtatgat tctgagagt 60
tctatagcac ttagtgtctg cttcatataa actaccagtt attatatatt tatgatgcaa 120
gtagttttcc aaatgtggtg aaagtctgag tctttttatc cccatgggta aaatctgaat 180
ctggctctct gtgtctctca gtgcttggtt attgctggtc agagagtaaa ttcttgataa 240
aagctgttga cttggctccc acagtttatg cagacattgg agagacaatt tggttatttc 300
aaacatcaca ggatttgagt aagaagacct gggtatgaaa caaggctctc ataattacta 360
gttatgactg ttgacaagtt accctttctt gtttacaagt tatttggcct ctttgaatta 420
cttgtaaaat agagataggg attctttctt gatcatggaa catcaaatga agttatttga 480
tgaaataact tgtcatctgg aaattataaa tataactaaa tgtaattat tatttgaat 540
ttgggcaccc catgg 555

<210> 500
<211> 340
<212> DNA
<213> Homo sapiens

<400> 500
ctgggggggc cgggaaaggg gttgggcat gagccaggca gctccgaagc agtcaactgag 60
gccaggagc ctgcaccag gtcattgggc gacctggctc tcaactcctgg cctgggtgct 120
cacctacaga ccacttcaat tcccctgtcc gcagcgtcac tatgtcctca taggtggctg 180
tctgtgcaat gtccaggccc tcgtaggtgt gatcttctc catgccagcc ttgctgtcat 240
ccttggtccag cagcagggaag ataggcacga tgatgaagag gatgatcagc agcgtctgga 300
tcatgatgat accatccttc agcgtgttcc tctgcttcag 340

<210> 501
<211> 482

<212> DNA

<213> Homo sapiens

<400> 501

```
aaaaaacag aacatttaca agacaccagt tattttgtgc cccatatgtc attaaaaaag 60
tttactttac ctttattatt atttccctag gctagtcaag cagcaaacca ttaatcggtc 120
ggagaaacct tcatgacata tgcccactg gctcttcgcc acccacttga aggacactac 180
ccaatcgatg gaagccttta atcgcacagc cctccctatt agcggactat tggcggatgc 240
agacatgttc tactcgagca gttaccaagg accactttac tgcgatcagg attccaacga 300
ccacctaatt tcgtatcttt caactctttt cgaccggacc tcttattcgg aagcgttaca 360
ggaagacagg tctcaactta gggatcagat cacgttatca acgctctggg atcgctgcaa 420
cctggcactt caaggaagtg caccgataac gtctagaccg gcaaacacag atctagaggt 480
gg                                         482
```

<210> 502

<211> 448

<212> DNA

<213> Homo sapiens

<400> 502

```
gaaagaatcc ctatctctat tttaacaagta attcaaagag gccaaataac ttgtaaacaa 60
gaaaaggtaa cttgtcaaca gtcataacta gtaattatga gaggcttgtt tcataaccag 120
gtcttcttac tcaaatcctg tgatgtttga aataaccaa ttgtctctcc aatgtctgca 180
taaaactgtga gagccaagtc aacagctttt atcaagaatt tactctctga ccagcaataa 240
acaagcactg agagacacag agagccagat tcagatttta cccatgggga taaaaagact 300
cagactttca ccacatttgg aaaactactt gcatcataaa tatataataa ctggtagttt 360
atatgaagca gacactaagt gctatagaca ctctcagaat atcatacttg gaaacaatgt 420
aattaaaatg ccgaatctga gtcaacag                                         448
```

<210> 503

<211> 573

<212> DNA

<213> Homo sapiens

<400> 503

```
ccaaaagaag taagacagct tgctgaagat ttcctgaaag actatatcca tataaacatt 60
gggtgcacttg aactgagtgc aaaccacaac attcttcaga ttgtggatgt gtgtcatgac 120
gtagaaaagg atgaaaaact tattcgtcta atggaagaga tcatgagtga gaaggagaat 180
aaaaccattg tttttgtgga aacaaaaaga agatgtgatg agcttaccag aaaaatgagg 240
agagatgggt ggcctgccat gggatatccat ggtgacaaga gtcaacaaga gcgtgactgg 300
gttctaaatg aattcaaaca tggaaaagct cctattctga ttgctacaga tgtggcctcc 360
agagggctag atgtggaaga tgtgaaattt gtcatacaatt atgactacc taactcctca 420
gaggattata ttcatcgaat tggagaact gctcgagta ccaaaacagg cacagcatac 480
actttcttta cacctaataa cataaagcaa gtgagcgacc ttatctctgt gcttcgtgaa 540
gctaatacag caattaatcc caagtgtgctt cag                                         573
```

<210> 504

<211> 340

<212> DNA

<213> Homo sapiens

<400> 504

```
ctgggggggtc cgggaaaggg gttgggcat gagccaggca gctccgaagc agtcactgag 60
gccagggagc ctgcaccag gtcattgggc gacctggctc tcaactcctg cctgggtgct 120
cacctacaga ccacttcact tcccctgtcc gcagcgtcac tatgtcctca taggtggctg 180
tctggtcaat gtccaggccc tcgtaggtgt gatcttcctc catgccagcc ttgctgtcat 240
ccttgccag cagcaggaag ataggcacga tgatgaagag gatgatcagc agcgtctgga 300
tcatgatgat accatccttc agcgtgttcc tctgcttcag                                         340
```

<210> 505

<211> 593

<212> DNA

<213> Homo sapiens

<400> 505

```
atctcgacat ctctgcttct catgctgctg gtcagcagcc tctctccagt ccaaggtgtt 60
ctggagggtct attacacaag cttgagggtg agatgtgtcc aagagagctc agtctttatc 120
cctagacgct tcattgatcg aattcaaatc ttgccccgtg ggaatgggtg tccaagaaaa 180
gaaatcatag tctggaagaa gaacaagtca attgtgtgtg tggaccctca agctgaatgg 240
atacaaagaa tgatggaagt attgagaaaa agaagttctt caactctacc agttccagt 300
tttaagagaa agattccctg atgctgatat ttccactaag aacacctgca ttcttccctt 360
atccctgctc tggattttag ttttgtgctt agttaaatct tttccaggaa aaagaacttc 420
cccatacaaa taagcatgag actatgtaaa aataaccttg cagaagctga tggggcaaac 480
tcaagcttct tcactcacag caccctatat acacttggag tttgcattct tattcatcgg 540
ggagggaaagt ttctttgaaa atagtatttc agttataagt aatacaggat tat 593
```

<210> 506

<211> 425

<212> DNA

<213> Homo sapiens

<400> 506

```
cctgggtgaa agaaggctct agaacctgct tatagagcca caacagggtg cagacaactg 60
tgatgtcaac caatgtcact cgttcgcca ccagaaaagt cctcgtcttc aagtaagcat 120
ccagcagccc cagaattcgc ctcaacttct cctttgcatt ctcaagtggc tgtttgtgtg 180
ggtgcatgat gcccaagggt gggaacaccc aggtactggc tgggggcaact atatcggaat 240
cagcaaagct caccactgc accacctggg ctgctgcctc tggagtactt ccccgagct 300
cctcattgct cacatagtag gcaatggcgt tgctctcaaa cacacagaat ccatcatcac 360
cctcaaagtc tgggaccttg ccggcaggaa atttgcggag aaattcaggg gtgcgggttg 420
tttgg 425
```

<210> 507

<211> 603

<212> DNA

<213> Homo sapiens

<400> 507

```
aaaaaaactt gtgcaaattg caatcactga gtgattatgg aaaggcaaag tatatacagt 60
aatgtgagag aaactcaaac caagtaaggg taaaaatgaa atgattaaca ccaccagagg 120
aggaagctac tatcaaaata aaaccatact tcctaataaa ggtaaggcca tcataacccc 180
agaaaatgct tcatacttta gataattaaa aacacattat aaccaaaagc agatagtaac 240
attgagtatg ctgatttcaa aaagaagatg ggtctagata ccaggacagc tctttttagt 300
gccttcctta aaaagggcaa aacttttttag agccatgtaa ttgtttatag ccatggcctg 360
gcttcaggca tctcataagt gaggcttcag aaagtcttg aagagtatat ggcagtga 420
ctgggctccc atctttacca taaagatgtt cttcttgaga ataagtgc ataggaagt 480
atcgcttatg acatcatttc attgatcttg aggccatata aagagacttg ctgatattag 540
agcagtttct ttctaataca tattccgctg aattccaagc aatgaggcac acaccagttt 600
gtc 603
```

<210> 508

<211> 578

<212> DNA

<213> Homo sapiens

<400> 508

```
ctgctgtgga agggctcctt caagcccagc gagcatgtga aaccaggggc cccaggaaac 60
ctgacagttc acaccaatgt ctccgacact ctgctgctga cctggagcaa cccgtatccc 120
cctgacaatt acctgtataa tcatctcacc tatgcagtca acatttgag tgaaaacgac 180
ccggcagatt tcagaatcta taacgtgacc tacctagaac cctccctccg catcgagccc 240
agcaccctga agtctgggat ttctacagg gcacgggtga gggcctgggc tcagtgtat 300
aacaccacct ggagtgaagt gagccccagc accaagtggc acaactccta cagggagccc 360
ttcgagcagc acctcctgct gggcgtagc gcttctgca ttgtcatcct ggccgtctgc 420
ctgttgtgct atgtcagcat caccaagatt aagaaagaat ggtgggatca gattcccaac 480
ccagcccgca gccgcctcgt ggctataata atccaggatg ctcaggggtc acagtgggag 540
aagcgggtccc gagggcagga accagccaag tgcccaca 578
```

<210> 509
<211> 568
<212> DNA
<213> Homo sapiens

<400> 509
ctcagagctc aagtctgaac tctacctcca gacagaatga agttcatctc gacatctctg 60
cttctcatgc tgctggtcag cagcctctct ccagtcgaag gtgttctgga ggtctattac 120
acaagcttga ggtgtagatg tgtccaagag agctcagctt ttatccctag acgcttcatt 180
gatcgaattc aaatcttgcc ccgtgggaat ggttgccaa gaaaagaaat catagtctgg 240
aagaagaaca agtcaattgt gtgtgtggac cctcaagctg aatggataca aagaatgatg 300
gaagtattga gaaaaagaag ttcttcaact ctaccagttc cagtgtttaa gagaaagatt 360
ccctgatgct gatatttcca ctaagaacac ctgcattctt cccttatccc tgctctggat 420
tttagttttg tgcttagtta aatcttttcc aggaaaaaga acttccccat acaaataagc 480
atgagactat gtaaaaataa ccttgacaga gctgatgggg caaactcaag cttcttcact 540
cacagcacc c tatatacact tggagttt 568

<210> 510
<211> 125
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(125)
<223> n = A,T,C or G

<400> 510
ctgggggggc caggaaaggg gttggggccat gagccaggca gctccgaagc agtcactgag 60
gccagggagc ctgcaccagc nncatgggnc gaccnnggctc tcaactcctgg cctgggtgct 120
cacct 125

<210> 511
<211> 231
<212> DNA
<213> Homo sapiens

<400> 511
aaacttgatc caacctcttt gcatcttaca aagttaaaca gctaaaagaa gtaaaataag 60
aaggcaatgc ttgtggaatg tacagtgcac attggcgggc cagcctcat tacgattcgc 120
ctgcttgctt ctctgttcca atcgtttctt tggaaggcag tggatttttc tcttgcgtct 180
ctgtcttctt cagtttcgac ttatcgaatt tctcgatctc agccatatcg g 231

<210> 512
<211> 278
<212> DNA
<213> Homo sapiens

<400> 512
aaaatatccc tgaagtgaac cactcctttt ttgagaccga tactggtatt cttttattat 60
agagactaaa aggtctgcct tactagactt cccacttttt gttctgaaag gaattaagga 120
ctgcagggtt ccagctctgt cttcccgagg ccattatgaa cagattaaat ggaaggacaa 180
attctaaata actgggcttt caacatgaaa agggaaaggc tgatggggag ttcagaacct 240
tgaatactgt aactgaacat ccctcaaggt taatgcag 278

<210> 513
<211> 288
<212> DNA
<213> Homo sapiens

<400> 513
aaaaatacag cttttattct gagacattga ccttcactag agtgggacct gtggccccag 60
cctggctgga gaagcagtc agggcctgag tgacaccatt tccctttcct gaaataggaa 120

caagttattc caaaggagaa aggagagccc agagagatct gtacaggacc tctcttgac 180
atggtgactg gaggcagagg gtggggagct ggagaggagt ccagtcctc caacaaatat 240
tgagggcttc aaagagctct tcctggacgt ttctcttaat ctggattt 288

<210> 514
<211> 284
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(284)
<223> n = A,T,C or G

<400> 514
ggcggcaaga tggcagtga aatatccaag aagaggaagt ttgtcgtga tggcatcttc 60
aaagtgaac tgaatgagtt tcttactcgg gagctggctg aagatggcta ctctggagtt 120
gagggcgca gttacaccaa ccaggacaga aatcattatc ttanccacca gaacacanaa 180
tgttcttggt gagaagggcc ggcggattcg ggaactgact gctgtagttc agaagaggtt 240
tggtctttcca gagggcagtg tagagcttta tgctnaaaag gtgg 284

<210> 515
<211> 211
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(211)
<223> n = A,T,C or G

<400> 515
ctgtctcaca ctttacaagc tgtgagagac acatcagagc cctgggcact gtcactgctt 60
gcagcctgag agtagctccc tccttttcta tctgagctgt tcctcctcca catcacagca 120
gcgaccacag ctccagtgat cacagctcca aggagaacca ggccagcaat gatgccacg 180
atggggacgg tgggctggga aganggctcc n 211

<210> 516
<211> 212
<212> DNA
<213> Homo sapiens

<400> 516
ccaatgtggt tggctctcag cttgcagtta gccagggtcc atacctgac cagcttgtcc 60
cagccacagg agacgatgat agggttgctg ctgttggcg agaagcggac acaagacacc 120
cactctgagt ggctctcatc ctggacagtg tatttgcaca cccccagggt attccatagc 180
ttgatgggtt tatctcgaga tccaaaaaca at 212

<210> 517
<211> 272
<212> DNA
<213> Homo sapiens

<400> 517
ccaaaagaag taagacagct tgctgaagat ttcctgaaag actatatcca tataaacatt 60
ggtgcacttg aactgagtgc aaaccacaac attcttcaga ttgtggatgt gtgtcatgac 120
gtagaaaagg atgaaaaact tattcgtcta atggaagaga tcatgagtga gaaggagaat 180
aaaaccattg tttttgtgga aaccaaaga agatgtgatg agcttaccag aaaaatgagg 240
agagatgggt ggctgcatc gggtatccat gg 272

<210> 518
<211> 285
<212> DNA

<213> Homo sapiens

<400> 518

```
cctttccttg agctgcacgt gaacctgtgt gggcaggcag cgtttgcagg cgtgtttacg 60
ggcagggcagc gtttgcaggc gtgtttaccg gcaggcagcg tttgcaggcg tgtttacatg 120
caggcgtagc accatgtgag accactggtc cagggtttca gaggtcctgc tcagggtgaat 180
cggctgtgtt ctcacaagtt cacggagctg agtgggtgtg caacatgaaa tactagtgtc 240
gtgagggaca gaaaggacag aaagaggctg aagaccatca tccag 285
```

<210> 519

<211> 287

<212> DNA

<213> Homo sapiens

<400> 519

```
ctctggcctc ttactcaccc tctaccacag acatggctca gtcactggct ctgagcctcc 60
ttaccctggt tctggccttt ggcattccca ggaccaagc cagtgatgga ggggctcagg 120
actgttgctt caagtacagc caaaggaaga ttcccgcctc ggtgtgtccg agctaccgga 180
agcaggaacc aagcttaggc tgctccatcc cagctatcct gttcttgccc cgcaagcgct 240
ctcaggcaga gctatgtgca gaccctaaag agctctgggt gcagcag 287
```

<210> 520

<211> 286

<212> DNA

<213> Homo sapiens

<400> 520

```
ccagagcggg gagtcccacc acctcgaact ctgggaattc gagccacagc tctgccagta 60
ccccaagact cagcactagt ctgatgacct gctaattcac tgacagcata gggctgtctg 120
ttgtttttgc gcaagttggt gtgaacaaag ttcacaatat ctggtcgaat aggagccttg 180
aatacagcag gcaaagtgc atttttgccg gatgactccc ccttttcgga gtacaccgat 240
atcagtgggc gagcacacgc catggcgagg agaggagaca gccacg 286
```

<210> 521

<211> 242

<212> DNA

<213> Homo sapiens

<400> 521

```
ctgggagagc tagactaagt tggatcatgat gcagaagcta ctcaaatgca gtcggcttgt 60
cctggctctt gccctcatcc tggttctgga atcctcagtt caagggtatc ctacgcagag 120
agccaggtag caatgggtgc gctgcaatcc agacagtaat tctgcaaat gccttgaaga 180
aaaaggacca atgttcgaac tacttccagg tgaatccaac aagatcccc gtctgaggac 240
tg 242
```

<210> 522

<211> 132

<212> DNA

<213> Homo sapiens

<400> 522

```
ctgcttccat tggtaggtca tttttgctgt caccagcaac gttgccacga cgaacatcct 60
tgacagacac attcttgaca ttgaagccca cattgtcccc aggaagagct tcaactaaag 120
cttcatggtg ca 132
```

<210> 523

<211> 414

<212> DNA

<213> Homo sapiens

<400> 523

```
cctgacacaa tatccctgtt cactttgaag tgaattttga ctctatatc agaaccttcc 60
tttaacacaa tggtttcctt tttgagggt tccagatctc cagtaaggct catggtgatt 120
```

```
gggtcccgagg cactctcaca aaccagggtg agccgggtga caacgacatt gggggctttc 180
ggatctgtca ccacaggacc atctcccagc agcgttttct tgtacttaat tagactctca 240
tcatttttgt ccatttcctg cagctctttc agggacttct gtgggtggagg cttataattg 300
agcttgctgt ccagctcatc atcgtcatcc tcctccacat gtgggctctg gggctttttc 360
agtcattctg atctatttat tcagtgtctc acgtctctgt ccgggggtgcc tctg 414
```

<210> 524

<211> 104

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(104)

<223> n = A,T,C or G

<400> 524

```
tatttaaaaa ctcaacagga cctacactac ntgttcaaat ctgtaatctt tcacaccnca 60
ctaacaaagt tnttaggaaa acaggactac ccaaanatgt tacc 104
```

<210> 525

<211> 423

<212> DNA

<213> Homo sapiens

<400> 525

```
attgacactt cctgggtggga tccgagttag ggcacggggg aggggttggc gctcaggcgg 60
cgaccatggc gtatcacggc ctcaactgtg ctctcattgt gatgagcgtg ttctggggct 120
tcgtcgggct cttgggtgct tgggtcatcc ctaagggtcc taaccgggga gttatcatta 180
ccatgttggt gacctgttca gtttgcctgt atctcttttg gctgattgca attctggccc 240
aactcaaccc tctcttttga ccgcaattga aaaatgaaac catctgggat ctgaagtatc 300
attggccttg aggaagaaga catgctctac agtgctcagt ctttgaggtc acgagaagag 360
aatgccttct agatgcaaaa tcacctccaa accagaccac ttttcttgac ttgcctgttt 420
tgg 423
```

<210> 526

<211> 478

<212> DNA

<213> Homo sapiens

<400> 526

```
ctggctaggt gtgtgtgtat gtgagttagg gtgctattga ttggcacata tttccccccc 60
tggagtttag ggggtggcaga aagcttttat agtaccaaaa aagtaaacat tgataatatg 120
gcctgacaac aatcagatat gctaagctct agaagcaaaa gcaaggtagg attgcctcca 180
aatgttgaca ggtattagcc ataccacagt aactagatct aatgtgaggg ctaaatgcct 240
ggagaggcag aaccctaaag gatgcttagt tatagctcca tgctgccgcc gagtggcttg 300
atgctccatt acaccctcct tggatccaac cttccattaa ggctgaaggc tctagagggc 360
agagtattca agatgttaga tctggtccaa gcccaaatte tagagttaaa agcagagggg 420
ttcttagtgg ctgaaaaaaaa acaaaacctg atgacatttg ggactccagt tttgagga 478
```

<210> 527

<211> 384

<212> DNA

<213> Homo sapiens

<400> 527

```
cctgacacaa tatccctgtt cactttgaag tgaattttga ctctatattc agaaccttcc 60
tttaacacaa tggtttcctt tttgagggtc tccagatctc cagtaaggtc catggtgatt 120
gggtcccgagg cactctcaca aaccagggtg agccgggtga caacgacatt gggggctttc 180
ggatctgtca ccacaggacc atctcccagc agcgttttct tgtacttaat tagactctca 240
tcatttttgt ccatttcctg cagctctttc agggacttct gtgggtggagg cttataattg 300
agcttgctgt ccagctcatc atcgtcatcc tcctccacat gtgggctctg ggctttttca 360
gtcattctga tctatttatt cagt 384
```

<210> 528
<211> 208
<212> DNA
<213> Homo sapiens

<400> 528
aagctactca aatgcagtcg gcttgtcctg gctcttgccc tcacccctggt tctggaatcc 60
tcagttcaag gttatcctac gcagagagcc aggtaccaat ggggtgcgctg caatccagac 120
agtaattctg caaactgcct tgaagaaaaa ggaccaatgt tcgaactact tccaggtgaa 180
tccaacaaga tcccccgctc gaggactg 208

<210> 529
<211> 330
<212> DNA
<213> Homo sapiens

<400> 529
ccacacagcc cctgtgctag acatcgccctg gtgcccgcac aatgacaacg tcattgccag 60
tggctccgag gactgcacag tcattggtgtg ggagatcccg gatggggggcc tgatgctgcc 120
cctgctggag cccgtcgtca ccctggaggg ccacaccaag cgtgtgggca ttgtggcctg 180
gcacaccaca gcccagaacg tgctgctcag tgcaggttgt gacaacgtga tcattggtgtg 240
ggacgtgggc actggggcgg ccattgctgac actggggcca gaggtgcacc cagacacgat 300
ctacagtgtg gactggagcc gagatggagg 330

<210> 530
<211> 294
<212> DNA
<213> Homo sapiens

<400> 530
ccaaactcct ccagatgccg gacggtctcc ttcttgtcca gatccacata gaacatctca 60
tcttcatcaa attcaaacat aaactcccct gttggtctat gcgtctgtac aaacggggca 120
taagttagca catggtccgc cttgatggcc ccagctcctc ggagactcag caggaaagcc 180
aaggagaggg ctctcaagat cacagctctg atatggaaca ttctgtcttc agggcgcatg 240
ttgtggggtc tataattgat gactgtgagc acaggaacag tgatgaggaa ctga 294

<210> 531
<211> 269
<212> DNA
<213> Homo sapiens

<400> 531
ccacaggctt ctaccccgac cacgtggagc tgagctggtg ggtgaatggg aaggaggtgc 60
acagtggggg cagcacagac ccgagccccc tcaaggagca gcccgcctc aatgactcca 120
gatactgcct gagcagccgc ctgaggggtc cggccacctt ctggcagaac ccccgcaacc 180
acttccgctg tcaagtccag ttctacgggc tctcggagaa tgacgagtgg acccaggata 240
gggccaaacc tgcacccag atcgtcagc 269

<210> 532
<211> 197
<212> DNA
<213> Homo sapiens

<400> 532
cctgaacaag gacctctgcc ctccctattc agacccttcg ttgcctcacc tgggtcaatac 60
aaccacttca cctctgaccg caggggcagg ggactagata gaatgaccta ctgagcctcg 120
tctgtctgtc tgtctgtctg tctctctctc tctgtttgtc tctttgtgtg tccgacaaga 180
accagactg agggggc 197

<210> 533
<211> 364
<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(364)

<223> n = A,T,C or G

<400> 533

```
ggcatcatatc tcctatngtn atgagaagcc ctctgccatc cagcagcgag ccattctacc 60
ttgtatcaag ggttatgatg tgattgctca agcccaatct gggactggga aaacggccac 120
atttgccata tcgattctgc ancagattga attagatcta aaagccaccc aggccttggc 180
cctagcacc cactcgagaat tggctcagca gatacagaag gtggtcatgg cactaggaga 240
ctacatgggc gcctcctgtc acgcctgtat ccggggcacc aacgtgcngt gctgacgtgc 300
ataaactgca natggaactc cccacatcat cgtgggtacc cctggccgng tgnnttga 360
tgcn 364
```

<210> 534

<211> 382

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(382)

<223> n = A,T,C or G

<400> 534

```
tcaggacaca gcatggacat gagggctccc gctcagctcc tggggctcct gctgctctgg 60
ctcccagggtg ccaaattgta catccagatg acccaatctc cttccaccct gtctgcatct 120
gtcggagata caagttacaa taagtgtcgc gccctctcag aatatagac ggtggttggc 180
ctggcatcaa cagaaaccag gcaaagcccc taatgtccta atttatgcga cttccagttt 240
agaagaagggt gtctcattaa gatttactgg cagtggatct gggacacaat tcaatttaac 300
catcaccagt ctgcagcctg acgattcagc aacttattat tgncaacatt attctgcac 360
tcttcgcagt ttttgacct cg 382
```

<210> 535

<211> 349

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(349)

<223> n = A,T,C or G

<400> 535

```
aaaaaattta ctcatcttcc ataaagcgac ttttaattgta tcaacactta aagatacaca 60
gtgacttaaat gaaatatcag cacaactgca tagaattgag ctccagagaa ttatacactc 120
gagctgcttt cctgggctct ggtttataag ggtattggct tagagaccag cttggagtca 180
tttgccccta ccggggaat gcaggccagg aaacttaaga ttttgcgggc cttttctgtt 240
tctaggtaaa atgcagggag ctccctgaag gncttgaaaa ccatcaacca ttcaaatatg 300
gtatcctctgg gacctttcct cttgagttaa nggaagaaag gaggtttgg 349
```

<210> 536

<211> 170

<212> DNA

<213> Homo sapiens

<400> 536

```
ccgcccgggg tccgtgcgcc cagcgtccca gggcccaggc cgagcagaca aagatcatc 60
cactcagcct gggacgatgg ggaggaaaaa aatccagatc tcccgcaccc tggaccaaa 120
gaatcggcag gtgacgttca ccaagcggaa gttcgggctg atgaagaagg 170
```


<210> 537
<211> 387
<212> DNA
<213> Homo sapiens

<400> 537
aaattttctca aataactaag tcttactaa ggcagcagtt caaaactgtt ccaggaatta 60
aaatatattc ccatttgagg agtcttcctt cacaccttca cctcctcagc cttaagtata 120
tacacacaca cccaacaccc tcaatacttg actagcaaca ggctttacca tctttacctg 180
acaatgaccc cagggcggag atcgaaattc ttcttcacaa tctctaatag ctctctctca 240
ctcttctgag aggtaccata atggaaaatg gagatagata atggatgaga aactccaata 300
gcataagaga cctgaacaag aaccctccgg cacagacctc ctttaacaag ggattttgcc 360
accacaacgag cagcataaag agacctg 387

<210> 538
<211> 533
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(533)
<223> n = A,T,C or G

<400> 538
cttgccctgct gctctggccc ctggctctgt cctgttctcc agcatgggtg gtctgaggct 60
ccctggaggc tcctgcatgg cagttctgac agtgacactg atgggtgctga gctccccact 120
ggctttggct ggggacacca gaccacgttt cttggagtag tctacgtctg agtgtcattt 180
cttcaatggg acggagcggg tgcggttcct ggacagatac ttctataaac aagaggagta 240
cgtgcgcttc gacagcgacg tgggggagtt ccgggcggtg acggagctgg ggcggcctga 300
tgaggagtag tggaaacagcc agaaggactt cctggaagac agggggggcc cggtggacac 360
ctactgcaga cacaactacg gggttggtga gagcttcaca gtgcagcggc gagtccatcc 420
taaggtgact gtgtatcctt caaagaccca cccctgcagc accacaacct cctggtctgt 480
tctgngagtg gtttctatcc aggcagcatt gaatcangtg gttccggaat ggn 533

<210> 539
<211> 332
<212> DNA
<213> Homo sapiens

<400> 539
tcgccctgaa cgaggacctg cgctcttgga ccgcggcgga catggcggct cagatcacca 60
agcgcaagtg ggaggcgccc catgaggcgg agcagttgag agcctacctg gatggcacgt 120
gcgtggagtg gctccgcaga tacctggaga acgggaagga gacgctgcag cgcacggacc 180
ccccaagac acatatgacc caccacccca tctctgacca tgaggccacc ctgagggtgt 240
gggccctggg cttctaccct cgggagatca cactgacctg gcagcgggat ggggaggacc 300
agaccagga cacggagctc gtggagacca gg 332

<210> 540
<211> 375
<212> DNA
<213> Homo sapiens

<400> 540
ccaaaactgc gaagagatgc agaataatgt tgacaataat aagttgctga atcgtcaggc 60
tgcagactgg tgatgggttaa attgaattgt gtcccagatc cactgccagt aaatcttaat 120
gagacccctt cttctaaact ggaagtcgca taaattagga cattaggggc ttgacctggt 180
ttctgttgat gccaggccaa ccaccgatct atattctgag agggccgaca acttattgta 240
actgtatctc cgacagatgc agacaggggtg gaaggagatt gggtcactct gatgtcacat 300
ttggcacctg ggagccagag cagcaggagc cccaggagct gagcggggac cctcatgtcc 360
atgctgtgtc ctgac 375

<210> 541

<211> 443
<212> DNA
<213> Homo sapiens

<400> 541
ccatttgact aaccagtcct acaaatttca catatccgtc actcagatga gcatatacca 60
agtcagagga aacaaaacat gcacatatatc aaaagtagaa agagaaaaca ctcatgcctt 120
cagaagtcca caaattaaaa gccctttaat aatataaaac agttgaacac tggaaatgtt 180
ttttctaggt catgaaaaaa gtgaattcca aatctatgta ataaatctaa aataatacag 240
catcactgtc ttctgttctg gtgtttatca aacctgcaca tgagttttta gaagggtgaat 300
tggggatgct tcagaatgta ttttctccaa acagatggag cctgaaaact gtgtgatttt 360
ccaaaccaag tggagaaaaa caggaagaaa ttggtgttta gctggtcagc agacggggat 420
ccccgggatg caatcagcct tgg 443

<210> 542
<211> 232
<212> DNA
<213> Homo sapiens

<400> 542
gctaaaccaa aagaagcctc cagacagccc tgagatcacc taaaaagctg ctaccaagac 60
agccacgaag atcctaccaa aatgaagcgc ttctcttccc tcctactcac catcagcctc 120
ctggttatgg tacagatata aactggactc tcaggacaaa acgacaccag ccaaaccagc 180
agcccctcag catccagcag catgagcgga ggcattttcc ttttcttcgt gg 232

<210> 543
<211> 392
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(392)
<223> n = A,T,C or G

<400> 543
ngtcttgctt gctgctctgg cccctgggtc tgtcctgttc tccagcatgg tgtgtctgag 60
gctccctgga ggctcctgca tggcagttct gacagtgcaca ctgatgggtc tgagctcccc 120
acttgctttg ggctggggac accagaccac gtttcttga gtactctacg tctgagtgtc 180
atttcttcaa tgggacggag cgggtgcggt tcctggacag atacttctat aaccaagag 240
agtacgtgag cttcgacagc gacgtggggg agttccgggc ggtgacngag ctggggcggg 300
ctgatgagga gtactggaac agccannaag gacttcctgg aanacagcgg ggnccgggtg 360
gacacctact gcanacacaa ctacgggggt gg 392

<210> 544
<211> 371
<212> DNA
<213> Homo sapiens

<400> 544
ggacacagca tggacatgag ggtccccgct cagctcctgg ggctcctgct gctctggctc 60
ccagggtgcca aatgtgacat ccagatgacc caatctcctt ccaccctgtc tgcattctgcc 120
ggaaatacag ttacaataag ttgtcggggc tctcagaata tagatcgggtg gttggcctgg 180
catcaacaga aaccaggcaa agcccctaatt gtcctaattt atgcgacttc cagtttagaa 240
gaaggggtct cattaaagatt tactggcagt ggatctggga cacaattcaa tttaaccatc 300
accagtctgc agcctgacga ttcagcaact tattattgtc aacattatcc tgcattctctt 360
cgcagttttg g 371

<210> 545
<211> 187
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(187)
<223> n = A,T,C or G

<400> 545
gacctgctcg gaggaatggc gccgccgggt tcaagcactg tcttcctgtt ggccctgaca 60
atcatagcca gcacctgggc tctgacgccc actcactacc tcaccaagca tgacngggag 120
agactaaaag cctcgctgga tccgcccttt cacaaagtgt gaagtctngt cttctactcc 180
atcntgg 187

<210> 546
<211> 558
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(558)
<223> n = A,T,C or G

<400> 546
ccatgggatg gctcttctga ccattggggg ccaggccagg ccaggccagg cttagggcag 60
caaggaccag gccaaaaggg cagggcctcc tttggagggg ttgaggggta catcctcggc 120
tggtgtttgc atccaggggt ccagcaggat ctcttcagt gagggtcggg aagaagggtt 180
gggggccagg caccggcgga ttagggcaca gcaatcttgg ggaaaacatg ggcttgggaa 240
gtggagctca gcttcagaa tctcctgtgc cctctcaaag ggaatgtccc cacacacat 300
gtcatagagg aggatgccca gtgaccagac agtggccggg agtgcatggt actggtgtcg 360
agagatccac tctggggggc tgtacaccct tgtcccatca aagtcagtgt agggttcatc 420
atgaagcagg gcaccagaac caaatcaat gagtttggca cagccacggc gtaggtctat 480
caggatgntc tcaccttga tgtcacgatg gacaactnca cgggaaatgg cagtgtctga 540
tggtgccac tactttgg 558

<210> 547
<211> 357
<212> DNA
<213> Homo sapiens

<400> 547
catgagggtc cccgctcagc tcctggggct cctgtgtctc tgggtcccag gtgccaaatg 60
tgacatccag atgacccaat ctccctccac cctgtctgca tctgtcggag atacagttac 120
aataagttgt cgggcctctc agaatataga tcggtggttg gcctggcatc aacagaaacc 180
aggcaaagcc cctaattgtc taatttatgc gacttcagt ttagaagaag ggggtctcatt 240
aagatttact ggcagtggat ctgggacaca attcaattta accatcacca gtctgcagcc 300
tgacgattca gcaacttatt attgtcaaca ttattctgca tctcttcgca gttttgg 357

<210> 548
<211> 260
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(260)
<223> n = A,T,C or G

<400> 548
ccaagtagtg gcanccatcc agcactgcc a tccccgtgga gttgtccatc gtgacatcaa 60
ggatgagaac atcctgatag acctacgccc tggctgtgcc aaactcattg attttggttc 120
tggtgccctg cttcatgatg aaccctacac tgactttgat gggacaaggg tgtacagccc 180
cccagagtgg atctctcgac accagtacca tgcactccc gccactgtct ggtcactggg 240
catcctnctc tatgacatgg 260

<210> 549
<211> 366
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(366)
<223> n = A,T,C or G

<400> 549
caggacacag catggacatg aggggtccccg ctcagctcct ggggctcctg ctgctctggc 60
tcccagggtgc caaatgtgac atccagatga cccaatctcc ttccaccctg tctgcatctg 120
tcggagatgac agttacaata agttgncggg cctctcnaaa tatagatcgg tgggtggcct 180
ggcatcaaca gaaaccaggc aaagccccta atgtcctaata ttatgcgact tccagttag 240
aagaaggggt ctcattaaga ttacttgga gtggatctgg gacacaattc aatttaacca 300
tcaccagtct gcagcctgac gattcagcaa cttattattg tcaacattat tntgcatctc 360
ttngca 366

<210> 550
<211> 368
<212> DNA
<213> Homo sapiens

<400> 550
acagcatgga catgaggggc cccgctcagc tcctggggct cctgctgctc tggctccag 60
gtgcaaatg tgacatccag atgacccaat ctccttccac cctgtctgca tctgtcggag 120
atacagttac aataagttgt cgggcctctc agaatataga tcgggtggtg gcctggcatc 180
aacagaaaacc aggcaaaagcc cctaattgtc taatttatgc gacttcagtt ttagaagaag 240
gggtctcatt aagatttact ggcagtggtat ctgggacaca attcaattta accatcacca 300
gtctgcagcc tgacgattca gcaacttatt attgtgcaac attattctgc atctcttcgc 360
agtttttg 368

<210> 551
<211> 539
<212> DNA
<213> Homo sapiens

<400> 551
ccttggtcct agcaccact cgagaattgg ctcagcagat acagaaggtg gtcattggac 60
taggagacta catgggcgcc tcctgtcacg cctgtatcgg gggcaccaac gtgcgtgctg 120
agggtcagaa actgcagatg gaagctcccc acatcatcgt gggatccctt ggccgtgtgt 180
ttgatatgct taaccggaga tacctgtccc ccaaatacat caagatgttt gtactggatg 240
aagctgacga aatgttaagc cgtggattca aggaccagat ctatgacata ttccaaaagc 300
tcaacagcaa caccaggtg gttttgctgt cagccacaat gccttctgat gtgcttgagg 360
tgaccaagaa gttcatgagg gacccattc ggattcttgt caagaaggaa gagttgacct 420
tggaggggtat ccgccagttc tacatcaacg tggaacgaga ggagtggag ctggacacac 480
tatgtgactt gtatgaaacc ctgaccatca ccagggcagt catcttcatc aacaccgg 539

<210> 552
<211> 529
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(529)
<223> n = A,T,C or G

<400> 552
aaatcctgag tcaagccaaa aaaaaaaaaa ccaaaacaaa acaaaaaaaaaa caaataaagc 60
catgccaatc tcatcttgtt ttctgcgcaa gttaggtttt gtcaagaaag ggtgtaacgc 120
aactaagtca tagtccgcct agaagcattt gcggtggacg atggaggggc cggactcgtc 180

```
atactcctgc ttgctgatcc acatctgctg gaagggtggac agcgaggcca ggatggagcc 240
gccgatccac acggagtact tgccctcagg aggagcaatg atcttgatct tcattgngct 300
gggtgccagg gcagngatct ccttctgcat cctgtcggna atgccagggt acatggtggt 360
gccgccagac agcactgngt tggcgtagag gtctttgcgg atgtccacgt cacacttcat 420
gatggagtgg aaggtagttt cgtggatgcc acaggactcc atgcccagga aggaaggctg 480
naanagtgcc tcagggcagc ggaaccgctc attgccaatg gtgatgacc 529
```

<210> 553

<211> 375

<212> DNA

<213> Homo sapiens

<400> 553

```
gtcaggacac agcatggaca tgagggtccc cgctcagctc ctggggctcc tgctgctctg 60
gctcccagggt gccaaatgtg acatccagat gacccaatct ccttccaccc tgtctgcatc 120
tgtcggagat acagttacaa taagctgtcg ggccctctcag aatatagatc ggtggttggc 180
ctggcatcaa cagaaaccag gcaaagcccc taatgtccta atttatgcga cttccagttt 240
agaagaagggt gtctcattaa gatttactgg cagtggatct gggacacaat tcaatttaac 300
catcaccagt ctgcagcctg acgattcagc aacttattat tgtcaacatt attctgcatc 360
tcttcgcagt ttgg 375
```

<210> 554

<211> 193

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(193)

<223> n = A,T,C or G

<400> 554

```
gaaccgnacc cgctccgtcc cattgaagaa atgacactca gacgtagagt actccaagaa 60
acgtggngctg gtgtccccag ccaaagccag tggggagctc ancaccatca ntgtcactgn 120
cagaactgnc atgcaggaac ctccaggag cctnagacac accatgctgg anaacaggac 180
aggaccagggt gcc 193
```

<210> 555

<211> 421

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(421)

<223> n = A,T,C or G

<400> 555

```
ccaatcatag agatatctgc accagcctgc aaagcttcca tgaacgcttt ggtcccagac 60
ttggcgatag taccaagggtt attgatcaag tcagccttgg tcattccaat tccagtatcc 120
acaatagtga gagttcgatc ttgtttgttc ggtataagggt taatatgcag ctctttctca 180
gagtctaatt tactgggatc tgtcaagctt tcataccgga ttttgtccaa tgcattctgat 240
gaatttgaaa tgagctctct cagaaagatc tctttgttcg agtagaaagt attgatgatc 300
aatgacatca actgggcaat ttctgcctga aaggcgaacg tntnaacctc ctntcctcc 360
atcggttgggt cttgggtctg gggttctcctca ngcatntgga acgacaccgc gccggtntac 420
c 421
```

<210> 556

<211> 372

<212> DNA

<213> Homo sapiens

<400> 556

```
aggacacagc atggacatga gggccccgc tcagctcctg gggctcctgc tgctctggct 60
cccaggtgcc aaatgtgaca tccagatgac ccaatctcct tccaccctgt ctgcatctgt 120
cggagataca gttacaataa gttgtcgggc ctctcagaat atagatcggg ggttggcctg 180
gcatcaacag aaaccaggca aagcccctaa tgtcctaatt tatgcgactt ccagtttaga 240
agaaggggtc tcattaagat ttactggcag tggatctggg acacaattca atttaaccat 300
caccagtctg cagcctgacg attcagcaac ttattattgt caacattatt ctgcatctct 360
tcgcagtttt gg 372
```

<210> 557
<211> 119
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(119)
<223> n = A,T,C or G

```
<400> 557
ggacacagcn tggacatgag ggtccccgct cagctcctgg ggctcctgct gctctggctn 60
ccaggtgcc aatgtganat ccagatgacc caatctcctt ccaccctgtc tgcattctgt 119
```

<210> 558
<211> 375
<212> DNA
<213> Homo sapiens

```
<400> 558
ccaaaactgc gaagagatgc agaataatgt tgacaataat aagttgctga atcgtcaggc 60
tgcagactgg tgatgggtaa attgaattgt gtcccagatc cactgccagt aaatcttaat 120
gagacccctt cttctaaact ggaagtcgca taaattagga cattaggggc tttgcctggg 180
ttctgttgat gccaggccaa ccaccgatct atattctgag aggcccgaca acttattgta 240
actgtatctc cgacagatgc agacagggtg gaaggagatt gggctcatctg gatgtcacat 300
ttggcacctg ggagccagag cagcaggagc cccaggagct gagcggggac cctcatgtcc 360
atgctgtgtc ctgac 375
```

<210> 559
<211> 130
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(130)
<223> n = A,T,C or G

```
<400> 559
atggacatga gggccccgc tcagctcctg gggctcctgc nngctctggc tcccaggtgc 60
caaattgtgac atncagatga cccaatctcc tncaccctng tctgcatctg ncggagatac 120
anntncaata 130
```

<210> 560
<211> 464
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(464)
<223> n = A,T,C or G

```
<400> 560
caggcagagg ctctgggtca gtgcaggaag cagagtcaca gccagcgcct tgggggtggg 60
```

```
atgaaaggag atgacctggt ggctgctgta cagccactgt aggactctga tctcaggggg 120
acaggctgac acaggcagtt gggaattctg ggcagggaca agcaggcgtt acagaaaagt 180
gataaccaat cccagttaaa atagtctcag gagtccagtc aggagccctt tctgactcct 240
gtgatggata ataaggccca ncccgaggaa gatgagcccc agcacgaagc ctccaatgcc 300
actcagcatc ttgctctggg cagattcaga ctgagcccg cactccacgg tgatgggggt 360
ctggaggctg ggggtgctca cgtggcaggt gtagacgtct ccatgctggg gagtcatctt 420
cagcatcacc aggatctgga aggnccagtc accgnttcct aata 464
```

<210> 561

<211> 332

<212> DNA

<213> Homo sapiens

<400> 561

```
aaatattgta cagggaataa tcgagcatgc aaaattgaaa accccatgta aagacagcat 60
gataagctca ctggaatttt tttaattaaa taagcttaaa aagacattgg actaaatgct 120
aatatatgga atataagatt tcccaatggt aatttagtta acaacttttt tgtagtagca 180
tacacacaca taccaccttt atgtactatc tctagaagta aaatagtaaa ctatataaga 240
tagatatata tgagtagaac aaggaggaca tcttgaggtc atttcagaaa tgtatcatgat 300
tttattgagt ctgcacacag tttatgattt tt 332
```

<210> 562

<211> 237

<212> DNA

<213> Homo sapiens

<400> 562

```
ccagtatttc tggaggatat aacactgaca tcagcagggt tttcaatggc aacaattgca 60
cgagctgcca gcagaagctt ctcccaggtc ctcttgagat ttatgatata gatgccatca 120
cttttccttt tatagatgta ctgttccatc tggaagtcaa gattgggtgc acctaaagtg 180
gttcctgctg caaggaaact aaggacatcc tcctccttca ttgcaggac atcaagg 237
```

<210> 563

<211> 443

<212> DNA

<213> Homo sapiens

<400> 563

```
aaactcattg attaaataat gattaatgca ttctccacat tttaatatg caaaggccca 60
ttggagtttc tgaagtggct ccacagaatt gaaataattt caaataactg taaagggaact 120
gaaaatcttc acagagatga agtggggttt ccattaggtg ctttgaaatt tgataacaaa 180
tcatcaactt cactgggtca atatatagat tttgggtgtc tgaggcccca agattagatg 240
ccactaatct ccaaagattc cctccaatta tgaaatatat taatgtctac ttttagagag 300
cactagccag tatatgacca tgtgattaat ttcttttcac actagataaa attacctggt 360
tcaaaaagtg tttttgttta ttaaatttgg taataaatat atataataca cagacaggat 420
agtttttatg ctgaagtttt tgg 443
```

<210> 564

<211> 524

<212> DNA

<213> Homo sapiens

<400> 564

```
gctctggccc ctggtcctgt cctgttctcc agcatggtgt gtctgaggct ccctggaggc 60
tcctgcatgg cagttctgac agtgacactg atggtgctga gctccccact ggctttgggt 120
ggggacacca gaccacgttt ctggagtagt tctacgtctg agtgtcattt cttcaatggg 180
acggagcggg tgcggttcct ggacagatac ttctataacc aagaggagta cgtgcgcttc 240
gacagcgacg tgggggagtt ccgggcggtg acggagctgg ggcggcctga tgaggagtag 300
tggaacagcc agaaggactt cctgggaagac aggcggggcg cgggtggacac ctactgcaga 360
cacaactacg gggttgtgga gagcttcaca gtgcagcggc gagtccatcc taaggtagact 420
gtgtatcctt caaagaccca gccctgcag caccacaacc tcctgggtctg ttctgtgagt 480
ggtttctatc caggcagcat tgaagtcagg tggttccgga atgg 524
```

<210> 565
<211> 556
<212> DNA
<213> Homo sapiens

<400> 565
cagagctcaa gtctgaactc tacctccaga cagaatgaag ttcattctcga catctctgct 60
tctcatgctg ctggtcagca gcctctctcc agtccaaggt gttctggagg tctattacac 120
aagcttgagg ttagatgtg tccaagagag ctcatgtctt atccctagac gcttcattga 180
tcgaattcaa atcttgcccc gtgggaatgg ttgtccaaga aaagaaatca tagtctggaa 240
gaagaacaag tcaattgtgt gtgtggaccc tcaagctgaa tggatacaaa gaatgatgga 300
agtattgaga aaaagaagtt cttcaactct accagttcca gtgtttaaga gaaagattcc 360
ctgatgtgta tatttccact aagaacacct gcattcttcc cttatccctg ctctggattt 420
tagttttgtg cttagttaaa tcttttccag gaaaaagaac ttccccatac aaataagcat 480
gagactatgt aaaaataacc ttgcagaagc tgatggggca aactcaagct tcttctactca 540
caacacccta tataca 556

<210> 566
<211> 353
<212> DNA
<213> Homo sapiens

<400> 566
cgcagccatg gctcgtggtc ccaagaagca tctgaagcgg gtggcagctc caaagcattg 60
gatgctggat aaattgaccg gtgtgtttgc tcctcgtcca tccaccggtc cccacaagtt 120
gagagagtgt ctccccctca tcattttcct gaggaacaga ctttaagtatg ccctgacagg 180
agatgaagta aagaagattt gcatgcagcg gttcattaaa atcgatggca aggtccgaac 240
tgatataacc taccctgctg gattcatgga tgtcatcagc attgacaaga cgggagagaa 300
tttccgtctg atctatgaca ccaagggctc ctttgcgtga catcgtatta cac 353

<210> 567
<211> 286
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(286)
<223> n = A,T,C or G

<400> 567
ctgtctcaca ctttacaagc tgtgagagac acatcagagc cctgggcact gtcactgctt 60
gcagcctgag tgtaactccc tccttttcta tctgagctct tcctcctcca catcacggca 120
gcgaccacag ctccagtgat cacagctcca aggagaacca ggccagcaat gatgcccacg 180
atggggatgg tgggctggga agacagctcc catctcangg tgaggggctt gggcagaccc 240
tcatgctgca catggcaggt gtatctctgc tcctctccag aaggca 286

<210> 568
<211> 529
<212> DNA
<213> Homo sapiens

<400> 568
cgcggtgcga cgaaggagta ggtggtggga tctcaccgtg ggtccgatta gccttttctc 60
tgccctgctt gcttgagctt cagcggaatt cgaaatggct ggcggtaagg ctggaaaagga 120
ctccggaaaag gccaaagaca aggcggtttc ccgctcgcag agagccggct tgcagtccc 180
agtgggcccgt attcatcgac acctaaaatc taggacgacc agtcatggac gtgtgggccc 240
gactgccgct gtgtacagcg cagccatcct ggagtacct accgcagagg tacttgaact 300
ggcaggaaat gcatcaaaag acttaaagggt aaagcgtatt acccctcgtc acttgcaact 360
tgctattcgt ggagatgaag aattggattc tctcatcaag gctacaattg ctgggtggtg 420
tgtcattcca cacatccaca aatctctgat tgggaagaaa ggacaacaga agactgtcta 480
aaggatgcct ggattccttg ttatctcagc actctaaata ctctaacag 529

<210> 569
<211> 556
<212> DNA
<213> Homo sapiens

<400> 569
gtttgatgac cgctcgcggac gccagtgagg atttcccatg cggggaagag gtgggtttga 60
cagaatgcct cctgggtcggg gtgggctgcc catgcctcca tctagaagag attatgatga 120
tatgagccct cgctcgcggac cactccccc tcctcccga cgaggcggcc ggggtggtag 180
cagagctcgg aatcttctc tcctccacc accaccacct agagggggag acctcatggc 240
ctatgacaga agagggagac ctggagaccg ttacgacggc atggttggtt tcagtgtctga 300
tgaaacttgg gactctgcaa tagatacatg gagcccatca gaatggcaga tggcttatga 360
accacagggg ggctccggat atgattattc ctatgcaggg ggtcgtggct catatggtga 420
tcttggtgga cctattatta ctacacaagt aactattccc aaagatttgg ctggatctat 480
tattggcaaa ggtggtcagc ggattaaaca aatccgtcat ggtcgggag ctctgatcaa 540
aattgatgag ccttta 556

<210> 570
<211> 598
<212> DNA
<213> Homo sapiens

<400> 570
ccatctgac tataaatgcg gtggcatcga caaaagaacc attgaaaaat ttgggaagga 60
ggctgtgtag atgggaaagg gctcctcaa gtatgcctgg gtcttgata aactgaaagc 120
tgagcgtgaa cggtggtatca ccattgatat ctcttctgtg aaatttgaga ccagcaagta 180
ctatgtgact atcattgatg cccagggaca cagagacttt atcaaaaaca tgattacagg 240
gacatctcag gctgactgtg ctgtcctgat tgttgctgct ggtgttggtg aatttgaagc 300
tggtatctcc aagaatgggc agaccgaga gcacgccctt ctggcttaca cactgggtgt 360
gaaacaacta attgtcgggtg ttaacaaaat ggattccact gagccacctt acagccagaa 420
gagatatgag gaaattgtta aggaagtcag cacttacatt aagaaaattg gctacaacct 480
cgacacagta gcatttgtgc caatttctgg ttggaatggt gacaacatgc tggagccaag 540
tgctaacatg ccttggttca agggatggaa agtcaccctg aaggatggca atgccagt 598

<210> 571
<211> 647
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(647)
<223> n = A,T,C or G

<400> 571
ctgagggagg ggtcaggggt ggtgcgcggt gacggggagg gcaaagggtg tgtcagtatc 60
ttcattttga ggattgggtg tcagagcact tctggggtgt cagctcctcc ttgtccccc 120
gtggggctcc gtaggactgg aaagaggaca tgaagagctc tgacagagag cagcagaaac 180
tctggaactg tttccagagg gcctgcactg catggaccag gccaccacc ttctccttca 240
cccaggccag aaccccgtgc caccaggtct gcagccgctg cagcatggcc tgaaccatc 300
tcatgacctt gtcacaaaag ctctccccc gctcctcggt tgcgggatcc tcaacatccg 360
ggacagggga tctgttgctt cggcacctga atccatctct ttctttttca agtagaggag 420
tgagctctag gtgctgctcc tcataataag ccgccactgt ctccaggtag ccctctttga 480
agtcgtcctc cagctctgcc aggtctgaca tcacctgtcc acgtcctgat tctgcatttt 540
gcattttatc ataaaaatct tctatggcct ggtgcattcg gcccttcagc ttcttcatgt 600
catcagagag gaccttcggg aagcacatgg cggccaaang ttcaagg 647

<210> 572
<211> 360
<212> DNA
<213> Homo sapiens

<400> 572

```
cctgacacaa tatccctggt cactttgaag tgaattttga ctctatattc agaacccttc 60
tttaacacaa tggtttcctt tttgagggct tccagatctc cagtaaggte catggtgatt 120
gggtccgggg cactctcaca aaccaggggtg agccgggtga caacgacatt gggggctttc 180
ggatctgtca ccacaggacc atctcccagc agcgttttct tgtacttaat tagactctca 240
tcattcttgt ccatttcctg cagctctttc agggacttct gtgggtggagg cttataattg 300
agcttgctgt ccagctcatc atcgtcatcc tcctccacat gtggctctgg ggctttttca 360
```

<210> 573
<211> 457
<212> DNA
<213> Homo sapiens

```
<400> 573
ccacggctgc ttccagctcc tccctggaga agagctacga gctgcctgac ggccagggtca 60
tcaccattgg caatgagcgg ttccgctgcc ctgaggcact cttccagcct tccttcctgg 120
gcatggagtc ctgtggcatc cacgaaacta cttcaactc catcatgaag tgtgacgtgg 180
acatccgcaa agacctgtac gccaacacag tgtgtcttgg cggcaccacc atgtaccctg 240
gcattgccga caggatgcaa aaggagatca ctgccctggc acccagcaca atgaagatca 300
agatcattgc tcctcctgag cgcaagtact ccgtgtggat cggcggtctc atcctggcct 360
cgctgtccac cttccagcag atgtggatca gcaagcagga gtatgacgag tccggcccct 420
ccatcgtcca ccgcaaatgc ttctaggcgg actatga 457
```

<210> 574
<211> 388
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(388)
<223> n = A,T,C or G

```
<400> 574
aaaaacaaaa caaacgatac cttttgattg tgtggtgcag acgcaggact gaagccacag 60
gcttttgggg tgctgtgagc ccagggtctt gctcagctca cagctagcgc ggcggggcaga 120
gcaacccttc ggcccaagcc atcctcgcag cttgtacaga agcttctcga acctaaggga 180
tccgttccca gctctcctta aattcccagt ccccaccctg ggcctctctc cctaacgatc 240
ttgtcgtctt gggagcctct gaagtgaacc ctgaaatact ccctccgtca actctgggct 300
cagacctttg cccttctctg ngtcacaagg aaatttcggt caaganggtg ggaacagggtg 360
gtttcagacc gtgcagcaaa gccactgc 388
```

<210> 575
<211> 571
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(571)
<223> n = A,T,C or G

```
<400> 575
cagagctcaa gtctgaactc tacctccaga cagaatgaag ttcattctga catctctgct 60
tctcatgctg ctggtcagca gcctctctcc agtccaaggt gttctggagg tctattacac 120
aagcttgagg tgtagatgtg tccaagagag ctgagctctt atccctagac gcttcattga 180
tcgaattcaa atcttgcccc gtgggaatgg ttgtccaaga aaagaaatca tagtctggaa 240
gaagaacaag tcaattgtgt gtgtggaccc tcaagctgaa tggatacaaa gaatgatgga 300
agtattgaga aaaagaagtt cttcaactct accagttcca gtgtttaaga gaaagattcc 360
ctgatgctga tatttccact aagaacacct gcattcttcc cttatccctg ctctggattt 420
tagttttgtg cttagttaaa tcttttccag gaaaaagaac ttccccatc aaataagcat 480
ganactatgt aaaaataacc cttgcagaag ctgatggggc aaactcaagc ttcttcactc 540
acagaccct atatacactt ggagtttgca t 571
```

<210> 576
<211> 306
<212> DNA
<213> Homo sapiens

<400> 576
ctgctgcacc cagagctcct ttgggtctgc acatagctct gcctgagagc gcttgcgggg 60
caagaacagg atagctggga tggagcagcc caagcttggg tcctgcttcc ggtagctgcg 120
gacaaccttg gcgggaatct tcctttggct gtacttgagg caacagtcct gagccctcc 180
atcactgcct tgggtcctgg ggatgccaaa ggccagaacc aggataagga ggctcagagc 240
cagtactga gccatgtctg tggtagaggg tgagtaagag gccagagctg aggggtaggt 300
gggcag 306

<210> 577
<211> 342
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(342)
<223> n = A,T,C or G

<400> 577
aaaaacaaaa caaacgatac cttttgaatg tgtggngcag acgcaggact gaagccacag 60
gcttttgggg tgctgtgagc ccagggcttt gctcagctca cagctagcgc ggccgggcaga 120
gcaacccttc ggcccaagcc atcctcgcag cttgcacaga agcttcttga acctaaggga 180
tccgttccca gctctcctta aattcccagt cccaccctg ggcctctctc cctaacgatac 240
ttgtcgcctt gggagccctt gaagngaacc ctgaaatact ccctccgtca actctgggct 300
cagacctttg cccttctctg tgtcacaagg aaatttcggt ca 342

<210> 578
<211> 560
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(560)
<223> n = A,T,C or G

<400> 578
ctcagagctc aagtctgaac tctacctcca gacagaatga agttcatctc gacatctctg 60
cttctcatgc tgctgggtcag cagcctctct ccagtcacaag gtgttcttga ggtctattac 120
acaagcttga ggtgtagatg tgtccaagag agctcagctt ttatccctag acgcttcatt 180
gatcgaattc aaatcttgcc ccgtgggaat ggtgttccaa gaaaagaaat catagtctgg 240
aagaagaaca agtcaattgt gtgtgtggac cctcaagctg aatggataca aagaatgatg 300
gaagtattga gaaaaagaag ttcttcaact ctaccagttc cagtgtttaa gagaaagatt 360
ccctgatgct gatatttcca ctaagaacac ctgcattctt cccttatccc tgctctggat 420
tttagttttg tgcttagtta aatcttttcc aggaaaaaga ncttcccat acaataaagc 480
atgagactat gtaaaaataa ccttgagaa gctgatggg caaactcaag cttcttcaat 540
cacagcacc tatatacact 560

<210> 579
<211> 504
<212> DNA
<213> Homo sapiens

<400> 579
aaatcctgag tcaagccaaa aaaaaaaaaa aaaacccaaa caaaacaaaa aaaacaaata 60
aagccatgcc aatctcatct tgttttctgc gcaagttagg ttttgtcaag aaaggggtga 120
acgcaactaa gtcatagtcc gcctagaagc atttgcggtg gacgatggag gggccggact 180
cgtcatactc ctgcttgctg atcacatctg ctggaagggtg gacagcgagg ccaggatgga 240

```
gcccgcgac caccggagt acttgcgctc aggaggagca atgatcttga tcttcattgt 300
gctgggtgcc agggcagtga tctccttctg catcctgtcg gcaatgccag ggtacatggt 360
ggtgcccga gacagcactg tgttggcgta caggctcttg cggatgtcca cgtcacactt 420
catgatggag ttgaaggtag tttcgtggat gccacaggac tccatgcccc ggaaggaagg 480
ctggaagagt gcctcagggc agcg 504
```

```
<210> 580
<211> 303
<212> DNA
<213> Homo sapiens
```

```
<400> 580
ctggagatgg cagccgttgt ttgcggagcc caggctgact ccggattcaa cggtgctggg 60
gagagaaaag cagtatagac tccaccttcc aggatgtcca tttcggggag agggagcagg 120
gggaccctca agaaaatgac ggagaacatc ccagacagat gggactcaag caggatgggt 180
gctatatcca agaagccaag aaggagaggt ttcgtgcact gtggttaaca ggagggctgc 240
ctggaggcag tggctgagcc agaaagtaac acagagctca tgcttgagga gagagagtct 300
tgg 303
```

```
<210> 581
<211> 363
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(363)
<223> n = A,T,C or G
```

```
<400> 581
tctatgaggc cctagagctc cgggacaatg ataagactcg ctatatgggg aaggggtgtct 60
caaaggctgt tgagcacatc aataaaaacta ttgcgcctgc cctgggttagc aagaaactga 120
acgtcacaga acaagagaag attgacaaac tgatgatcga gatggatgga acagaaaata 180
aatctaantt tgggtcggaac gccattctgg ggggtgtccct tgccgtctgc aaagctgggt 240
ccgttgagaa ggggggtcccc ctgtaccgcc acatcgtctga cttggctggc aactctgaag 300
tcatcctgcc agtcccggcg ttcaatgtca tcaatggcgg ttctcatgct ggcaacaagc 360
tgg 363
```

```
<210> 582
<211> 584
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(584)
<223> n = A,T,C or G
```

```
<400> 582
aaataatcca ggcaggagaa gagaggaggg cactcttga actcccctcc ccacaatacg 60
tgattattta catttttagta attggacaat cccggctcag gaggagggtt caagaatctg 120
caaaagtgg agggagcgcc ccaggagaac aaacagcaag ccttatttcc cctagcccat 180
cccccaaaa accatccatc ccattcctagt gtctggtggt gtccggtggt gtccatcttc 240
cattccttcc caaattatgg aagtaagggt cttctacca gaataagagc acttgggata 300
acagagtagg gtcccctcac ccaaaaaaaa aaaaaaaan gaagccttgg ggtaacaaca 360
gggcattacc tccccagaa taaagaatcc tgggctgagg caggtaagca gcttgaccca 420
atatgggacc ctaggctagg ggaaagggtc ctttactaa aataaaagct actggggtat 480
tgaaggaaa gcacccttgc ccaagtaaga gcatatgaac taagtttng tgngngtagt 540
aggaggngcc aatgtggggt. gacacatcat cagaataaga gtcc 584
```

```
<210> 583
<211> 547
<212> DNA
```

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(547)

<223> n = A,T,C or G

<400> 583

```
ctgattgnnc acctgaccac acgccccac aggctctgac cagcagccta tgaggggggtt 60
tggcaccaag ctctgtccaa tcaggtaggc tgggcctgaa ctagccaatc agatcaactc 120
tgtcttgggc gtttgaactc agggagggag gcccttggga gcagggtgctt gtggacaagg 180
ctccacaagc gttgagcctt ggaaaggtag acaagcgttg agccactaag cagaggacct 240
tgggttccca atacaaaaat acctactgct gagagggctg ctgaccattt ggtcaggatt 300
cctgttgccct ttatatccaa aataaactcc cctttcttga ggttgtctga gtcttgggtc 360
tatgccttga aaaaagctga attattggac agtctcacct cctgccatag ggtcctgaat 420
gtttcagacc acaaggggct ccacacctt gctgtgtgtt ctggggcaac ctactaatcc 480
tctctgcaag tcggtctcct tatcccccca aatggnaatt gnatttgcct tctccacttt 540
gggaggc 547
```

<210> 584

<211> 400

<212> DNA

<213> Homo sapiens

<400> 584

```
ccaggtagca atgggtgctg tgcaatccag acagtaattc tgcaaaactgc cttgaagaaa 60
aaggaccaat gttcgaacta cttccagggtg aatccaacaa gatccccgt ctgaggactg 120
acctttttcc aaagacgaga atccaggact tgaatcgtat cttcccactt tctgaggact 180
actctggatc aggtctcggc tccggctccg gctctggatc aggatctggg agtggcttcc 240
taacggaaat ggaacaggat taccaactag tagacgaaag tgatgctttc catgacaacc 300
ttagggtctc tgacaggaat ctgccctcag acagccagga cttgggtcaa catggattag 360
aaggagattt tatgttataa aaggagattt tcccaccttg 400
```

<210> 585

<211> 393

<212> DNA

<213> Homo sapiens

<400> 585

```
ctgctcatca gatggcggga agatgaagac agatgggtgca gccacagttc gtttgatctc 60
taccttgggtc cctccccga aagtgaagca aggaggccac ttggcacgac cgtgacagta 120
ataaactgca aaatcttcag gctctaggct gctgacgggtg agagtgaagt ctgtcccaga 180
tccactgcca gtgaatctgg cggggatgcc agcgccctg taggatgtat cataaatgat 240
gatcctggga gcctggccag gtttctgttg ggaccagcct aagtaggtgg caacactctg 300
actggccctg caggagaggg tggctctctc ccctggagac aaagacaggg tggctggaga 360
ctgtgacaac acaagttctc cgtgggagtc tgg 393
```

<210> 586

<211> 425

<212> DNA

<213> Homo sapiens

<400> 586

```
cctggtggaa agaaggctct agaacctgct tatagagcca caacagggtg cagacaactg 60
tgatgtcaac caatgtcact cgttcgcccc ccagaaaagt cctcgtcttc aagtaagcat 120
ccagcagccc cagaattcgc ctcaactcct cctttgcatt ctcaagggtc tgtttgttgt 180
ggtgcatgat gcccagggtg gggaacaccc aggtactggc tgggggcact atatcggaat 240
cagcaaaagt caccactgc accacctggg ctgctgcctc tggagtactt ccccgagct 300
cctcattgct cacatagtag gcaatggcgt tgctctcaaa cacacagaat ccatcatcac 360
cctcaaatgc tgggaccttg ccggcaggaa atttcggag aaattcaggg gtgcggttgg 420
tttgg 425
```

<210> 587

<211> 595
<212> DNA
<213> Homo sapiens

<400> 587
ctgagggagg ggtcaggggt ggtgcgcggt gacggggagg gcaaagggtg tgtcagtatc 60
ttcatTTTTga ggattgggggt tcagagcact tctgggggtg cagctcctcc ttgtcccccc 120
gtgggggtcc gtaggactgg aaagaggaca tgaagagctc tgacagagag cagcagaaac 180
tctggaaactg tttccagagg gcctgcactg catggaccag ggccaccacc ttctccttca 240
cccaggccag aacccccgtgc caccaggcct gcagccgctg cagcatggcc tggaaccatc 300
tcatgacctt gtcacaaaag ctctccccag gctcctcggt tgcgggatcc tcaacatccg 360
ggacagggga tctgttgctt cggcacgta atccatctct ttctttttca agtagaggag 420
tgagctctgg gtgctgctcc tcataataag ccgccactgt ctccaggtag ccctctttga 480
agtctctctc cagctctgcc aggcctcgaca tcaccattcg ggccttcagc tttttcatgt 540
catcagagag gaccttcggg aagcacatgg cggccaaaag ttcaaggagc caagg 595

<210> 588
<211> 278
<212> DNA
<213> Homo sapiens

<400> 588
aaaatatccc tgaagtgaca cactcctttt ttgagaccga tactggtatt cttttattat 60
agagactaaa aggtctgcct tactagactt cccacttttt gttctgaaag gaattaagga 120
ctgcagggtt ccagctctgt cttcccgagg ccattatgaa cagattaaat ggaaggacaa 180
attctaaata actgggcttt caacatgaaa agggaaaggc tgatggggag ttcagaacct 240
tgaatactgt aactgaacat ccctcaaggt taatgcag 278

<210> 589
<211> 284
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(284)
<223> n = A,T,C or G

<400> 589
ggcggcaaga tggcagtga aatatccaag aagagggaagt ttgtcgctga tggcatcttc 60
aaagctgaac tgaatgagtt tcttactcgg gagctggctg aagatggcta ctctggagtt 120
gagggtgcga gttacaccaa ccaggacaga aatcattatc ttanccacca gaacacanaa 180
tgttcttggg gagaagggcc ggcggattcg ggaactgact gctgtagttc agaagaggtt 240
tggctttcca gagggcagtg tagagcttta tgctnaaaag gtgg 284

<210> 590
<211> 211
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(211)
<223> n = A,T,C or G

<400> 590
ctgtctcaca ctttacaagc tgtgagagac acatcagagc cctgggcact gtcactgctt 60
gcagcctgag agtagctccc tccttttcta tctgagctgt tcctcctcca catcacagca 120
gcgaccacag ctccagtgat cacagctcca aggagaacca ggccagcaat gatgcccacg 180
atggggacgg tgggctggga aganggtcc n 211

<210> 591
<211> 286

<212> DNA

<213> Homo sapiens

<400> 591

```
ccagagcggg  gagtcccacc  acctcgaact  ctgggaattc  gagccacagc  tctgccagta  60
ccccaagact  cagcactagt  ctgatgacct  gctaattcac  tgacagcata  gggctgtctg  120
ttgtttttgc  gcaagttggg  gtgaacaaag  ttcacaatat  ctggtcgaat  aggagccttg  180
aatacagcag  gcaaagtgac  atttttgcca  gatgactccc  ccttttcgga  gtacaccgat  240
atcagtgggc  gagcacacgc  catggcggag  agaggagaca  gccacg      286
```

<210> 592

<211> 242

<212> DNA

<213> Homo sapiens

<400> 592

```
ctgggagagc  tagactaagt  tggtcatgat  gcagaagcta  ctcaaatgca  gtcggcttgt  60
cctggctctt  gccctcatcc  tggttctgga  atcctcagtt  caaggttatc  ctacgcagag  120
agccaggtag  caatgggtgc  gctgcaatcc  agacagtaat  tctgcaaat  gccttgaaga  180
aaaaggacca  atgttcgaac  tacttccagg  tgaatccaac  aagatcccc  gtctgaggac  240
tg          242
```

<210> 593

<211> 132

<212> DNA

<213> Homo sapiens

<400> 593

```
ctgcttccat  tgggtgggtca  tttttgctgt  caccagcaac  gttgccacga  cgaacatcct  60
tgacagacac  attccttgaca  ttgaagccca  cattgtcccc  aggaagagct  tcactcaaag  120
cttcatggtg  ca          132
```

<210> 594

<211> 108

<212> DNA

<213> Homo sapiens

<400> 594

```
ccatggggaat  ctaattaatt  tcataatgat  gttggttgaa  catgatacca  aaaaatgcag  60
gtattttcaa  gaacaataag  atagataaca  gcattaaagc  ataatcct    108
```

<210> 595

<211> 206

<212> DNA

<213> Homo sapiens

<400> 595

```
gaatccaaca  agatcccccg  tctgaggact  gaccttttcc  caaagacgag  aatccaggac  60
ttgaatcgta  tcttcccact  ttctgaggac  tactctggat  caggcttcg  ctccggctcc  120
ggctctggat  caggatctgg  gagtggcttc  ctaacggaaa  tggacaagga  ttccaactag  180
tagacgaaag  tgatgctttc  catgac      206
```

<210> 596

<211> 322

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(322)

<223> n = A,T,C or G

<400> 596

```

ttctgccacc tatgggggncc aggcagggtgt ggtgccttgg ctaagtccac anacttctga 60
gaggccacg ctttcttctt ctccanaaat aaaccctgaa actcaagcag ctttaatacag 120
agggcaggat tccacgatag cagcatcaga acagcaagtg gcancnaga attcttgatt 180
ccnatgatca ngcaacagta aaccctgttg aatttaatac tgaggttgca acaccaccat 240
tttcccttct gganacttct aatgaaacan atttcctgat tggcattaat gaagagncac 300
tggaaggcac ngcaatctat tt                                     322

```

<210> 597

<211> 500

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(500)

<223> n = A,T,C or G

<400> 597

```

atgatgcaga agctactcaa atgcagtcgg gttgtcctgg ctcttgccct catcctgggt 60
ctggaatcct cagttcaagg ttatcctacg cagagagcca ggtaccaatg ggtgcgctgc 120
aatccagaca gtaattctgc aaactgcctt gaagaaaaag gaccaatgtt cnaactactt 180
ccagggtgaat ccaacaagat cccccgtctg aggactgacc tttttccaaa gaccagaatc 240
caggacttga atcgatatctt cccnctttct gaggactact ctggatcagg cttcggctcc 300
ggctccggnt ctggatcagg atctgggagt ggcttcctaa cggaaatgga acaggattac 360
caactagtag accaaagtga tgctttccat gacaacctta ggtctcttga caggaatctg 420
ccctcanaca gccnggactt gggtaacat ggattagaag aggattttat gttataaaag 480
aggattttcc ccccttgncn                                     500

```

<210> 598

<211> 511

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(511)

<223> n = A,T,C or G

<400> 598

```

ggtcatgatg cagaagctac tcaaatgcag tcggcttgtc ctggctcttg ccctcactct 60
ggttctggaa tcctcagttc aaggttatcc tacgcagaga gccaggtagc aatgggtgag 120
ctgcaatcca gacagtaatt ctgcaaactg ccttgaagaa aaaggaccaa tgttcgaact 180
acttccagggt gaatccaaca agatcccccg tctgaggact gacctttttc caaagacgag 240
aatccaggac ttgaatcgta tcttccnct ttctgaggac tactctggat caggcttcgg 300
ctcccgtctc ggctctggat caggatctgg gagtggcttc ctaacggaaa tggaaccngg 360
attacccaac tagtagacga aagtgatgct ttccatgaca acccttaggt ctcttgacag 420
gaatctgccc tcacacngcc aggacttggg tcaacatgga ttagaagagg attttattgn 480
tataaaagag gattttcccc nccnttgacc c                                     511

```

<210> 599

<211> 101

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(101)

<223> n = A,T,C or G

<400> 599

```

gttngtaatn atgcanaagc tactcnaatg cagtccnnct ttttctggct cttgccctca 60
tcctggttct ngaatcctca cttcaaggtt atcctacnca c                                     101

```


<210> 600
<211> 414
<212> DNA
<213> Homo sapiens

<400> 600
gcttcctaac ggaaatggaa caggattacc aactagtaga cgaaagtgat gctttccatg 60
acaaccttag gtctcttgac aggaatctgc cctcagacag ccaggacttg ggtcaacatg 120
gattagaaga ggattttatg ttataaaaga ggattttccc accttgacac caggcaatgt 180
agtttagcata ttttatgtac catgggtata cgattaatct tgggacaaag aattttatag 240
aaatttttaa acatctgaaa aagaagctta agttttatca tccttttttt tctcatgaat 300
tcttaaagga ttatgcttta atgctgttat ctatcttatt gttcttgaaa atacctgcat 360
tttttggtat catgttcaac caacatcatt atgaaattaa ttagattccc atgg 414

<210> 601
<211> 525
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(525)
<223> n = A,T,C or G

<400> 601
ctgggtgtaa gacctgggtt agaggtttgt caaacagagg caggggcccag tcacctcttt 60
ggaggggagt gatgagaagg ggattttggt cacctgagag ggttgagtaa acttggatca 120
gggcacaggc ttctctcacc atactcagct ttttgcactc actccctagt tgagcctact 180
ggcatcaagc tctagatgcc aaggctggga tggctgtgga gcaggagcta tggcccaagt 240
agctctgaga ggggaagaga cctaaaaccc ctacgaggga aaatactgac gctaggtgtg 300
aacataacct ctcttttcac aagagtcctg atggggcttg ctgagctttt ggggtactcat 360
ccctactgtt atagctggag aggatttggg tattgaagca gggaggggca gatccacga 420
agtgactgca gatctggaat aataagtaag gggtagatct gcccatagag ctacactttag 480
accggcctat actcctacaa ggaattgggg tangatcttc tactc 525

<210> 602
<211> 433
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(433)
<223> n = A,T,C or G

<400> 602
tgnnatgat gcanaagcta ctcaaatgca gtcggcttgt cctggctctt gccctcatcc 60
tggttctgga atcctcagtt caaggttatc ctacgcagag agccaggtag caatgggtgc 120
gctgcaatcc agacagtaat tctgcaaaact gccttgaaga aaaaggacca atgttcgaac 180
tacttccang tgaatccaac aagatccccc gtctgaggac tgaccttttt ncaaagacga 240
gaatccagga cttgaatcgt atcttccac tttctgagga ctactctgga tcaggcttng 300
gntccggctc cggctctgga tcangatctg ggagtggctt cctaaccgaa atggaacagg 360
attaccaact agnngacgaa agtgaatgct tccatgacaa ccttaggtct cttgacagga 420
atctgcccctc aga 433

<210> 603
<211> 510
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(510)

<223> n = A,T,C or G

<400> 603

```
gaggaagaaa cagctcccta atgacaaatg catctgtggg cgggagggga cttgggattg 60
tgctggaact ggatttctga attgctacta catctttttt cctctcatcc aggtctcttc 120
agagctgctg tgcccagtggt tgcttcaact ggtatctatg aggccctaga gctccgggac 180
aatgataaga ctgcctatat ggggaagggt gtctcaaagg ctggttagca catnaataaa 240
actattgctg ctgccctggt tagcaagaaa ctgaacgtca cagaacaaga gaagattgac 300
aaactgatga tcgagatgga tggaaacagaa aataaatcta agtttgggtg gaacgccatt 360
ctgggggtgt cccttgccgt ctgcaaagct ggtgccgttg agaagggggg cccctgttac 420
cgccacatcg ctgacttggc tggcaactct gaagtcattc tgccagtcct ggcgttcaat 480
gtcatcaatg gcggntctca tgctggcaac 510
```

<210> 604

<211> 478

<212> DNA

<213> Homo sapiens

<400> 604

```
ctggctaggt gtgtgtgtat gtgagtaggg gtgctattga ttggcacata ttttcccccc 60
tggagtttag ggggtggcaga aagcttttat agtaccacaaa aagtaaacat tgataaatatg 120
gcctgacacac aatcagatat gctaagctctc agaagcaaaa gcaaggtagg attgcctcca 180
aatgttgaca ggtattagcc ataccacagt aactagatct aatgtgaggg ctaaagtgcct 240
ggagaggcag aaccctaaag gatgcttagt tatagctcca tgctgccgcc gagggtgctg 300
atgctccatt acaccctcct tggatccaac cttccattaa ggctgaaggc tctagagggc 360
agagtattca agatgttaga tctgttccaa gcccaaattc tagagttaaa agcagagggg 420
ttcttagtgg ctgaaaaaaa acaaaacctg atgacatttg ggactccagt tttgagga 478
```

<210> 605

<211> 384

<212> DNA

<213> Homo sapiens

<400> 605

```
cctgacacaa tatccctggt cactttgaag tgaattttga ctctatatcc agaacccttc 60
tttaacacaa tggtttcctt tttgagggtc tccagatctc cagtaagggt catggtgatt 120
gggtccgggg cactctcaca aaccagggtg agccgggtga caacgacatt gggggctttc 180
ggatctgtca ccacaggacc atctcccagc agcgttttct tgtacttaat tagactctca 240
tcacttttgt ccatttcctg cagctctttc agggacttct gtggtggagg cttataattg 300
agcttgctgt ccagctcatc atcgtcattc tcctccacat gtggctcttg ggctttttca 360
gtcattctga tctatttatt cagt 384
```

<210> 606

<211> 208

<212> DNA

<213> Homo sapiens

<400> 606

```
aagctactca aatgcagtcg gcttgtcctg gctcttgccc tcattcctgt tctggaatcc 60
tcagttcaag gttatcctac gcagagagcc aggtaccaat ggggtgcgctg caatccagac 120
agtaattctg caaactgcct tgaagaaaaa ggaccaatgt tcgaactact tccagggtgaa 180
tccaacaaga tccccctgtc gaggactg 208
```

<210> 607

<211> 550

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(550)

<223> n = A,T,C or G

<400> 607
gcagaagcta ctcaaatgcn gtcggcttgt cctggctctt gccctcatcc tggttctgga 60
atcctcagtt caaggttata ctacgcagag agccaggtag caatgggtgc gctgcaatcc 120
agacagtaat tctgcaaaact gccttgaaga aaaaggacca atgttcgaac tacttccagg 180
tgaatccaac aagatccccc gtctgaggac tgaccttttt ccaaagacga gaatccagga 240
cttgaatcgt atcttcccac tttctgagga ctactctgga tcaggcttcg gctccggctc 300
cggctctgga tcaggatctg ggagtggctt cctaaccgaa atggaacagg attaccaact 360
agtagacgaa agtgategct tccatgacaa ccttaggtct cttgacagga atctgccctc 420
agacagccag gacttgggtc aacatggatt agaagaggat tttatgttat aaaagaggat 480
tttccacct tgacaccagg caatgtagtt agcatatttt atgtaccatg gttatatgat 540
taatcttggg 550

<210> 608
<211> 564
<212> DNA
<213> Homo sapiens

<400> 608
ccagaggatc agtgtccgat gaggaaatga tggagctcag agaagctttt gccaaagtgt 60
cttcaatgag ttgaatgact tgttcaaggc tgcttgcttg cctttgcctg ggtatagagt 120
acgagaaatt acagaaaacc tgatggctac aggtgatctg gaccaagatg gaaggatcag 180
ctttgatgag ttatcaaga ttttccatgg cctaaaaagc acagatgttg ccaagacctt 240
tagaaaagca atcaataaga aggaaggat ttgtgcaatc ggtggtactt cagagcagtc 300
tagcgttggc acccaacact cctattcaga ggaagaaaag tatgccttg tcaactggat 360
aaacaagacc ctggaaaatg atcctgattg tcggcatgtc atcccaatga acccaaacac 420
gaatgatctc tttaatgctg ttggagatgg cattgtcctt tgtaaaatga tcaacctgtc 480
agtgcacgac acaattgatg aaagaacaat caacaaaaag aagctaacc ctttcacat 540
tcaggaaaat ctgaacttgg ctct 564

<210> 609
<211> 564
<212> DNA
<213> Homo sapiens

<400> 609
tgcagatgga agctccccac atcatcgtgg gtacccttgg ccgtgtgttt gatatgctta 60
accggagata cctgtccccc aaatacatca agatgtttgt actggatgaa gctgacgaaa 120
tgtaagccg tggattcaag gaccagatct atgacatatt ccaaagctc aacagcaaca 180
cccaggtagt tttgctgtca gccacaatgc cttctgatgt gcttgaggtg accaagaagt 240
tcatgagga cccattcgg attcttgtca agaaggaaga gttgacctg gagggtatcc 300
gccagtctca catcaacgtg gaacgagagg agtggagct ggacacacta tgtgacttgt 360
atgaaacctc gaccatcacc caggcagtc tcttcatcaa caccggagg aagggtggact 420
ggctcaccga gaagatgcat gctcgagatt tcaactgtat cgccatgcat ggagatattg 480
acaaaagga acgagacgtg attatgaggg agtttcgttc tggctctagc agagttttga 540
ttaccactga cctgctggac ctgc 564

<210> 610
<211> 550
<212> DNA
<213> Homo sapiens

<400> 610
ccagatgcc aagtacaaga ccattggggg aggagatgat tccttcaaca ccttcttcag 60
tgaacgggt gctggcaagc atgtacccc ggagtggtt gtagacttg aaccacagt 120
cattgatgaa gttcgactg gcacttaccg ccagctcttc caccctgagc aactcatcac 180
aggcaaggaa gatgctgcc ataactatgc ccgagggcac tacaccattg gcaaggagat 240
cattgacctc gtgttgacc gaattcgcaa gctggctgac cagtgcaccg gtcttcaggg 300
cttcttgggt ttccacagct ttgggtgggg aactggttct gggttcacct cgctgctcat 360
ggaacgtctc tcagttgatt atggcaagaa gtccaagctg gaggttctca ttaccgggc 420
gccccagggt tccacaggag aggagaccag agtctgcctg gagtgcagac tgggagggg 480
cagatgactg ggggtggagca tgaagaaatt tctggggtga ttatcctatc ttatttggg 540
tgatatttac 550

<210> 611
<211> 349
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(349)
<223> n = A,T,C or G

<400> 611
aaaaaattta ctcatcttcc ataaagcgac ttttaattga tcaacactta aagatacaca 60
gtgactttaat gaaatatcag cacaactgca tagaattgag ctccagagaa ttatacactc 120
gagctgcttt cctgggctct ggtttataag ggtattggct tagagaccag cttggagtca 180
tttgcacctt cccgggaaat gcaggccagg aaacttaaga ttttgccggc cttttctgtt 240
tctaggtaaa atgcaggagg ctccctgaag gncttgaaaa ccatcaacca ttcaaatatg 300
gtatcctggg gacctttcct cttgagttaa nggaagaaag gaggtttgg 349

<210> 612
<211> 342
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(342)
<223> n = A,T,C or G

<400> 612
ngtctcacag gtagtctcct gagtagttga cggctagcgg ggagctagtt ccgccgcata 60
gttatagtgt tgatgtgtga acgctgacct gtcctgtgtg ctaagagcta tgcagcttag 120
ctgaggcgcc tagattacta gatgtgctgt atcacgggga atgagggtgg ggtgcttatt 180
ttttaatgaa ctaatcagag cctcttgaga aattgttact cattgaactg gagcatcaag 240
acatctcatg gaagtggata cggagtgatt tgggtgccat gcttttcacc ctnaggacat 300
ttaatcngag aacctcctgt ngaattttgt gggagacact tg 342

<210> 613
<211> 246
<212> DNA
<213> Homo sapiens

<400> 613
aaatcttttag agataccata aatcaacatt taatctttgt aacacatctg aaggaatatt 60
cttgaaatag cgtgatgatg gtctttaagg attctagaaa gggagtgatg agtcagaatt 120
tgccagaatg tcccagcata gtcaggagaa agagaacctc tctggtcgat gtacatgttc 180
taatcccatg gagattaggg caccagacta tgagatttgg taacatttgc tatcaagatg 240
aaccag 246

<210> 614
<211> 178
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(178)
<223> n = A,T,C or G

<400> 614
gcccnggnag gtccaaatgt ctgagacacc ttcaaatggg ccagtgcca gccaaactggg 60
ctcctcactg gcaccacgtc ccagatgccc ttctctgccc acaccctgca ggctgaggcc 120
agaggaggnc acccctccgg agatggggna tgtgngtgtg tgtgngtatg ttctgcgn 178

<210> 615
<211> 406
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1)...(406)
<223> n = A,T,C or G

<400> 615
ncgaggtcct ccccaaagcc agtcctgtgt caccaatcaa aggaaaggaa gccgtcagca 60
gagatgaaca gaataaccac caaggaagcc acttctctct gcccccaaa atcccccttt 120
ggagagaccc gccagaaact ctggaggagc ctcaaaatgc tccccgagag aggccagagg 180
gtccggcagc agctaaaaag ccacctcgcc actgtgaact tgtcgtcact cttggatgtc 240
cggagatcca cggatgatctc aggcctggg accggaaaag gcagccaaga tcaactcagg 300
gateccacct cgggggacag aggtacacg gatccctgtg cggccacatc tntnaaaagc 360
ccctcacagc cccaggcacc aaaanacana aaggtcccca ccagga 406

<210> 616
<211> 445
<212> DNA
<213> Homo sapiens

<400> 616
ctgccgccgt ggaatccaaa atttcgggag ctgtgaccct ttcctcatgt aaaacgagta 60
gtcttggacg atctgggcat aggaaccaat cagaaacaat cgcttcagca atcaagacca 120
ttgttcacatc tggaggaacc cgtggatacc tctgagcctc tatctgcatt accattcact 180
gggcagcagc cttttgagcc aagtggcaaa tttggacagt atccatcgat gcagatgaac 240
cacatccagg cactggggaa gtggaggaca tagaacagct caatcagtgt ttgatccaac 300
acttccatct cattaagaca agtttgattt ttctttgctt tttatttcatt ggaatcacatg 360
agaatctctt aactgttggg gtttccaagg aggcatacct catgacttca gttaatggga 420
agaacaaaac taaaatgctg tatgg 445

<210> 617
<211> 240
<212> DNA
<213> Homo sapiens

<400> 617
cctaagccgc ctaaggggct gcctcggctg tccatcagtt acctcgttc ctgagcagag 60
taattgggtg agattgttca tggaggcatt gctggctctc tagtcctgga acctacagtt 120
gggtccaattc attatgccaag aggtccgctc taggagggtc ttgttccaag tattgagatt 180
cccgagagaa gtaggtcccc ttagatagaa gcagagtttc tcagagggtat ttagcagcag 240

<210> 618
<211> 268
<212> DNA
<213> Homo sapiens

<400> 618
aaaatttatt ttattttaca atacttttag atttatagaa aagttgggaa gatggtacaa 60
agagtcccca tatataccat acccagtttc ccctaataac atcttacatt ggtatattat 120
ggttgcacaa attaaatggg ctaatatgta tacattagta ttaactaaag tccatacttt 180
gttcagattt cattagtttt tatgtaatgt cttttgtctg ttctaggatc ccgttgaaga 240
taccacatta cacttaggct cctgttgg 268

<210> 619
<211> 277
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (1)...(277)
<223> n = A,T,C or G

<400> 619
cgctttttta ggcctagtgt aaagtcaaga aggacagcag caagcatagg ctcaggatta 60
aagaaaaaaa tctgctcaca gtctgttctg gaggtcacat caccaacaaa gtcacgccc 120
tatgcagttc tgagaagggt gaggcaccag gctcaaaaaga ggaaatttan aatttctcat 180
tgaggagagt aggtaccccc atcccagaat gataactgca cagtggcaga acaaactcca 240
ccctaattgtg ggtggacccc atccagtctg ttgaagg 277

<210> 620
<211> 233
<212> DNA
<213> Homo sapiens

<400> 620
ctgtgcgtgc tcacgggctc ctccctgctgg aagagagaga gatgtgcacg ccactccat 60
ggcatgtcta gcaggctctga gcagtggttca tagaagaaaa atgttttaac agtctcagat 120
tttgggaggt agggggaaaa aaatcattga aatctgggaa agacattttt aagctgctga 180
cttcacctgc aaaatctaac aggttggtatt agtttttttt ttttttttta cct 233

<210> 621
<211> 311
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(311)
<223> n = A,T,C or G

<400> 621
ctgcaagaca gcagagaanc tgccaatatc cagtttagcag atgactttgc tggcaagcag 60
aggaagncgg taaaagcttg tctcccagcc aggaacttg acaccaagnt aagatttga 120
gctaggaaac aaacccaaaa ggctcacagc aagcggagaa aaaaaccca aaatctgtaa 180
cctgtatcac aaagcgttca tatccttcag atataaagag ttattagata tcaataagaa 240
aaatgcaaac actcctgaaa agtagaaaaa agctatgaac aggcaattca ctgaaattaa 300
aaaaaaaaa a 311

<210> 622
<211> 243
<212> DNA
<213> Homo sapiens

<400> 622
ctgtggctta gctggctttg ctggtcgtaa tggaggacaa aagtgccttc tggtgaaact 60
cagcttccat agtgatgaa cctaagggtg gcagagtta tggtgaccct gtagtgtatc 120
tccagaaatg gtgattgttt gaatgcatgt aagacattcc ctagggactc caagaaatat 180
tgattagagg aagatgtggt gctttgaaag ggacttggtg ttcctacatg aaccaagtga 240
agg 243

<210> 623
<211> 388
<212> DNA
<213> Homo sapiens

<400> 623
ggacattcaa atgtctttat ccacattcct gaaggataat tggtatagat tccctacctc 60
cataggaatg cttataatgg attatctata caatctccac attcccacat tttgcattag 120
agaatggaat cagtcaaac ctgttcccag agtttccctt agagtctca cctgttgtct 180
tatatccatc taggaatccc catctctaata gtaagcttgg agatccgggc ccccggggga 240
caggtgactg aaggacaaaa actgatcctg ctctgctcag tggctggggg tacaggaaat 300

gtcacattct cctggtacag agaggccaca ggaaccagta tgggaaagaa aaccagcgt 360
tccctgtcag cagagctgga gatcccag 388

<210> 624
<211> 529
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(529)
<223> n = A,T,C or G

<400> 624
cctgtggaac cgggcccctc ccggagccca nggaaaagac tgcttctctc tcagcagccc 60
cattcctggt tattccaggg ctgaccaaca aggacatttc caccctacaa gctgctgctc 120
actgatgttc ccgtgggata agaggggaaa ttaagtgaca accgcagcag catccgctgg 180
gtctgtccct gtatcgcatg ccagaggctt gcgcatcacc aagggtcggg cgtagctgtg 240
ctgcccctgcg ttgtgtgcat agcctctctc tcctctgctt gcttaagtcc ttcttancca 300
ccctctccct tanggctcta ccaggtatgc cacggggagc aggaatatta atcctagaat 360
cctgactctc agtggcaata cagagtgtac tccagggatg ctgggtgaaa cccgggggaat 420
tctactcacc attaaccttg ggagtaagag gccatacctc atctgaaact ttacctgccc 480
gggcgggccc ttcaaaaggc cnattccccc nccctttgcg ccnttatag 529

<210> 625
<211> 571
<212> DNA
<213> Homo sapiens

<400> 625
ctgagctcct ctggttcttc tctagacctg ctccctctct gaaatgcaag gccgtgcctt 60
taatgggctt ttggcattct gtctccagac ctcccttctc atctgaaggg ctctcaggag 120
aacagagaaa aaaccagcct gtctccaaac tggcccgtct cagggaactgg gggcctttac 180
ccccagtgaag agatgcagac tttacagcgc tgcatgacag tagagttaag tgactccttc 240
agatagttgg atgggtctct cgatcattcc tgataataac attttgccta tgttaagtgc 300
tttccaccta tcatgttacc ttctaactac tcccttggtt ggatacaggt attagcccca 360
tttcacaatt aagaaattga ggcttaaaag gattaaagag ttttttagag gagaacacgc 420
tcttcccttac agaaggatcc caagtaataa atgtgaatgc tccctctcca gaagggtgca 480
cttaattccc ctgtcctgga gtttgacctc gcttagtgac tggcttctga tgaataaaa 540
ggggaaaagg aaaaatagta actccacagt g 571

<210> 626
<211> 449
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(449)
<223> n = A,T,C or G

<400> 626
aaaattgac acaacnaggg aaaacaaaat aaaattaggg ggcaaagggt aggagtatgg 60
ggggagggga gagcaaacct atcgaatata tcttagaatt ttgctcagaa atcactgctg 120
cctctcaagt gttgcattgt ccctgcctaa accaagaagg ctaaacaagg cccctcctgt 180
ttgaattctt aaggtaagaa atttctaagc taagaaaaca ctattgccta aaaccaatga 240
tagtgagact catttacaaa taggcatgcc tcacacacac agtccaaagg caagacactg 300
gctttgaaat taggctcatg atgtgattcc tattatatgt acctgatttt tttaggcccc 360
aggatatgg accagagtta atgtcatgac tcttcaaaga tatgatgaaa agttgcccta 420
gaaatctaga gatgcatgtt tatttaatt 449

<210> 627
<211> 410

<212> DNA

<213> Homo sapiens

<400> 627

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cctgggtcaaa tgtcacctcc actgggaagc cctccttgat ctcccaggct gttaggggcc 60
tgccccaggt tcctgcagac tccctgcttc tctccatcac aaacctgagc agtgtggggc 120
tgtcattatc atgtgtgagg ttttagtacc aggaagtggg gtactaccat agcaaatacc 180
caaaaatggg gaaatggctt ggggaatgga aagaattgga caatgagcac ttgatagaaa 240
aagcctagat tgcctgaag aggtggtcag tagaaatatg gatgttaaag gtgcccctgc 300
tgaggtccta ggaggaaatg agggacatga cattggacgt gaagatggag gtggggactg 360
cagtgatgca tccacagatc tgggagacca ggatgctgca gccatcacag 410
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<210> 628

<211> 343

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(343)

<223> n = A,T,C or G

<400> 628

```
cccggcaggn aaatgccact gctgnggaca aaaaactgaa tgaantctat tagaagcttc 60
tgaaaaatgt taaatgttaa atcctgctat ggtctgatna gaanaactca agacttagaa 120
ttagatattt tcttccttcg aattatgtat tagattatct ccctacatat tttctcccag 180
ccataagtaa ctgagttatg ctggaaaaaa aaacacanaa atcttaagat ctctttttct 240
actgggtgaaa ttgggggttt gataataatt tttagagaaa aatctanaat tctctgtgta 300
tagctggtca acncataaac cangtaaatt ttgattttct tgg 343
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<210> 629

<211> 117

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(117)

<223> n = A,T,C or G

<400> 629

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ngtaaatccc tgtaataaaa gggaaattga gggcagagca atcaggctgg agttgcaagg 60
accaggggga tcacctaatg ccagaagcca gccatccaaa actctgtttg tcaaagg 117
```

<210> 630

<211> 111

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(111)

<223> n = A,T,C or G

<400> 630

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agcactgggtg gtgctcacca tggctggacg tctctctcgg ctctctctca ctgacagact 60
ctggactcta tgnatctca acaccctagt gcagtggcca cgaaaacagc a 111
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<210> 631

<211> 303

<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(303)
<223> n = A,T,C or G

<400> 631
ctggacgang aangntnctg acactcacta ggactgtgac tagatgttcc agtggcagaa 60
agtcctcctg gtttccttcg ggccctggcg taatgcagca gagcagcagc anctacnann 120
acnaagatgt tgaccaccag ccccntgatt cccgcagtgg taaggcctgt tctgttcctg 180
gaagtctcctg taacattgag tgtcaccact ttactgtgct gggcccccag gccattgtca 240
agcctcacat gagtagtttc cagaatgntc tgtagtcaga gagaggttga aggatgcccc 300
tcc 303

<210> 632
<211> 246
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(246)
<223> n = A,T,C or G

<400> 632
ncgangtctg aagcccacta aggaatccag gagatgtgct gggccctgga gtgggagcac 60
cttgccactg gattagaaaa cctgccagtc agggctttaa ctgggaaaca ggtgacagtc 120
cagcagggcc ctgcattctg gtcagactga gaatgaggac atgtgaaaca aaggccagta 180
gatatggtct ggggcagnct aaatcttcca cttcaatgct gcttctcccc aaggggaaact 240
ttgcgg 246

<210> 633
<211> 544
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(544)
<223> n = A,T,C or G

<400> 633
aaatgcgcat gtaatttatt tatgataatg taaatacttc ttaaattgtct gtaactcttc 60
aaaagtgatg cttcaggata aatgagctgc taagcatttt aagaatttac cgttaactcta 120
atatactgga ggggaaggga tggatctgaa aggctaccat cagtaagagg aataaaaactt 180
gctctgtgtc ctccagaagt ctggacagtg atcagcaggt aatagacaca gaggaactga 240
tttcaacttt tgaaaaagag ttttccacta attaacactg tcccacggcg gaatagggttc 300
cctgaagatg ttgagtgtcg aaagtgatca agcagaggct agagggttc ttgcctggga 360
gcaggggagg gttgggggag aaggacaaga ggacagtggg gtaggtgacc tctagcatca 420
ttgtcactgc taatattcta tcttgtgcat tcatttgctc attcacacag cttcccaaga 480
tggccccc aa tgatccttgc cagtggngta ttcatgccct tgggcaattc cttncacagac 540
tgaa 544

<210> 634
<211> 220
<212> DNA
<213> Homo sapiens

<400> 634
ccacctgggg gcaggtagcc ccggcttgct tgttctctct ttccctagccc aggaatcggg 60
tccttgggtc taaagcacag ggccaagtgc tcaaggatca acatcccaga cagctcccat 120
ggtctggggc ttggagctgg tatgaagggt gaaccagggt ccatcctgga ctgtttatgg 180
ttggagggcc tgggccctg gcaccaagac cttcacttcc 220

<210> 635
<211> 224
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(224)
<223> n = A,T,C or G

<400> 635
cctaaaaaag cggcctcggg gggaaatgcat ttctcttgct ccacgtctat tttagttgca 60
tatctgtagt gatgacaaat gcctccagcc ttgtcctctg caaggctgca ctgggctgca 120
tacaggctcc tgtctcagggt gtctggtttc ctccttgaaa ggttggggca gcggagtcag 180
ccctgtctat ctgggcaagg ncctgacact tggaancatg aaaa 224

<210> 636
<211> 453
<212> DNA
<213> Homo sapiens

<400> 636
ctgtcatgag gtctcttcta tagccatcag gtcttctcac agggatattc accaccttgc 60
tctggatagg cacatggccg ttgtcagctc tacagtaata ttggccggca tcaactctctt 120
tcacagctgg gatctccagc tctgctgaca gggaaacgctg ggttttcttt ccatactgg 180
ttcctgtggc ctctctgtac caggagaatg tgacatttcc tgtaccccca gccactgagc 240
agagcaggat cagtttttgt ccttcagtca cctgtccccc gggggcccg atctccaagc 300
ttacattaga gatggggatt cctagatgga tataagacaa caggtgagaa ctctaaggga 360
aactctggga acaggggttg actgattcca ttctctaata caaaatgtgg gaatgtggag 420
attgtataga taatccatta taagcattcc tat 453

<210> 637
<211> 215
<212> DNA
<213> Homo sapiens

<400> 637
ccgccccggc aggtccaccc aggaactcct gactgcttcc ctccccctgc ttgctataca 60
ttgtctggaa ctggctaaga aatggggaac atttgtgaaa accaagaaat gtaatggtt 120
tggtatgaata aaatagacca aagttaaggt aagtgcacaa atatcagtgt caggctatgg 180
aagaaagata aagagatact tctttttttt ttttt 215

<210> 638
<211> 497
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(497)
<223> n = A,T,C or G

<400> 638
gttcggggag aggttggtan cacagggctt gggatatcgg cagtgtggga aatgcgaagc 60
atttctcatc atcatcatct ctgctacagn catgtttctg catgtcagcg agcgacactg 120
tccctgcctc aggttgagg ttttatcanc caaagtgttt ttttcagtga tcgttcgttc 180
cattcatcca ctctgnncct tgnacgctt tgaaaggctt ggttgctccc aggctgctgt 240
tctcagggac cttaaaaggg acctggtag tcttggggca gagagtatct acttgggcac 300
tctcttccaa gaaagacctt gtctccattt tcattaggac aatgcttctt gtgtgtgttc 360
tggaagatct tctaaatgga atgcttgttg cactgntccc ancgagtggt ntgccatgag 420
acctgangac cacacttggg ggaccaatca tgncttnac cactgngcct tagaatcgcc 480
cctggacaga gttcctg 497

<210> 639
<211> 591
<212> DNA
<213> Homo sapiens

<400> 639
ctgataacgt tcacagcccc atcctcagca cgtggattcg agtcaccgtg agaattccgg 60
tatctcacc tgctctcacc ttcagggtc ccagggccca cactgtggtg ggggacctgc 120
tggagcttca ctgtgagtc ctgagaggct ctccccgat cctgtaccga ttttatcatg 180
aggatgtcac cctggggaac agctcagccc cctctggagg aggagcctcc ttcaacctct 240
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agcacagtca tggagttagt ctcagggtca cagttccggt gtctcgcccc gtcctcacc 360
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tgagaggctc ctcccgatc ctgtactggt tttatcacga ggatgacacc ttggggaaca 480
tctcgcccca ctctggagga ggggcaccc tcaacctctc tctgactaca gaacattctg 540
gaaactactc atgtgaggct gacaatggcc tggggccag cacagtaaag t 591

<210> 640
<211> 349
<212> DNA
<213> Homo sapiens

<400> 640
ccagagtga gatacatca ttggcaccaa ggtctctttt caattcttgg tcaatccctct 60
gcagcaagca cccccggatg acgtcctcat agatgccctc agtggtcaga gcctggctgc 120
ccacggcaag gacatcccc tcgaactcag gcagctcctt ttgagcct ggctcgagtt 180
ggctcagcac aaaaggtaaa aagatgcaga gacccagcc tcggatgaac ctccctctgcg 240
ccaacccgct gtccgatttg aatttcttca gcacgcgccc cctgactctc tccagcctct 300
gggcagcctg gtcacagttg agggccgctg tcagacactg gtcagccag 349

<210> 641
<211> 555
<212> DNA
<213> Homo sapiens

<400> 641
aaaggatgca ctcttgccat tttatgtact ggaagatcat tggtcagatg aatactgtgt 60
ctgacaaaaa tgtaaaactgt ataaactgag gaacctcagc taatcagtat tactttgtag 120
atcaccatgc ccaccacatt tcaaaactcaa actatctgta gatttcaaaa tccattgtgt 180
ttgagtttgt ttgcagttcc ctcagcttgc tggtaattgt ggtgttttgt tttttgtttt 240
gttttcaatg caaatgtgat gtaaatattct tattttcttt ggatcaaaagc tggactggaa 300
attgtatcgt gtaattattt ttgtgttctt aatgttattt ggtacttaag ttgtaataaa 360
cgtctactac tgtttattcc agtttctact acctcagggtg tcctatagat ttttcttcta 420
ccaaagtcca ctttcacaat gaaattatat ttgctgtgtg actatgatcc ctaagatttc 480
cagggcttaa gggctaactt ctattagcac cttactgtgt aagcaaatgt taaaaaaaaa 540
aaaaaaaaatc tctgg 555

<210> 642
<211> 179
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(179)
<223> n = A,T,C or G

<400> 642
aatgtttcat tgnactcaac atgtgaagaa aactattggt nntgncccat gactgtttgc 60
acttntctgn taacctgaca aattcctact ctttcccat gagcattgta aanccttgtg 120
cacaantnga aaacttatga gtgacctgag atnttatcta tcccctanct ttttaccta 179

<210> 643

<211> 582
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(582)
<223> n = A,T,C or G

<400> 643
ccattggatg gctggggatt caccagagaa acggacacac caggttctat tctaaaaaca 60
ttaagtgggt tcccaggaca gcagtcttcc ctgattttat cttctgcttc ggaggcaaac 120
ttgactttcta tgtgttctag ctcaagcgaa ttagtcagat agactatatt ctccataagc 180
acagcctttt catcaaattc taattgcaaa tccagaatac gagggcccat cttctccaga 240
ttttccttaa tcatggcaac aaatggcatg actttcttca tgtatttctt cagtctctgc 300
atactgctta gttcactagc aatgactttg ttgtcaggca gttttccgtt attggcctca 360
aagtgtttac gtagaacaga caggggtgta tgttgccaag gtggatagtt ctttgccaca 420
tagatgggtc aatgtgaggg cttctgcagg ggttggttgt cagtcttctt ccctttagct 480
ggcatcatat agttcttgag tcgtagtcta aggtcatgtg ttacttccat aagatactgn 540
gaggagtgtta ttaaaacttc attaacagga cctgccacag gc 582

<210> 644
<211> 420
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(420)
<223> n = A,T,C or G

<400> 644
ctggggcaca cagaggaggg gcctgggtac cccttttggg gaaactgaga cgaagctatt 60
tagaacagct tgaataaag agacttttct agaattgggt ggagcctaaa gtagcttctt 120
tttctttctt tcagaatgct cagatgcac agttccttaa tatacacgtg aaatttgaaa 180
actgtacatt cggtgagatt aaattttata tacaactagc aattgtccag ctttgttgc 240
cattttcaat taaggctaaa gtgttcaaca tgagaaaatg tgatacattt gatacagtg 300
ggggtgggag tggatgggca gctcttggtg gtactggacc ttncacaagg ctgtgtccac 360
ccagaatcca tgctggcagg agggaggcag aggtatcaaa ccanacctct caccaagcgc 420

<210> 645
<211> 505
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(505)
<223> n = A,T,C or G

<400> 645
aaagacagaa tccctgagtg ctgagcagat tctcaaaaca catttanaat ccctgaaatt 60
agaaagatca atgacaaaat atctgtcagc caggccacaa acaggtgtta aattatgaaa 120
ggagtgggtg gatgtgcaa gtttggtaaa gtggtgactg catctgagaa agaggctgtg 180
aggctgaact cttggtggct tccttctgta acttccagag ggagtcttca acacaggccc 240
cgtgctcgta ggaatacggc agcacctatg taggaagtgc gtggagtttt ctgtcttctt 300
tctgtgtgat ttttggcctt tttatcagca cttctccctt ccaggagacc tggggatgcc 360
aaacatccag aatgtgatgg gacaagatgg gggcaggggc ctcacctccc tgcagaggtc 420
cggccaggtc tccttgctcc tggacaatct cctgagcctc tctgcttggt ggagcaggca 480
cctgtgtgca gaattcccac tgttg 505

<210> 646
<211> 474

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(474)
<223> n = A,T,C or G

<400> 646
gtgcgaaggt ccagctcagt ggcacaagt aaagcaatga tcgagactaa gacgggtata 60
atccctgaga cccagattgt gacttgcaat ggaaagagac tggaaagatgg gaagatgatg 120
gcagattacg gcatcagaaa gggcaactta ctcttctctg catgttattg tattggaggg 180
tgaccaccct ggycatgggg tgttggcagg gatcaaaaag cttatttctt ttaatctctt 240
actcaacgaa cacatcttct gatgatttcc caaaattaat gagaatgaga tgagtagagt 300
aagatttggg tgggatgggt aggatgaagt atattgccc actctatgtt tctttgattc 360
taacacaatt aattaagtga catgattttt actaatgtat tactgagact agtaataaaa 420
ttttaaggc aaaaatagagc attccnaaaa aaaaaaaaaa aaaaaaaaaa aagg 474

<210> 647
<211> 478
<212> DNA
<213> Homo sapiens

<400> 647
ccagcatcac cacagcctgg ggcccagaag gagccataac ctgttgctgc ctgatggagg 60
gcccagcatg ggacacaagc cagatcatca tcaccgggag tcaagacggc atggtccggg 120
tttggaagac tgaggatgtg aagatgtctg ttcttgagcg gccagcagga gaggagcccc 180
tggctcagcc tccaagccca agaggccaca agtgggagaa gaacctggcc ttgagtcgag 240
agctggacgt tagcattgct ttgacaggga agcccagcaa aaccagcccc gcagtgactg 300
ctctggccgt gtccagaaac cacaccaaac tcctgggttg tgatgagagg gggagaatat 360
tctgtctgtc tgcagatggg taggaagaga gaggcagcag aggcctctggc acaacagtgc 420
caggctgagg gtggcagagg tgactggggc ctgagctctg cctacagaag aaaccccc 478

<210> 648
<211> 443
<212> DNA
<213> Homo sapiens

<400> 648
aaactcattg attaaataat gattaatgca ttctccacat tttaatatg caaaggccca 60
ttggagtttc tgaagtggct ccacagaatt gaaataattt caaataactg taaaggaact 120
gaaaatcttc acagagatga agtgggggtt ccattaggtg ctttgaaatt tgataacaaa 180
tcatacaact ccaactgttc atatatagat ttggggtgtc tgaggcccca agattagatg 240
ccactaatct ccaaagattc cctccaatta tgaaatattt taatgtctac ttttagagag 300
cactagccag tatatgacca tgtgattaat ttcttttcac actagataaa attacctggt 360
tcaaaagtgg tttttgttta ttaaatgtg taataaatat atataatata cagacaggat 420
agtttttatg ctgaagtttt tgg 443

<210> 649
<211> 563
<212> DNA
<213> Homo sapiens

<400> 649
aaaaaaaaact acatctcttt attgcagaat ttatacttgt ttgaaaaata caaaatgtag 60
cgttgataag attgaagcat gttgaaaggt aagtacagg aaaggtcctt tcagaatgac 120
tgcaacagtg cagcaaggat tccatttccc cgcctaaagg acaatacctt tttaatagaa 180
ataaatgagt tagttagtta gatttttatt acagattgaa ttaaacagtt agttacaaag 240
acattctctg atacattcat tcataagagg cttaacgtat aaatacatag taaatatcct 300
ataaaatggt aggcattctc atcgtgcatt atctttttgt gctcagactt gacttcacat 360
tcagtctcta catacagctt gattagaatc ataaaaacaa tatgaagacg attgcataaa 420
gggatagttt gacaaagcat attcagatat tgtaacattt atgggtggga aaaatgtatc 480
ttttgaaaca atatattaga ctccattttt agctgaaatg aaatttactg attcaatctt 540

tttaagaatt tgtggatggt tac

563

<210> 650

<211> 306

<212> DNA

<213> Homo sapiens

<400> 650

aaaaacaatc tacaggcagt tctttacaag tctcatattt acagatagca caagctatgg 60
catggcgat ggctccctc ctaaatatac gattctttgg catattggaa ttggtcagcc 120
tcaaagaccg gctgggtaca tcgtcgacac agacagtcctt gcttattcct ctgcacggac 180
tcggagacgg tcctcagcgg gaggagctca ggtctccctg ggccagacac gtgcccaga 240
gagtcctccag aagcatggac agttctgctc tgtttccatc gctcaggcag gggagagagt 300
ccgtgg 306

<210> 651

<211> 561

<212> DNA

<213> Homo sapiens

<400> 651

ccaagagggt gactcagagc ctcccttgag ctaaaactcgg ccaaccaagg cagcagcat 60
gtccctcag gtctccagtc agtccagggt gacctcagt tctggacgtg tgatatagc 120
tgtaattaat acctcaagggt cattgtggct ctggggatgc cggggcagga ggacgagggt 180
gcgctgtgga cacagcagtc cgcggaattc cgttctggga agccaatggt cgccggcacc 240
ccttgcttcc tcctctgtgt gtctgcctgt gtgacacaca tcaatggcaa taacttcttc 300
caactcctcg cagaagtggg agaggccggc agcctgcacc gagaggggct ttcctctctc 360
ttgctccccg ctctgttctg ttttggtgc agagagtgggt tcatccatac tctcattccc 420
tcgcctcccc ttgtggacgg gggctctgcc ttttcaattc ctgtgttttg gtgtcttccc 480
ttatctgcta ccctgaatca cctgccttg tcttgctgtg tgatgggaac atgcttgtaa 540
actgcgtaac aaatctactt t 561

<210> 652

<211> 420

<212> DNA

<213> Homo sapiens

<400> 652

ctgtagcctc tgcaagtga aatccaggcc gacttgacgt cattggactg atgtccaagt 60
gcaatcacca tacagcagct acaggcaggg ctggctgata gggagtatgg gagaaggaca 120
cgctcagatg aaaacatgca tgcaacgatt ttcaccactg aacacactgt tttctgtgat 180
agaaactgtc ggccctgctg ggggacaaga tattcacggc ctactagacc agtgagatgc 240
caccagggcg gcctgcccct gatgctcctt tgttacctgc taaagaagga ccataaggta 300
aaaggcacct taccttatgg agtgagccca gacccagggg aaaagcttgg gtagaacaat 360
ccaaggggca gcctgggtgt gagaatccag cccaagctag ctgctctaga agcctggagg 420

<210> 653

<211> 196

<212> DNA

<213> Homo sapiens

<400> 653

tcagaagtgt gctcctctgg cctcagttct cctcttttgg aacaacataa aacaaattta 60
atthttctacg cctctgggga tatctgctca gccaatggaa aatctgggtt caaccagccc 120
ctgccatttc ttaagacttt ctgctgcact cacaggatcc tgagctgcac ttacctgtga 180
gagctttcaa actttt 196

<210> 654

<211> 581

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature
<222> (1)...(581)
<223> n = A,T,C or G

<400> 654
ctgctcgaca gcatatggca ccagcccatt ttcaatttgc tgagcatcgg ccaaagcctg 60
tatgcgaaag ccaaggagct ggacagagtg aaggaaattc aggagcagct cttccatata 120
aagaagctgt tgaagacctg taggtttgct aacagtgcac taaaggagtt tgtagggcag 180
gtgccgggac acttgactga tgagctccac ctgttctccc ttgaggacct ggtcaggatc 240
aagaagggc tgctggcacc cttactcaag gacattctga aagcttccct tgcacatgtg 300
gctggctgtg agctgtgtca aggaagggc tttatttgtg aattttgccga gaatacgact 360
gtcatcttcc catttcagac agcaacatgt agaagatgtt cagcgtgcag ggcttgcttt 420
cacaacagct gcttccagtc ctccgagtg ccccggtgtg cgaggatcac agcgaggaga 480
aaacttctgg aaagtgtggc ctctgcagca acatgatgcc cctgagtact gngaaaaaga 540
ctgttcaaca tgccttatga taacaccgat ttgngtctat t 581

<210> 655
<211> 482
<212> DNA
<213> Homo sapiens

<400> 655
aaaaaaacag aacatttaca agacaccagt tattttgtgc cccatatgtc attaaaaaag 60
tttactttac ctttattatt atttccctag gctagtcaag cagcaaaacca ttaatcggtc 120
ggagaaacct tcatgacata tgcccgaactg gctcttcgcc acccacttga aggacactac 180
ccaatcgatg gaagccttta atcgcacagc cctccctatt agcggactat tggcggatgc 240
agacatgttc tactcgagca gttaccaagg accactttac tgcgatcagg attccaacga 300
ccacctaat tcttatcttt caactctttt cgaccggacc tcttattcgg aagcgttaca 360
ggaagacagc tctcaactta gggatcagat cacgttatca acgctctggg atcgctgcaa 420
cctggcactt caaggaagtg caccgataac gtctagaccg gcaaacacag atctagaggt 480
gg 482

<210> 656
<211> 252
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(252)
<223> n = A,T,C or G

<400> 656
aaaatacttt tataaaatta taaattgata ataatcccn caaactgaag ngaaatactt 60
ttaatactac ttgaaattaa agtacagttg nttatacaac aatgaataag gacaagatat 120
naaaactgaaa attcaaaaat aaacagaaga aatgtaaaac gttctaaaat atcagtattt 180
ataaatgttg cttagaggaa ggctattcaa agcatgggcc attaactatt tgtgagctgt 240
ccagaatgaa ag 252

<210> 657
<211> 379
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(379)
<223> n = A,T,C or G

<400> 657
aaaataagct atgggtttttc cagtagccaa aatgatcctg caccanagct catanactga 60
gaacctganc atgcaaancc acagtctggg tgaagggatg tctgctttgt aaatgacctg 120
ctaattcttt gcaaccacaa gtaatttggt ttctgtgaac ccacagaagc agggccacca 180

```
aaaagggcct tgtctgctag cctggagtat acatgantca ctggcggtgg gatcagtcac 240
tttttaggct gcccatttt cctaacatgt taaaatgtgt gttctcagtc ttttcaagag 300
aggaagaagc aaagcggcac ttacagagtg tgtgatanga cacagatctg tggcgaggga 360
ttggggaagg tgggtggca 379
```

<210> 658
<211> 551
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(551)
<223> n = A,T,C or G

```
<400> 658
ctgaatatat taaacnttgc tctattatct gttgaattgc tgtatttcac tttttcagca 60
tttggggatc attatttaac tgaatttgta gagatcgatt ttccagacag gtctctgttc 120
ttcaatgaac aaatgataag aaacaatttg actccttata tgacaatgga attaaataaa 180
ttgacactca tctaggaata attctacaat catctccatc tctaagatta cctactgcaa 240
acaaagaatt gatcttttct tctcaaaaac cacatgggta agatgatcat tgtgactctg 300
aatgcaagaa taagtgaagt gaagctacaa ggggagatta tctgccaaac tagaaagaat 360
ctagaagaaa agattttatt acaggtaaca tgacatagct tggagccatc tttttgggtct 420
cttgcataca ttttctctgc atgtctaagg aagaattcac aaggtagcaa gcaccaatac 480
tttctgcttt ggagtttcac aaattgaaaa tttgtccctc tcttgtaaag tcaatcaaac 540
atctaccaat g 551
```

<210> 659
<211> 278
<212> DNA
<213> Homo sapiens

```
<400> 659
aaaatatccc tgaagtgaca cactcctttt ttgagaccga tactgggtatt cttttattat 60
agagactaaa aggtctgcct tactagactt cccacttttt gttctgaaag gaattaagga 120
ctgcagggtt ccagctctgt cttcccaggg ccattatgaa cagattaaat ggaaggacaa 180
attctaaata actgggcttt caacatgaaa agggaaaggc tgatggggag ttcagaacct 240
tgaatactgt aactgaacat ccctcaaggt taatgcag 278
```

<210> 660
<211> 414
<212> DNA
<213> Homo sapiens

```
<400> 660
cctgacacaa tatccctgtt cactttgaag tgaattttga ctctatattc agaaccttcc 60
tttaacacaa tggtttcctt tttgagggtc tccagatctc cagtaaggtc catgggtgatt 120
ggtccccggg cactctcaca aaccagggtg agccgggtga caacgacatt gggggctttc 180
ggatctgtca ccacaggacc atctcccagc agcgttttct tgtacttaac tagactctca 240
tcattctttg ccattttcctg cagctctttc agggacttct gtggtggagg cttataattg 300
agcttgctgt ccagctcatc atcgtcatcc tcctccacat gtgggctctg gggctttttc 360
agtcattctg atctatttat tcagtgttcc acgtctctgt ccggggtgcc tctg 414
```

<210> 661
<211> 353
<212> DNA
<213> Homo sapiens

```
<400> 661
gtttcagccg aaggactctt ctattcggaa gtacaccctc actattagga agattcttag 60
gggtaatttt tctgaggaag gaggactagc caacttaaga attacaggaa gaaagtgggt 120
tggaagacag ccaaagaaat aaaagcagat taaactgtat caggtacatt ccagctgttt 180
ggcaactcca taaaaacatt tcagatttta atccgaattt agctaataag actggatttt 240
```


tggttttttat gttgtgtgtc acagagctaa aaactcagtt cccaaatccc cagttttatgc 300
agccgccatc aggtatttta agctaaactt cttcaccctt gagagcatgt cag 353

<210> 662
<211> 101
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(101)
<223> n = A,T,C or G

<400> 662
agggggntgg tggctgncnt natnaggacc tggacggcct ggncctgagct gaccnatgcc 60
ngatntactg gtncnctact gaangtacac aanatcntta a 101

<210> 663
<211> 442
<212> DNA
<213> Homo sapiens

<400> 663
cctccaattc cacagagcac aattttaaac tacagcatat gaaaatagca aatgcaaaaa 60
aacaaaaaca aaaacacacac acaaaatgcc acatgtaaat ggtggagtat gtattttatac 120
ataacatccc cacatacata catacactca aaacaatact atataatatt tctatgtgaa 180
catacaatgt ccttctggaa gaacatacaa aaactggtaa cagtagctaa ctttagggga 240
gaatccttga ttaggggttg tagatgaaaa gacttcagcc ctttctgtaa ggtgggcagc 300
acatatattac aaaagggaatg tatctctgta ttgtgtgtga atataccatt aatttctaaa 360
aggttccatg agaaaatttt cgaagaattg cacaacatc ctttgctatg tagacaaaga 420
tgggtgactcg gcacaaagcc ag 442

<210> 664
<211> 317
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(317)
<223> n = A,T,C or G

<400> 664
ctgggtggta acaagtggat cgtcatgttc agtagtttat acattatgtg agaagtaacg 60
ttctgattct ttttcttaca cagaattggc agaggggggtc gatttgggag gaaaggtgtg 120
gctataaact ttgttactga agaagacaag aggattcttc gtgacattga gactttctac 180
aatactacag tggaggagat gccatgaat gtgactgacc ttattttaatt cctgggatga 240
gagttttcga tgcagtgtc gctgttgntg aataggcnat cacnacgtgc attgtgcttc 300
tttctttggn aatattt 317

<210> 665
<211> 1324
<212> DNA
<213> Homo sapiens

<400> 665
cttgagagge tctgtctctt gcttcttagg cggcccagag acgccatggc cgagtgcctg 60
acactcgggg aggcagtcac cgaccaccgg gaccgcctgt gggcctggga gaagttcgtg 120
tatttggacg agaagcagca cgcttgctg cccttaacca tcgagataaa ggataggtta 180
cagttacggg tgctcttgcg tcgggaagac gtcgtccttg ggaggcctat gacccccacc 240
cagataggcc caagcctgct gcctatcatg tggcagctct accctgatgg acgataccga 300
tcctcagact ccagtttctg gcgcttagtg taccacatca agattgacgg cgtggaggac 360

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<210> 666
<211> 114
<212> PRT
<213> Homo sapiens
```

```

<400> 666
Met Ala Glu Cys Pro Thr Leu Gly Glu Ala Val Thr Asp His Pro Asp
      5                      10                      15

Arg Leu Trp Ala Trp Glu Lys Phe Val Tyr Leu Asp Glu Lys Gln His
      20                      25                      30

Ala Trp Leu Pro Leu Thr Ile Glu Ile Lys Asp Arg Leu Gln Leu Arg
      35                      40                      45

Val Leu Leu Arg Arg Glu Asp Val Val Leu Gly Arg Pro Met Thr Pro
      50                      55                      60

Thr Gln Ile Gly Pro Ser Leu Leu Pro Ile Met Trp Gln Leu Tyr Pro
      65                      70                      75                      80

Asp Gly Arg Tyr Arg Ser Ser Asp Ser Ser Phe Trp Arg Leu Val Tyr
      85                      90                      95

His Ile Lys Ile Asp Gly Val Glu Asp Met Leu Leu Glu Leu Leu Pro
      100                      105                      110

Asp Asp

```

```
<210> 667
<211> 1659
<212> DNA
<213> Homo sapiens
```

<400> 667									
tcagcggggc	agtcccccgc	tcctccagct	ccttcctcct	cttcctcctc	ctctccacc	60			
tcggcgcttt	ggggcgctac	tgctcctctc	ggcgagcaga	atgagccggc	agbtggtcgc	120			
tcgcgcgaag	tttccgccac	tggttgga	gccggccaag	gccgaccagt	gctatgaaga	180			
tggtgcgcgtc	tcacagacca	cctgggacag	tgccctctgt	gctgtcaacc	ctaagtttgt	240			
ggccctgatc	tgtagggcca	gcgggggagg	ggccttctgt	gtgctgcgcc	tgggcaagac	300			
tggaactgtgt	gacaagaatg	cgcgccaggt	ctgtggccac	acagcccctg	tgttagacat	360			
cgctcgggtgc	ccgcacaatg	acaacgtcat	tgccagtgtc	tccgaggact	gcacagtcat	420			
gggtctgggag	atcccggaat	ggggcctgat	gtgcgccctg	ccggagcccg	tcgtcacctc	480			
ggaagcccac	accaagctat	tggcacttgt	ggcttggcac	accagagccc	agaaactgtc	540			

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gctcagtgca ggttggtgaca acgtgatcat ggtgtgggac gtgggcactg gggcggccat 600
gctgacactg ggcccagagg tgcaccagga cagcatctac agtgtggact ggagccgaga 660
tggaggcctc atttgtacct cctgccgtga caagcgctg cgcatcatcg agccccgcaa 720
aggcactgtc gtagctgaga aggaccgtcc ccacgagggg acccggcccg tgcgtgcagt 780
gttcgtgtcg gagggggaaga tcctgaccac gggcttcagc cgcatgagtg agcggcaggt 840
ggcgctgtgg gacacaaagc acctggagga gccgctgtcc ctgcaggagc tggacaccag 900
cagcggtgtc ctgctgccct tctttgaccc tgacaccaac atcgtctacc tctgtggcaa 960
gggtgacagc tcaatccggt actttgagat cacttccgag gccctttcc tgcactatct 1020
ctccatgttc agttccaagg agtcccagcg gggcatgggc tacatgcccc aacgtggcct 1080
ggaggtgaac aagtgtgaga tcgccagggt ctacaagctg cacgagcgga ggtgtgagcc 1140
cattgccatg acagtgcctc gaaagtcgga cctgttccag gaggacctgt acccaccac 1200
cgcaggggcc gaccctgccc tcacggctga ggagtggctg gggggtcggg atgctgggct 1260
cctcctcatc tccctcaagg atggctacgt acccccaaag agccgggagc tgagggtcaa 1320
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ccagaagcgc ttggacaggc tggaggagac agtccaggcc aagtagagcc ccgaggggcc 1500
tccagcaggg tcagccattc acaccatcc actcacctcc cattcccagc cacatggcag 1560
agaaaaaaat cataataaaa tggctttatt ttctggtaaa aaaaaaaaaa aaaaaaaaaa 1620
aaaaaaaaaa aaaaaaaaaa aaaaaaaagg gggggggga 1659

```

<210> 668

<211> 461

<212> PRT

<213> Homo sapiens

<400> 668

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Met Ser Arg Gln Val Val Arg Ser Ser Lys Phe Arg His Val Phe Gly
              5                      10                      15

Gln Pro Ala Lys Ala Asp Gln Cys Tyr Glu Asp Val Arg Val Ser Gln
              20                      25                      30

Thr Thr Trp Asp Ser Gly Phe Cys Ala Val Asn Pro Lys Phe Val Ala
              35                      40                      45

Leu Ile Cys Glu Ala Ser Gly Gly Gly Ala Phe Leu Val Leu Pro Leu
              50                      55                      60

Gly Lys Thr Gly Arg Val Asp Lys Asn Ala Pro Thr Val Cys Gly His
              65                      70                      75                      80

Thr Ala Pro Val Leu Asp Ile Ala Trp Cys Pro His Asn Asp Asn Val
              85                      90                      95

Ile Ala Ser Gly Ser Glu Asp Cys Thr Val Met Val Trp Glu Ile Pro
              100                     105                     110

Asp Gly Gly Leu Met Leu Pro Leu Arg Glu Pro Val Val Thr Leu Glu
              115                     120                     125

Gly His Thr Lys Arg Val Gly Ile Val Ala Trp His Thr Thr Ala Gln
              130                     135                     140

Asn Val Leu Leu Ser Ala Gly Cys Asp Asn Val Ile Met Val Trp Asp
              145                     150                     155                     160

Val Gly Thr Gly Ala Ala Met Leu Thr Leu Gly Pro Glu Val His Pro
              165                     170                     175

Asp Thr Ile Tyr Ser Val Asp Trp Ser Arg Asp Gly Gly Leu Ile Cys
              180                     185                     190

Thr Ser Cys Arg Asp Lys Arg Val Arg Ile Ile Glu Pro Arg Lys Gly

```

195					200					205					
Thr	Val	Val	Ala	Glu	Lys	Asp	Arg	Pro	His	Glu	Gly	Thr	Arg	Pro	Val
210					215							220			
Arg	Ala	Val	Phe	Val	Ser	Glu	Gly	Lys	Ile	Leu	Thr	Thr	Gly	Phe	Ser
225					230					235					240
Arg	Met	Ser	Glu	Arg	Gln	Val	Ala	Leu	Trp	Asp	Thr	Lys	His	Leu	Glu
				245					250					255	
Glu	Pro	Leu	Ser	Leu	Gln	Glu	Leu	Asp	Thr	Ser	Ser	Gly	Val	Leu	Leu
			260					265					270		
Pro	Phe	Phe	Asp	Pro	Asp	Thr	Asn	Ile	Val	Tyr	Leu	Cys	Gly	Lys	Gly
		275					280					285			
Asp	Ser	Ser	Ile	Arg	Tyr	Phe	Glu	Ile	Thr	Ser	Glu	Ala	Pro	Phe	Leu
290					295					300					
His	Tyr	Leu	Ser	Met	Phe	Ser	Ser	Lys	Glu	Ser	Gln	Arg	Gly	Met	Gly
305				310					315						320
Tyr	Met	Pro	Lys	Arg	Gly	Leu	Glu	Val	Asn	Lys	Cys	Glu	Ile	Ala	Arg
				325					330					335	
Phe	Tyr	Lys	Leu	His	Glu	Arg	Arg	Cys	Glu	Pro	Ile	Ala	Met	Thr	Val
			340					345					350		
Pro	Arg	Lys	Ser	Asp	Leu	Phe	Gln	Glu	Asp	Leu	Tyr	Pro	Pro	Thr	Ala
		355					360					365			
Gly	Pro	Asp	Pro	Ala	Leu	Thr	Ala	Glu	Glu	Trp	Leu	Gly	Gly	Arg	Asp
370					375					380					
Ala	Gly	Pro	Leu	Leu	Ile	Ser	Leu	Lys	Asp	Gly	Tyr	Val	Pro	Pro	Lys
385				390					395						400
Ser	Arg	Glu	Leu	Arg	Val	Asn	Arg	Gly	Leu	Asp	Thr	Gly	Arg	Arg	Arg
				405					410					415	
Ala	Ala	Pro	Glu	Ala	Ser	Gly	Thr	Pro	Ser	Ser	Asp	Ala	Val	Ser	Arg
			420					425					430		
Leu	Glu	Glu	Glu	Met	Arg	Lys	Leu	Gln	Ala	Thr	Val	Gln	Glu	Leu	Gln
			435				440					445			
Lys	Arg	Leu	Asp	Arg	Leu	Glu	Glu	Thr	Val	Gln	Ala	Lys			
450					455					460					

<210> 669

<211> 79

<212> PRT

<213> Homo sapiens

<400> 669

Gly	Lys	His	Pro	Asp	Pro	Ser	Ala	Trp	His	Arg	Pro	Ser	Asp	Thr	Glu
				5					10					15	

Pro	Leu	Asn	Lys	Gly	Thr	Pro	Thr	Pro	His	His	Ile	Leu	Arg	Ser	Gly
				20				25					30		

Ala Pro Gln Val Asp Thr Arg Thr Leu Thr Pro Cys Pro Ser Ser Thr
 35 40 45
 Pro Gln Val Ser Pro Arg Leu Pro Pro Arg Ser Leu Cys Ser Arg Pro
 50 55 60
 Pro Leu Arg Ser Phe Lys Pro Thr Arg Pro His Trp Cys Val Ser
 65 70 75

<210> 670
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 670
 Thr Phe Arg His Arg Ala Pro Glu Gln Gly His Pro Asn Thr Ser Ser
 5 10 15
 Tyr Thr Glu Val Arg Gly Ser Pro Gly Gly His Gln Asp Ser Asp Pro
 20 25 30
 Leu Pro Leu Ile His Pro Ala Gly Gln Pro Lys Ala Ala Pro Ser Val
 35 40 45
 Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr
 50 55 60
 Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala
 65 70 75 80
 Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr
 85 90 95
 Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser
 100 105 110
 Leu Thr Pro Glu Gln Trp Lys Ser His Lys Ser Tyr
 115 120

<210> 671
 <211> 50
 <212> PRT
 <213> Homo sapiens

<400> 671
 Pro Ala Gly Trp Met Arg Gly Arg Gly Ser Glu Ser Trp Cys Pro Pro
 5 10 15
 Gly Glu Pro Leu Thr Ser Val Tyr Asp Glu Val Leu Gly Cys Pro Cys
 20 25 30
 Ser Gly Ala Leu Cys Leu Lys Val Tyr Ala Arg Gln Arg Gly Gln Gly
 35 40 45
 Val Phe
 50

<210> 672
 <211> 108

```

<400> 672
Val Ala Phe Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Val Ala
          5                               10                      15

Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
          20                               25                      30

His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
          35                               40                      45

Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
          50                               55                      60

Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
          65                               70                      75                      80

Ser Leu Gly Leu Thr Cys Gly Val Asp Glu Gly Gln Gly Val Arg Val
          85                               90                      95

Leu Val Ser Thr Trp Gly Ala Pro Asp Leu Ser Ile
          100                               105

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```
<210> 673
<211> 58
<212> PRT
<213> Homo sapiens
```

```

<400> 673
Gln Arg His Cys Gln Trp Leu Arg Gly Leu His Ser His Gly Val Gly
          5              10              15
Asp Pro Gly Trp Gly Pro Asp Ala Ala Pro Ala Gly Ala Arg Arg His
          20              25              30
Pro Gly Gly Pro His Gln Ala Cys Gly His Cys Gly Leu Ala His His
          35              40              45
Ser Pro Glu Arg Ala Ala Gln Cys Arg Leu
          50              55

```

```
<210> 674
<211> 109
<212> PRT
<213> Homo sapiens
```

<400> 674

His	Thr	Ala	Pro	Val	Leu	Asp	Ile	Ala	Trp	Cys	Pro	His	Asn	Asp	Asn
				5					10					15	
Val	Ile	Ala	Ser	Gly	Ser	Glu	Asp	Cys	Thr	Val	Met	Val	Trp	Glu	Ile
			20					25					30		
Pro	Asp	Gly	Gly	Leu	Met	Leu	Pro	Leu	Arg	Glu	Pro	Val	Val	Thr	Leu
		35					40					45			
Glu	Gly	His	Thr	Lys	Arg	Val	Gly	Ile	Val	Ala	Trp	His	Thr	Thr	Ala
	50					55				60					

Gln Asn Val Leu Leu Ser Ala Gly Cys Asp Asn Val Ile Met Val Trp
 65 70 75 80
 Asp Val Gly Thr Gly Ala Ala Met Leu Thr Leu Gly Pro Glu Val His
 85 90 95
 Pro Asp Thr Ile Tyr Ser Val Asp Trp Ser Arg Asp Gly
 100 105

<210> 675
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 675
 Ile Val Ser Gly Cys Thr Ser Gly Pro Ser Val Ser Met Ala Ala Pro
 5 10 15
 Val Pro Thr Ser His Thr Met Ile Thr Leu Ser Gln Pro Ala Leu Ser
 20 25 30
 Ser Thr Phe Trp Ala Val Val Cys Gln Ala Thr Met Pro Thr Arg Leu
 35 40 45
 Val Trp Pro Ser Arg Val Thr Thr Gly Ser Arg Arg Gly Ser Ile Arg
 50 55 60
 Pro Pro Ser Gly Ile Ser His Thr Met Thr Val Gln Ser Ser Glu Pro
 65 70 75 80
 Leu Ala Met Thr Leu Ser Leu Cys Gly His Gln Ala Met Ser Ser Thr
 85 90 95
 Gly Ala Val Trp
 100

<210> 676
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 676
 Ser Ile Ser Ala Pro Val His Thr Val Asp Arg Val Trp Val His Leu
 5 10 15
 Trp Ala Gln Cys Gln His Gly Arg Pro Ser Ala His Val Pro His His
 20 25 30
 Asp His Val Val Thr Thr Cys Thr Glu Gln His Val Leu Gly Cys Gly
 35 40 45
 Val Pro Gly His Asn Ala His Thr Leu Gly Val Ala Leu Gln Gly Asp
 50 55 60
 Asp Gly Leu Pro Gln Gly Gln His Gln Ala Pro Ile Arg Asp Leu Pro
 65 70 75 80
 His His Asp Cys Ala Val Leu Gly Ala Thr Gly Asn Asp Val Val Ile
 85 90 95
 Val Arg Ala Pro Gly Asp Val

100

<210> 677
<211> 89
<212> PRT
<213> Homo sapiens

<400> 677
Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly
 5 10 15
Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu Lys Glu
 20 25 30
Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg
 35 40 45
Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys Gln
 50 55 60
Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg
 65 70 75 80
Ala Lys Pro Val Thr Gln Ile Val Ser
 85

<210> 678
<211> 89
<212> PRT
<213> Homo sapiens

<400> 678
Ala Asp Asp Leu Gly Asp Arg Phe Gly Pro Ile Leu Gly Pro Leu Val
 5 10 15
Ile Leu Arg Glu Pro Val Glu Leu Asp Leu Thr Ala Glu Val Val Ala
 20 25 30
Gly Val Leu Pro Glu Gly Gly Arg Asp Pro Gln Ala Ala Ala Gln Ala
 35 40 45
Val Ser Gly Val Ile Glu Gly Gly Leu Leu Leu Glu Gly Leu Arg Val
 50 55 60
Cys Ala Asp Pro Thr Val His Leu Leu Pro Ile His Pro Pro Ala Gln
 65 70 75 80
Leu His Val Val Gly Val Glu Ala Cys
 85

<210> 679
<211> 59
<212> PRT
<213> Homo sapiens

<400> 679
Gln Arg Lys Trp Leu Arg Gly Phe Cys Gln Lys Val Ala Glu Thr Leu
 5 10 15
Arg Arg Leu Leu Arg Gln Tyr Leu Glu Ser Leu Arg Ala Gly Cys Ser

20 25 30
 Leu Arg Gly Cys Gly Ser Val Leu Thr Pro Leu Cys Thr Ser Phe Pro
 35 40 45
 Phe Thr His Gln Leu Ser Ser Thr Trp Ser Gly
 50 55

<210> 680
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(123)
 <223> Xaa = Any amino acid

<400> 680
 Thr Xaa Xaa Ile Asn Arg Xaa Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
 5 10 15
 Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly
 20 25 30
 Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
 35 40 45
 Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
 50 55 60
 Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
 65 70 75 80
 Lys Ala Xaa Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
 85 90 95
 Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu
 100 105 110
 Thr Pro Glu Gln Trp Lys Ser His Xaa Thr Thr
 115 120

<210> 681
 <211> 85
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(85)
 <223> Xaa = Any amino acid

<400> 681
 Cys Ser Xaa Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
 5 10 15
 Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30
 His Ser Arg Leu Asp Gly Ala Ala Xaa Cys Leu Pro Gly His Cys His

35 40 45
 Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
 50 55 60
 Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
 65 70 75 80
 Ser Leu Gly Leu Thr
 85

<210> 682
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 682
 Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
 5 10 15
 Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30
 His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45
 Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
 50 55 60
 Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
 65 70 75 80
 Ser Leu Gly Leu Thr
 85

<210> 683
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 683
 Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
 5 10 15
 Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly
 20 25 30
 Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
 35 40 45
 Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
 50 55 60
 Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
 65 70 75 80
 Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
 85 90 95
 Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu
 100 105 110

Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
 115 120

<210> 684
 <211> 161
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(161)
 <223> Xaa = Any amino acid

<400> 684
 Pro Cys Leu Arg Ser Lys Val Thr Arg Lys Arg Pro Cys Leu Pro Ser
 5 10 15
 Met Thr Leu Met Glu Glu Met Leu Arg Glu Ala Phe Arg Cys Met Thr
 20 25 30
 Gln Glu Pro Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro
 35 40 45
 Leu Phe Arg Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe
 50 55 60
 Met Arg Glu Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn Gly Leu
 65 70 75 80
 Phe His Ile Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly Ile Tyr
 85 90 95
 Ala Pro Ile Cys Val Thr Gly Val Val Pro Ser Leu Gly Arg His Tyr
 100 105 110
 Val Tyr Tyr Phe Arg Ile Thr Pro Gly Ser Asn Arg Lys Lys Asn Ser
 115 120 125
 Arg Lys Cys Leu Val Lys Gly Lys Asn Asp Asn Glu Phe Ile Xaa Pro
 130 135 140
 Ser Leu Leu Ala Phe Ser Gly Lys Asn Ser Phe Gln Ile Met Gly Pro
 145 150 155 160
 Tyr

<210> 685
 <211> 60
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(60)
 <223> Xaa = Any amino acid

<400> 685
 Leu Gly Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr Ile Ile Ser Gly
 5 10 15

Ser Leu Leu Ala Ala Thr Gly Lys Lys Thr Pro Gly Ser Val Trp Ser
 20 25 30
 Lys Glu Lys Met Ile Met Asn Ser Leu Xaa Pro Leu Cys Leu Pro Phe
 35 40 45
 Leu Glu Arg Ile Leu Phe Lys Ser Trp Asp His Thr
 50 55 60

<210> 686
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 686
 Leu Pro Gln Ile Gln Gly His Ser Glu Glu Ala Met Ser Thr Leu Asn
 5 10 15
 Asp Thr His Gly Gly Asn Ala Glu Arg Ser Ile Gln Met His Asp Thr
 20 25 30
 Arg Ala Asn Glu Arg Pro Tyr Cys Tyr Ala Ile Trp Ser Lys Thr Thr
 35 40 45
 Leu Gln Glu Asp Val Phe Thr Gly Gly Pro His Ala Lys Leu Leu His
 50 55 60
 Glu Gly Ile
 65

<210> 687
 <211> 68
 <212> PRT
 <213> Homo sapiens

<400> 687
 Asp Phe Gly Gly Cys Pro Asp Tyr Glu Trp Ala Leu Pro His Cys Pro
 5 10 15
 Gly Gly Ser Ser Asp Asp Pro Ser Arg Asp Leu Cys Thr His Leu Cys
 20 25 30
 Asp Trp Gly Gly Thr Leu Ser Gly Glu Ala Leu Cys Ile Leu Phe Pro
 35 40 45
 Asp His Ser Trp Gln Gln Pro Glu Lys Lys Leu Gln Glu Val Phe Gly
 50 55 60
 Gln Arg Lys Lys
 65

<210> 688
 <211> 106
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(106)

<223> Xaa = Any amino acid

<400> 688

```

Val Trp Ser His Asp Leu Lys Arg Ile Leu Ser Arg Lys Gly Lys Gln
              5              10              15

Arg Gly Xaa Asn Glu Phe Ile Ile Ile Phe Ser Phe Asp Gln Thr Leu
              20              25              30

Pro Gly Val Phe Phe Pro Val Ala Ala Arg Ser Asp Pro Glu Ile Ile
              35              40              45

Tyr Ile Met Pro Pro Gln Arg Gly Tyr His Pro Ser His Thr Asp Gly
              50              55              60

Cys Ile Asp Pro Cys Trp Asp His Gln Lys Thr Pro Gln Gly Asn Val
              65              70              75              80

Glu Glu Pro Ile His Asn Leu Asp Ser Pro Gln Ser Leu Arg Phe Pro
              85              90              95

His Glu Glu Ala Leu Arg Gly Ala His Gln
              100              105

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<210> 689

<211> 94

<212> PRT

<213> Homo sapiens

<400> 689

```

Ile Pro Ala Gly Ile Ile Arg Arg Pro Pro Arg Ala Met Trp Lys Ser
              5              10              15

Pro Phe Ile Ile Trp Thr Ala Pro Lys Val Leu Asp Ser Leu Met Lys
              20              25              30

Lys Leu Cys Val Gly Pro Thr Ser Glu Asp Ile Leu Leu Lys Ser Gly
              35              40              45

Phe Gly Pro Asp Cys Ile Ala Ile Gly Pro Phe Ile Gly Ser Cys Val
              50              55              60

Met His Leu Asn Ala Ser Leu Ser Ile Ser Ser Met Ser Val Ile Glu
              65              70              75              80

Gly Arg His Gly Leu Phe Arg Val Thr Leu Asp Leu Arg Gln
              85              90

```

<210> 690

<211> 151

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(151)

<223> Xaa = Any amino acid

<400> 690

```

Pro Gly Gly Gln His Gly Gly Asp Trp Ser Trp Arg Val Thr Val Glu
              5              10              15

```

Pro Gln Asp Ser Gly Thr Ser Ala Leu Pro Leu Val Ser Leu Phe Phe
 20 25 30
 Tyr Val Val Thr Asp Gly Lys Glu Val Leu Leu Pro Glu Val Gly Ala
 35 40 45
 Lys Gly Gln Leu Lys Phe Ile Ser Gly His Thr Ser Glu Leu Gly Asn
 50 55 60
 Phe Arg Phe Thr Leu Leu Pro Pro Thr Ser Pro Gly Asp Thr Ala Pro
 65 70 75 80
 Lys Tyr Gly Ser Tyr Asn Val Phe Trp Thr Ser Asn Pro Gly Leu Pro
 85 90 95
 Leu Leu Thr Glu Met Val Lys Ser Arg Leu Asn Ser Trp Phe Gln His
 100 105 110
 Arg Pro Pro Gly Ala Ser Pro Glu Arg Tyr Leu Gly Leu Pro Gly Ser
 115 120 125
 Leu Lys Trp Glu Asp Arg Xaa Pro Ser Gly Gln Gly Xaa Gly Ala Val
 130 135 140
 Leu Asp Thr Ala Gly Asp Pro
 145 150

<210> 691
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 691
 Trp Gly Ser Ala Arg Arg Gly Leu Glu Leu Glu Ser Asp Cys Arg Ala
 5 10 15
 Ser Gly Leu Arg Tyr Phe Cys Pro Pro Phe Gly Leu Pro Val Leu Leu
 20 25 30
 Cys Gly Asp Arg Trp Gln Gly Ser Pro Thr Thr Arg Gly Trp Gly Gln
 35 40 45
 Gly Ala Val Glu Val Tyr Gln Trp Ala His Gln
 50 55

<210> 692
 <211> 85
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(85)
 <223> Xaa = Any amino acid

<400> 692
 Phe Lys Gly His Leu Leu Tyr Gln Glu Leu Pro Xaa Ala Leu Ala His
 5 10 15
 Leu Asp Xaa Cys Pro Pro Thr Ser Gly Ile Leu Ala Ser Arg Gly Ser

20 25 30
 Val Gln Gly Arg Pro Leu Gly Ala Asp Ala Glu Thr Ser Tyr Leu Gly
 35 40 45
 Asp Ser Leu Pro Ser Leu Ser Ala Gly Ala Val Leu Gly Trp Arg Ser
 50 55 60
 Arg Arg His Cys Ser Cys His Thr Trp Gly Leu Tyr Pro Leu Asp Trp
 65 70 75 80
 Leu Val Ala Lys Val
 85

<210> 693
 <211> 53
 <212> PRT
 <213> Homo sapiens

<400> 693
 Thr Ser Thr Ala Pro Trp Pro Gln Pro Leu Val Val Gly Leu Pro Cys
 5 10 15
 His Leu Ser Pro His Arg Arg Thr Gly Arg Pro Lys Gly Gly Gln Lys
 20 25 30
 Tyr Leu Ser Pro Glu Ala Leu Gln Ser Leu Ser Ser Ser Pro Leu
 35 40 45
 Arg Ala Asp Pro Gln
 50

<210> 694
 <211> 62
 <212> PRT
 <213> Homo sapiens

<400> 694
 Ala Thr Leu Tyr His Leu Cys Gln Gln Gly Gln Ser Trp Val Gly Gly
 5 10 15
 Pro Glu Asp Ile Val Ala Ala Ile Leu Gly Gly Cys Ile Pro Trp Thr
 20 25 30
 Gly Trp Trp Gln Lys Cys Lys Ala Glu Val Thr Lys Phe Thr Gly Val
 35 40 45
 Pro Thr Asp Lys Leu Gln Leu Pro Leu Gly Pro Asn Leu Trp
 50 55 60

<210> 695
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 695
 Leu Pro Tyr Leu Gly Ala Val Ser Pro Gly Leu Val Gly Gly Lys Ser
 5 10 15
 Val Lys Arg Lys Leu Pro Ser Ser Leu Val Cys Pro Leu Ile Asn Phe

20

30

Val Thr Thr
50

```
<210> 696
<211> 71
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> variant  
<222> (1)...(71)  
<223> Xaa = Any amino acid
```

<400> 696
Ile Arg Ser Lys Ser His Pro Gly Leu Gly Pro Ser Thr His Ser Arg
 5 10 15

Ile Gly Ser Ala Asp Thr Glu Gly Gly His Gly Thr Arg Arg Leu His
20 25 30

Gly Arg Leu Leu Ser Arg Leu Tyr Pro Gly His Gln Arg Xaa Val Leu
35 40 45

Thr Cys Ile Asn Cys Xaa Trp Asn Ser Pro His His Arg Gly Tyr Pro
50 55 60

Trp Pro Xaa Xaa Leu Lys Cys
65 70

```
<210> 697
<211> 97
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> variant  
<222> (1)...(97)  
<223> Xaa = Any amino acid
```

<400> 697
Ala Ser Tyr Ser Tyr Xaa Xaa Glu Lys Pro Ser Ala Ile Gln Gln Arg
5 10 15

Ala Ile Leu Pro Cys Ile Lys Gly Tyr Asp Val Ile Ala Gln Ala Gln
20 25 30

Ser Gly Thr Gly Lys Thr Ala Thr Phe Ala Ile Ser Ile Leu Xaa Gln
35 40 45

Ile Glu Leu Asp Leu Lys Ala Thr Gln Ala Leu Val Leu Ala Pro Thr
50 55 60

Arg Glu Leu Ala Gln Gln Ile Gln Lys Val Val Met Ala Leu Gly Asp
65 70 75 80

Tyr Met Gly Ala Ser Cys His Ala Cys Ile Arg Gly Thr Asn Val Xaa

85

90

95

Cys

<210> 698
<211> 52
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(52)
<223> Xaa = Any amino acid

<400> 698
Pro Pro Ser Val Ser Ala Glu Pro Ile Leu Glu Trp Val Leu Gly Pro
 5 10 15

Arg Pro Gly Trp Leu Leu Asp Leu Ile Gln Ser Xaa Ala Glu Ser Ile
 20 25 30

Trp Gln Met Trp Pro Phe Ser Gln Ser Gln Ile Gly Leu Glu Gln Ser
 35 40 45

His His Asn Pro
 50

<210> 699
<211> 70
<212> PRT
<213> Homo sapiens

<400> 699
Ser Gly His Ser Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu
 5 10 15

Leu Leu Leu Trp Leu Pro Gly Ala Lys Cys Asp Ile Gln Met Thr Gln
 20 25 30

Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Thr Ser Tyr Asn Lys
 35 40 45

Leu Ser Gly Leu Ser Glu Tyr Arg Ser Val Val Gly Leu Ala Ser Thr
 50 55 60

Glu Thr Arg Gln Ser Pro
 65 70

<210> 700
<211> 97
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(97)
<223> Xaa = Any amino acid

<400> 700

Pro Asn Leu Leu Pro Pro Cys Leu His Leu Ser Glu Ile Gln Val Thr
 5 10 15
 Ile Ser Cys Arg Ala Ser Gln Asn Ile Asp Arg Trp Leu Ala Trp His
 20 25 30
 Gln Gln Lys Pro Gly Lys Ala Pro Asn Val Leu Ile Tyr Ala Thr Ser
 35 40 45
 Ser Leu Glu Glu Gly Val Ser Leu Arg Phe Thr Gly Ser Gly Ser Gly
 50 55 60
 Thr Gln Phe Asn Leu Thr Ile Thr Ser Leu Gln Pro Asp Asp Ser Ala
 65 70 75 80
 Thr Tyr Tyr Xaa Gln His Tyr Ser Ala Ser Leu Arg Ser Phe Trp Thr
 85 90 95
 Ser

<210> 701
 <211> 72
 <212> PRT
 <213> Homo sapiens

<400> 701
 Asp Ile Arg Gly Phe Ala Trp Phe Leu Leu Met Pro Gly Gln Pro Pro
 5 10 15
 Ile Tyr Ile Leu Arg Gly Pro Thr Thr Tyr Cys Asn Leu Tyr Leu Arg
 20 25 30
 Gln Met Gln Thr Gly Trp Lys Glu Ile Gly Ser Ser Gly Cys His Ile
 35 40 45
 Trp His Leu Gly Ala Arg Ala Ala Gly Ala Pro Gly Ala Glu Arg Gly
 50 55 60
 Pro Ser Cys Pro Cys Cys Val Leu
 65 70

<210> 702
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 702
 Glu Ala Arg Gln Leu Ile Val Thr Cys Ile Ser Asp Arg Cys Arg Gln
 5 10 15
 Gly Gly Arg Arg Leu Gly His Leu Asp Val Thr Phe Gly Thr Trp Glu
 20 25 30
 Pro Glu Gln Gln Glu Pro Gln Glu Leu Ser Gly Asp Pro His Val His
 35 40 45
 Ala Val Ser
 50

<210> 703
<211> 61
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(61)
<223> Xaa = Any amino acid

<400> 703
Leu Leu Ala Ala Tyr Leu Leu Leu Cys Leu Glu Gly Val Val Xaa
 5 10 15

Ser Thr Pro Ala Leu Thr Gly Leu Ala Ile Cys Leu Pro Gly His Cys
 20 25 30

His Xaa Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Xaa Gly Leu
 35 40 45

Val Gly Leu Lys Leu Leu Xaa Gly Gly Arg Glu Thr Glu
 50 55 60

<210> 704
<211> 56
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(56)
<223> Xaa = Any amino acid

<400> 704
Val Ala Ala Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
 5 10 15

Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Xaa Leu
 20 25 30

His Ser Arg Leu Asp Gly Ala Cys Tyr Leu Pro Ser Arg Pro Leu Ser
 35 40 45

Xaa Leu Pro Gly Arg Ser His Leu
 50 55

<210> 705
<211> 76
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(76)
<223> Xaa = Any amino acid

<400> 705
Val Ser Pro Xaa Leu Pro Pro Arg Ser Phe Cys Phe Pro Pro Ser Xaa
 5 10 15

Glu Glu Leu Gln Ala Asn Lys Ala Xaa Leu Val Cys Leu Ile Ser Asp

20 25 30
 Phe Tyr Pro Gly Xaa Val Thr Val Ala Trp Lys Ala Asp Ser Lys Pro
 35 40 45
 Arg Gln Gly Gly Ser Gly Xaa His His Thr Leu Gln Thr Lys Gln Gln
 50 55 60
 Gln Val Arg Gly Gln Gln Leu Ser Glu Pro Asp Ala
 65 70 75

<210> 706

<211> 154

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(154)

<223> Xaa = Any amino acid

<400> 706

Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
 5 10 15
 Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly
 20 25 30
 Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
 35 40 45
 Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
 50 55 60
 Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
 65 70 75 80
 Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
 85 90 95
 Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu
 100 105 110
 Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Arg Pro Ala Arg Ala
 115 120 125
 Ala Lys Gly Glu Phe Gln His Thr Trp Arg Arg Tyr Tyr Gly Ser Xaa
 130 135 140
 Ser Val Pro Thr Trp Arg Asn His Xaa His
 145 150

<210> 707

<211> 67

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(67)

<223> Xaa = Any amino acid

<400> 707

Tyr Xaa His Asp Tyr Ala Lys Leu Val Pro Ser Xaa Ile His Ser Asn
 5 10 15

Gly Ala Lys Cys Ala Gly Ile Arg Pro Trp Pro Pro Gly Gln Val Cys
 20 25 30

Ser Phe Cys Gly Thr Ser Thr Ala Gln Ala Ser Gly Ser Asp Ser Cys
 35 40 45

Trp Pro Arg Thr Cys Cys Cys Phe Val Trp Arg Val Trp Trp Ser Pro
 50 55 60

Leu Pro Pro
 65

<210> 708

<211> 116

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(116)

<223> Xaa = Any amino acid

<400> 708

Met Xaa Met Ile Thr Pro Ser Trp Tyr Arg Xaa Gly Ser Ile Val Thr
 5 10 15

Ala Pro Ser Val Leu Glu Phe Ala Leu Gly Arg Pro Gly Arg Ser Val
 20 25 30

Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala Ala
 35 40 45

Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu His
 50 55 60

Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His Gly
 65 70 75 80

Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val Gly
 85 90 95

Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly Ser
 100 105 110

Leu Gly Leu Thr
 115

<210> 709

<211> 125

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(125)

<223> Xaa = Any amino acid

<400> 709

Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
5 10 15

Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly
20 25 30

Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
35 40 45

Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
50 55 60

Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
65 70 75 80

Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
85 90 95

Ser Lys Gln Ser Asn Asn Lys Tyr Ala Xaa Gln Gln Leu Ser Glu Ala
100 105 110

Leu Thr Pro Glu Gln Val Glu Ser Pro Thr Glu Ala Thr
115 120 125

<210> 710

<211> 70

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(70)

<223> Xaa = Any amino acid

<400> 710

Leu Leu Xaa Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly
5 10 15

Leu His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys
20 25 30

His Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu
35 40 45

Val Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly
50 55 60

Gly Ser Leu Gly Leu Thr
65 70

<210> 711

<211> 53

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(53)

<223> Xaa = Any amino acid

<400> 711

Val Ala Ser Val Gly Leu Ser Thr Cys Ser Gly Val Lys Ala Ser Asp
5 10 15
Ser Cys Xaa Ala Ala Tyr Leu Leu Leu Cys Leu Glu Gly Val Val
20 25 30
Val Ser Thr Pro Ala Leu Thr Gly Leu Leu Ser Ala Phe Gln Ala Thr
35 40 45
Val Thr Ala Pro Gly
50

<210> 712

<211> 56

<212> PRT

<213> Homo sapiens

<400> 712

Pro Pro Arg Val Arg Ala Pro Ser Val Pro Gly Pro Arg Pro Ser Arg
5 10 15
Gln Arg Ser Phe His Ser Ala Trp Asp Asp Gly Glu Glu Lys Asn Pro
20 25 30
Asp Leu Pro His Pro Gly Pro Lys Glu Ser Ala Gly Asp Val His Gln
35 40 45
Ala Glu Val Arg Ala Asp Glu Glu
50 55

<210> 713

<211> 56

<212> PRT

<213> Homo sapiens

<400> 713

Arg Arg Gly Ser Val Arg Pro Ala Ser Gln Gly Pro Gly Arg Ala Asp
5 10 15
Lys Asp His Ser Thr Gln Pro Gly Thr Met Gly Arg Lys Lys Ile Gln
20 25 30
Ile Ser Arg Ile Leu Asp Gln Arg Asn Arg Gln Val Thr Phe Thr Lys
35 40 45
Arg Lys Phe Gly Leu Met Lys Lys
50 55

<210> 714

<211> 56

<212> PRT

<213> Homo sapiens

<400> 714

Leu Leu His Gln Pro Glu Leu Pro Leu Gly Glu Arg His Leu Pro Ile
5 10 15
Pro Leu Val Gln Asp Ala Gly Asp Leu Asp Phe Phe Pro Pro His Arg

Pro Arg Leu Ser Gly Met Ile Phe Val Cys Ser Ala Trp Ala Leu Gly
35 40 45

Arg Trp Ala His Gly Pro Ala Ala
50 55

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<210> 715
<211> 120
<212> PRT
<213> Homo sapiens
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<220>  
<221> variant  
<222> (1)...(120)  
<223> Xaa = Any amino acid
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<400> 715
Pro Ala Ile Cys Thr Asp Lys Tyr Arg Cys Leu Lys His Asn Leu Asn
 5 10 15

Ser Leu Ile Lys Arg Ser Asn Ser Thr Ala Ala Thr Asn Glu Xaa Pro
20 25 30

Glu Val Thr Val Phe Ser Lys Ser Pro Val Thr Leu Gly Gln Pro Asn
35 40 45

Ile Leu Ile Cys Leu Val Asp Asn Ile Phe Pro Pro Val Xaa Asn Ile
50 55 60

Thr Trp Leu Ser Asn Gly His Ser Val Thr Glu Xaa Val Ser Glu Thr
65 70 75 80

Ser Phe Leu Ser Lys Ser Asp His Ser Phe Phe Lys Ile Ser Thr Ser
85 90 95

Pro Ser Ser Leu Leu Xaa Glu Glu Ser Tyr Asp Cys Lys Xaa Xaa His
100 105 110

Trp Gly Leu Gly Gln Ala Ser Ser
115 120

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<210> 716
<211> 52
<212> PRT
<213> Homo sapiens
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<220>
<221> variant
<222> (1)...(52)
<223> Xaa = Any amino acid
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<400> 716
Ala Met Gly Thr Gln Ser Gln Xaa Val Phe Leu Arg Pro Ala Ser Ser
 5 10 15

Pro Arg Val Ile Ile Pro Ser Ser Arg Ser Val Pro His Pro Pro Pro
20 25 30

Phe Trp Xaa Arg Arg Val Met Thr Ala Arg Xaa Xaa Thr Gly Asp Trp

35

40

45

Asp Lys Pro Leu
50

<210> 717
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(60)
<223> Xaa = Any amino acid

<400> 717
Val Pro Ile Ala Gln Pro Cys Asp Val Xaa His Arg Arg Lys Asp Val
5 10 15
Val His Lys Thr Asp Glu Asp Val Gly Leu Thr Gln Cys His Gly Arg
20 25 30
Leu Gly Lys His Cys Asp Leu Arg Xaa Leu Ile Gly Ser Ser Gly Arg
35 40 45
Val Gly Ala Phe Asn Gln Thr Val Gln Val Met Phe
50 55 60

<210> 718
<211> 52
<212> PRT
<213> Homo sapiens

<400> 718
Ser Asp Cys Ser Ser Tyr Val Leu Gly Ser Asp Ile Cys Gln Cys Lys
5 10 15
Leu Arg Val Lys Ser Lys Leu Ser Glu Asn Arg Gln Thr Pro Asp Ser
20 25 30
Leu Leu Pro Pro Gln Val His Val Glu Leu Leu Ile Ser Ile Lys Phe
35 40 45
Met Gly Val Leu
50

<210> 719
<211> 53
<212> PRT
<213> Homo sapiens

<400> 719
Gly Lys Ser Trp Ala Gly Leu Pro Gly His Arg Gly His Gly Gly Gly
5 10 15
Val Ser Gln Asp Leu Gly Ser Ala Glu Arg Arg Leu Gly Val Thr Gly
20 25 30
Ile Trp Asp Gly Gly Gly Cys Val Ser Thr Leu Leu Gly Pro Val Pro
35 40 45

Gly Leu Gly Pro Leu
50

<210> 720
<211> 59
<212> PRT
<213> Homo sapiens

<400> 720
Ala Ser Pro Gly Leu Ala Tyr Leu Gly Thr Val Gly Met Gly Glu Val
5 10 15

Cys His Lys Ile Trp Ala Leu Gln Arg Glu Asp Trp Glu Leu Arg Gly
20 25 30

Ser Gly Met Glu Val Asp Ala Ser Ala Pro Cys Trp Gly Leu Ser Leu
35 40 45

Asp Ser Gly His Ser Arg Ala Leu Val Pro Pro
50 55

<210> 721
<211> 68
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(68)
<223> Xaa = Any amino acid

<400> 721
Gln Val Leu Gly Trp Leu Thr Trp Ala Pro Trp Ala Trp Gly Arg Cys
5 10 15

Val Thr Arg Phe Gly Leu Cys Arg Glu Lys Ile Gly Ser Tyr Gly Asp
20 25 30

Leu Gly Trp Arg Trp Met Arg Gln His Pro Ala Gly Ala Cys Pro Trp
35 40 45

Thr Arg Ala Thr Leu Gly Leu Leu Ser Arg Leu Glu Leu Glu Gly Glu
50 55 60

Asp Leu Xaa Arg
65

<210> 722
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(51)
<223> Xaa = Any amino acid

<400> 722
Xaa Gly Xaa Gly Pro Arg Pro Pro Ala Gln Gly Gly Thr Arg Ala Leu

5 10 15
 Glu Trp Pro Glu Ser Arg Asp Arg Pro Gln Gln Gly Ala Asp Ala Ser
 20 25 30
 Thr Ser Ile Pro Asp Pro Arg Asn Ser Gln Ser Ser Leu Cys Arg Ala
 35 40 45
 Gln Ile Leu
 50

<210> 723
 <211> 52
 <212> PRT
 <213> Homo sapiens

<400> 723
 Ser Gly Pro Ser Pro Gly Thr Gly Pro Ser Arg Val Leu Thr His Pro
 5 10 15
 Pro Pro Ser Gln Ile Pro Val Thr Pro Asn Leu Leu Ser Ala Glu Pro
 20 25 30
 Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Gly Lys Pro
 35 40 45
 Ala Gln Asp Leu
 50

<210> 724
 <211> 57
 <212> PRT
 <213> Homo sapiens

<400> 724
 Arg Lys Gln His Trp Trp Cys Leu Ser His Gly Leu Asp Arg Ser Pro
 5 10 15
 Pro Arg Pro Pro Leu Ser Leu His Arg Leu Cys Asp Leu Leu Cys Val
 20 25 30
 Asp Ser Asp Thr Leu Ser Val Ser Gly Pro Arg Lys Asp Gly Gln Asp
 35 40 45
 Tyr Leu Trp Gly Lys Gln Tyr Trp Glu
 50 55

<210> 725
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 725
 Gly Ser Ser Thr Gly Gly Ala Ser Ala Met Ala Trp Thr Val Leu Leu
 5 10 15
 Leu Gly Leu Leu Ser His Cys Thr Asp Ser Val Thr Ser Tyr Val Leu
 20 25 30
 Thr Gln Thr Pro Ser Val Ser Val Ala Pro Gly Lys Thr Ala Lys Ile

35 40 45
 Thr Cys Gly Gly Asn Asn Ile Gly Ser Asn Asn Val His Trp Tyr Tyr
 50 55 60
 Gln Lys Pro Gly Gln Ala Pro Val Leu Ile Ile Ser Phe Asp Asn Asp
 65 70 75 80
 Arg Pro Ser Gly Ile Ser Glu Arg Phe Ser Gly Phe Asn Ser Gly Asp
 85 90 95

Met

<210> 726
 <211> 65
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(65)
 <223> Xaa = Any amino acid

<400> 726
 Gln Ala Xaa Asp Glu Ala Asp Tyr Tyr Cys Gln Xaa Trp Asp Arg Asn
 5 10 15
 Asn Asp His Val Val Phe Gly Gly Gly Thr Lys Leu Ala Xaa Leu Xaa
 20 25 30
 Xaa Pro Asn Ala Ala Pro Ser Xaa Thr Leu Phe Pro Pro Ser Ser Glu
 35 40 45
 Glu Leu Gln Ala Asn Xaa Ala Thr Xaa Val Cys Leu Ile Xaa Asp Phe
 50 55 60

Tyr
 65

<210> 727
 <211> 60
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(60)
 <223> Xaa = Any amino acid

<400> 727
 Lys Xaa Ala Met Arg Pro Thr Ile Thr Val Lys Xaa Gly Ile Val Ile
 5 10 15
 Met Thr Met Ser Ser Ser Ala Glu Gly Pro Asn Trp Xaa Ser Xaa Val
 20 25 30
 Xaa Pro Thr Leu Pro Pro Gln Xaa Leu Cys Ser Arg Pro Pro Leu Arg
 35 40 45
 Ser Phe Lys Pro Thr Xaa Pro His Xaa Cys Val Ser

50

55

60

<210> 728
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(59)
 <223> Xaa = Any amino acid

<400> 728
 Asp Thr Xaa Val Trp Xaa Cys Trp Leu Glu Ala Pro Gln Arg Arg Ala
 5 10 15
 Gly Thr Glu Xaa Leu Arg Gly Gln Arg Trp Xaa Asp Xaa Gly Xaa Pro
 20 25 30
 Val Trp Ser Leu Arg Arg Arg Arg His Gly His Tyr Tyr Asp Pro Xaa
 35 40 45
 Leu Asp Ser Asn Ser Arg Pro His Arg Xaa Leu
 50 55

<210> 729
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 729
 Gly Val Phe Leu His Thr Phe Thr Ser Ser Ala Leu Ser Ile Tyr Thr
 5 10 15
 His Thr Gln His Pro Gln Tyr Leu Thr Ser Asn Arg Leu Tyr His Leu
 20 25 30
 Tyr Leu Thr Met Thr Pro Gly Arg Arg Ser Lys Phe Phe Phe Thr Ile
 35 40 45
 Ser Asn Ser Ser Leu Ser Leu Phe
 50 55

<210> 730
 <211> 50
 <212> PRT
 <213> Homo sapiens

<400> 730
 Ile Ser Gln Ile Thr Lys Ser Ser Leu Arg Gln Gln Phe Lys Thr Val
 5 10 15
 Pro Gly Ile Lys Ile Tyr Ser His Leu Arg Ser Leu Pro Ser His Leu
 20 25 30
 His Leu Leu Ser Leu Lys Tyr Ile His Thr His Pro Thr Pro Ser Ile
 35 40 45
 Leu Asp
 50

<210> 731
<211> 70
<212> PRT
<213> Homo sapiens

<400> 731
Arg Ser Ala Tyr Ala Ala Arg Trp Val Ala Lys Ser Leu Val Lys Gly
 5 10 15
Gly Leu Cys Arg Arg Val Leu Val Gln Val Ser Tyr Ala Ile Gly Val
 20 25 30
Ser His Pro Leu Ser Ile Ser Ile Phe His Tyr Gly Thr Ser Gln Lys
 35 40 45
Ser Glu Arg Glu Leu Leu Glu Ile Val Lys Lys Asn Phe Asp Leu Arg
 50 55 60
Pro Gly Val Ile Val Arg
 65 70

<210> 732
<211> 53
<212> PRT
<213> Homo sapiens

<400> 732
Gly Leu Leu Met Leu Leu Val Gly Trp Gln Asn Pro Leu Leu Lys Glu
 5 10 15
Val Cys Ala Gly Gly Phe Leu Phe Arg Ser Leu Met Leu Leu Glu Phe
 20 25 30
Leu Ile His Tyr Leu Ser Pro Phe Ser Ile Met Val Pro Leu Arg Arg
 35 40 45
Val Arg Glu Ser Tyr
 50

<210> 733
<211> 76
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(76)
<223> Xaa = Any amino acid

<400> 733
Lys Gln His Trp Trp Cys Leu Ser His Gly Leu Asp Arg Ser Pro Pro
 5 10 15
Arg Pro Pro Leu Ser Leu His Arg Leu Cys Asp Leu Leu Cys Val Asp
 20 25 30
Ser Asp Thr Leu Ser Val Ser Gly Pro Xaa Lys Asp Gly Gln Asp Tyr
 35 40 45

Leu Trp Gly Lys Gln Tyr Trp Glu Leu Gln Cys Thr Leu Val Leu Pro
 50 55 60

Lys Ala Arg Pro Gly Pro Cys Pro Asn His Leu Phe
 65 70 75

<210> 734

<211> 96

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(96)

<223> Xaa = Any amino acid

<400> 734

Ser Ser Thr Gly Gly Ala Ser Ala Met Ala Trp Thr Val Leu Leu Leu
 5 10 15

Gly Leu Leu Ser His Cys Thr Asp Ser Val Thr Ser Tyr Val Leu Thr
 20 25 30

Gln Thr Pro Ser Val Ser Val Ala Pro Xaa Lys Thr Ala Lys Ile Thr
 35 40 45

Cys Gly Gly Asn Asn Ile Gly Ser Tyr Ser Val His Trp Tyr Tyr Gln
 50 55 60

Lys Pro Gly Gln Ala Pro Val Leu Ile Ile Ser Phe Asp Asp Xaa Arg
 65 70 75 80

Pro Ser Xaa Ile Ser Glu Arg Phe Ser Gly Leu Gln Phe Trp Gly Thr
 85 90 95

<210> 735

<211> 85

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(85)

<223> Xaa = Any amino acid

<400> 735

Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
 5 10 15

Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Xaa Gly Leu
 20 25 30

His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45

Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
 50 55 60

Gly Leu Lys Leu Leu Thr Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
 65 70 75 80

Ser Leu Gly Leu Thr
85

<210> 736
<211> 87
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(87)
<223> Xaa = Any amino acid

<400> 736
Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro
5 10 15
Ser Cys Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile
20 25 30
Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser
35 40 45
Ser Pro Val Lys Ala Gly Val Glu Thr Xaa Thr Pro Ser Lys Gln Ser
50 55 60
Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln
65 70 75 80
Trp Lys Ser His Arg Ser Tyr
85

<210> 737
<211> 125
<212> PRT
<213> Homo sapiens

<400> 737
Arg Ser Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp
5 10 15
Tyr Tyr Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly
20 25 30
Gly Gly Thr Lys Leu Ala Val Leu Ser Gln Pro Lys Ala Ala Pro Ser
35 40 45
Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala
50 55 60
Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val
65 70 75 80
Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr
85 90 95
Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu
100 105 110
Ser Leu Thr Pro Glu His Trp Lys Ser His Lys Ser Tyr
115 120 125

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Thr Cys Gly Gly Asn Asn Ile Gly Ser Asn Asn Val His Trp Tyr Tyr
 50 55 60
 Gln Lys Pro Gly Gln Ala Pro Val Leu Ile Ile Ser Phe Asp Asn Asp
 65 70 75 80
 Arg Pro Ser Gly Ile Ser Glu Arg Phe Ser Gly Phe Asn Ser Gly Asp
 85 90 95

Met

<210> 741
 <211> 57
 <212> PRT
 <213> Homo sapiens

<400> 741
 Ser Trp Pro Ser Phe Leu Gly Pro Leu Thr Leu Arg Val Ser Glu Ser
 5 10 15
 Thr His Arg Arg Ser Gln Ser Leu Cys Ser Glu Arg Gly Gly Arg Gly
 20 25 30
 Gly Glu Arg Ser Arg Pro Trp Leu Arg His His Gln Cys Cys Phe Leu
 35 40 45
 Arg Pro Arg Leu Ser Arg Phe Leu Pro
 50 55

<210> 742
 <211> 143
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(143)
 <223> Xaa = Any amino acid

<400> 742
 Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
 5 10 15
 Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly
 20 25 30
 Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
 35 40 45
 Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
 50 55 60
 Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
 65 70 75 80
 Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
 85 90 95
 Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Xaa Leu

100 105 110
 Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser Leu Gly Leu Ala
 115 120 125
 Tyr Leu Gly His Pro Trp Gly Asn Gly Gly Xaa Cys Val Thr Lys
 130 135 140

<210> 743
 <211> 53
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(53)
 <223> Xaa = Any amino acid

<400> 743
 His Xaa Phe Pro His Cys Pro Thr Gly Ala Gln Gly Lys Pro Ser Pro
 5 10 15
 Gly Cys Ser Phe Cys Gly Thr Ser Thr Ala Gln Ala Ser Xaa Ser Asp
 20 25 30
 Ser Cys Trp Pro Arg Thr Cys Cys Cys Phe Val Trp Arg Val Trp Trp
 35 40 45
 Ser Pro Leu Pro Pro
 50

<210> 744
 <211> 105
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(105)
 <223> Xaa = Any amino acid

<400> 744
 Phe Cys Asp Thr Xaa Ser Pro Ile Ala Pro Arg Val Pro Lys Val Ser
 5 10 15
 Gln Ala Gln Ala Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln
 20 25 30
 Xaa Gln Ile Ala Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly
 35 40 45
 Cys Gly Gly Leu His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro
 50 55 60
 Gly His Cys His Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln
 65 70 75 80
 Cys Gly Leu Val Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser
 85 90 95
 Asp Arg Gly Gly Ser Leu Gly Leu Thr

100

105

<210> 745
<211> 59
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(59)
<223> Xaa = Any amino acid

<400> 745
Xaa Gly Xaa Gly Pro Glu His Thr Phe Gly Trp Asn Ser Leu Arg Asp
 5 10 15
Gln Lys Ala Pro Val Ser His Arg Ala Glu Glu Pro Gly Gln Lys Ser
 20 25 30
Asn Pro Arg Val Arg Cys Ala Gly Glu Thr Gln Ser Ser Leu Tyr Leu
 35 40 45
Ser Gly Trp Gln Glu Gly Thr Gly Ser Gly Arg
 50 55

<210> 746
<211> 78
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(78)
<223> Xaa = Any amino acid

<400> 746
Gly Thr Lys Arg Pro Gln Tyr Pro Thr Glu Leu Arg Ser Gln Ala Arg
 5 10 15
Lys Val Thr Pro Glu Phe Ala Val Gln Gly Arg His Arg Ala Leu Phe
 20 25 30
Ile Cys Gln Asp Gly Arg Arg Gly Gln Gly Gln Gly Ala Glu Gly Xaa
 35 40 45
Met Ser Val Leu Gly Ala Lys Ala Pro Arg Asp Leu Arg Thr Gly Gly
 50 55 60
Gln Val Ser Lys Val Lys Gln Leu Pro Val Gln Ile Arg Ala
 65 70 75

<210> 747
<211> 50
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(50)
<223> Xaa = Any amino acid

<400> 747

Pro Gln Ser Ser Leu Cys Arg Gly Asp Thr Glu Leu Ser Leu Ser Val
 5 10 15

Arg Met Ala Gly Gly Asp Arg Val Arg Ala Leu Arg Val Xaa Cys Arg
 20 25 30

Cys Trp Gly Pro Arg Pro Arg Glu Ile Ser Gly Gln Val Val Arg Cys
 35 40 45

Leu Arg
 50

<210> 748

<211> 56

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(56)

<223> Xaa = Any amino acid

<400> 748

Asn Ser Ser Pro Cys Arg Ser Gly His Ser Gly Lys His Pro Asp Pro
 5 10 15

Ser Ala Trp His Arg Pro Ser Asp Thr Glu Pro Leu Asn Xaa Gly Thr
 20 25 30

Pro Thr Pro His His Ile Leu Arg Ala Gly Ala Pro Gln Val Asp Thr
 35 40 45

Arg Thr Leu Thr Pro Leu Pro Leu
 50 55

<210> 749

<211> 118

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(118)

<223> Xaa = Any amino acid

<400> 749

Gly Val Gly Val Xaa Leu Phe Arg Gly Ser Val Ser Glu Gly Leu Cys
 5 10 15

Gln Ala Glu Gly Ser Gly Cys Phe Pro Leu Cys Pro Asp Leu His Gly
 20 25 30

Glu Leu Phe Tyr Leu Arg His Leu Thr Thr Cys Pro Glu Ile Ser Arg
 35 40 45

Gly Leu Gly Pro Gln His Arg His Xaa Thr Leu Ser Ala Leu Thr Leu
 50 55 60

Ser Pro Pro Ala Ile Leu Thr Asp Lys Glu Ser Ser Val Ser Pro Leu

65 70 75 80
 His Ser Glu Leu Trp Gly Tyr Phe Ser Gly Leu Ala Pro Gln Leu Cys
 85 90 95
 Gly Ile Leu Gly Pro Phe Gly Pro Ser Gly Cys Ser Ser Gln Met Cys
 100 105 110
 Val Leu Asp Xaa Gly Arg
 115

<210> 750
 <211> 60
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(60)
 <223> Xaa = Any amino acid

<400> 750
 Gly Ala Arg Gly Ser Glu Ser Trp Cys Pro Pro Gly Glu Pro Leu Pro
 5 10 15
 Ser Val Tyr Asp Glu Val Leu Gly Cys Xaa Cys Ser Gly Ala Leu Cys
 20 25 30
 Leu Lys Val Tyr Ala Arg Gln Arg Gly Gln Gly Val Phe His Tyr Ala
 35 40 45
 Leu Ile Cys Thr Gly Ser Cys Phe Thr Leu Asp Thr
 50 55 60

<210> 751
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(67)
 <223> Xaa = Any amino acid

<400> 751
 Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln
 5 10 15
 Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly
 20 25 30
 Ala Val Thr Val Ala Trp Xaa Ala Asp Ser Thr Pro Xaa Lys Ala Gly
 35 40 45
 Val Glu Thr Thr Thr Pro Xaa Lys Gln Ser Asn Asn Lys Tyr Pro Ala
 50 55 60

Ser Ser Tyr
 65

<210> 752
<211> 67
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(67)
<223> Xaa = Any amino acid

<400> 752
Ile Ala Ala Gly Arg Val Leu Val Val Ala Leu Phe Xaa Gly Cys Gly
 5 10 15
Gly Leu His Ser Arg Leu Xaa Gly Gly Ala Ile Cys Xaa Pro Gly His
 20 25 30
Cys His Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly
 35 40 45
Leu Val Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg
 50 55 60
Gly Gly Ser
65

<210> 753
<211> 97
<212> PRT
<213> Homo sapiens

<400> 753
Gly Ser Ser Thr Gly Gly Ala Ser Ala Met Ala Trp Thr Val Leu Leu
 5 10 15
Leu Gly Leu Leu Ser His Cys Thr Asp Ser Val Thr Ser Tyr Val Leu
 20 25 30
Thr Gln Thr Pro Ser Val Ser Val Ala Pro Gly Lys Thr Ala Lys Ile
 35 40 45
Thr Cys Gly Gly Asn Asn Ile Gly Ser Asn Asn Val His Trp Tyr Tyr
 50 55 60
Gln Lys Pro Gly Gln Ala Pro Val Leu Ile Ile Ser Phe Asp Asn Asp
 65 70 75 80
Arg Pro Ser Gly Ile Ser Glu Arg Phe Ser Gly Phe Asn Ser Gly Asp
 85 90 95

Met

<210> 754
<211> 56
<212> PRT
<213> Homo sapiens

<400> 754
Lys Gln His Trp Trp Cys Leu Ser His Gly Leu Asp Arg Ser Pro Pro
 5 10 15

Arg Pro Pro Leu Ser Leu His Arg Leu Cys Asp Leu Leu Cys Val Asp
 20 25 30
 Ser Asp Thr Leu Ser Val Ser Gly Pro Arg Lys Asp Gly Gln Asp Tyr
 35 40 45
 Leu Trp Gly Lys Gln Tyr Trp Glu
 50 55

<210> 755
 <211> 139
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(139)
 <223> Xaa = Any amino acid

<400> 755
 Xaa Pro Xaa Xaa Arg Ser Lys Val Thr Arg Lys Arg Pro Cys Leu Pro
 5 10 15
 Ser Met Thr Leu Met Glu Glu Met Leu Arg Glu Ala Phe Arg Cys Met
 20 25 30
 Thr Gln Gly Lys Thr Ala Lys Lys Ser Cys Ser Cys Ser Pro His Phe
 35 40 45
 Val Ile Cys Phe Ile Phe Xaa Ser Phe Glu Ser Lys Met Thr Thr Pro
 50 55 60
 Arg Asn Ser Val Asn Gly Thr Phe Pro Ala Glu Pro Met Lys Xaa Pro
 65 70 75 80
 Ile Ala Met Gln Ser Gly Pro Lys Pro Leu Phe Arg Arg Met Ser Ser
 85 90 95
 Leu Val Gly Pro Thr Gln Ser Phe Phe Met Arg Glu Ser Lys Thr Leu
 100 105 110
 Gly Ala Val Gln Ile Met Asn Gly Leu Phe His Ile Ala Leu Gly Xaa
 115 120 125
 Leu Leu Met Ile Pro Xaa Gly Xaa Tyr Ala Pro
 130 135

<210> 756
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(51)
 <223> Xaa = Any amino acid

<400> 756
 Glu Gln Asn Asp Asn Thr Gln Lys Phe Ser Lys Trp Asp Phe Pro Gly
 5 10 15

Arg Ala Asn Glu Arg Xaa Tyr Cys Tyr Ala Ile Trp Ser Lys Thr Thr
 20 25 30
 Leu Gln Glu Asp Val Phe Thr Gly Gly Pro His Ala Lys Leu Leu His
 35 40 45
 Glu Gly Ile
 50

<210> 757
 <211> 92
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(92)
 <223> Xaa = Any amino acid

<400> 757
 Gly Ala Xaa Ile Pro Xaa Gly Ile Ile Arg Xaa Pro Pro Arg Ala Met
 5 10 15
 Trp Lys Ser Pro Phe Ile Ile Trp Thr Ala Pro Lys Val Leu Asp Ser
 20 25 30
 Leu Met Lys Lys Leu Cys Val Gly Pro Thr Ser Glu Asp Ile Leu Leu
 35 40 45
 Lys Ser Gly Phe Gly Pro Asp Cys Ile Ala Ile Xaa Pro Phe Ile Gly
 50 55 60
 Ser Ala Gly Lys Val Pro Phe Thr Glu Phe Leu Gly Val Val Ile Leu
 65 70 75 80
 Leu Ser Lys Leu Xaa Lys Ile Lys Gln Ile Thr Lys
 85 90

<210> 758
 <211> 53
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(53)
 <223> Xaa = Any amino acid

<400> 758
 Pro Ala Gly Trp Met Arg Gly Arg Gly Ser Lys Ser Trp Cys Pro Pro
 5 10 15
 Gly Glu Pro Leu Thr Ser Val Tyr Asp Glu Val Leu Gly Cys Pro Cys
 20 25 30
 Ser Gly Ala Leu Cys Leu Lys Val Tyr Ala Arg Gln Arg Gly Xaa Gly
 35 40 45
 Val Phe Thr Met Pro
 50

<210> 759
 <211> 108
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(108)
 <223> Xaa = Any amino acid

<400> 759
 Val Ala Phe Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Val Ala
 5 10 15
 Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30
 His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45
 Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
 50 55 60
 Gly Leu Lys Leu Leu Xaa Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
 65 70 75 80
 Ser Leu Gly Leu Thr Cys Gly Val Asp Glu Gly Gln Gly Val Lys Val
 85 90 95
 Leu Val Ser Thr Trp Gly Ala Pro Asp Leu Ser Ile
 100 105

<210> 760
 <211> 78
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(78)
 <223> Xaa = Any amino acid

<400> 760
 Lys His Xaa Xaa Pro Ser Ala Trp His Arg Pro Ser Asp Thr Glu Pro
 5 10 15
 Leu Asn Lys Gly Thr Pro Thr Pro His His Ile Leu Arg Ser Gly Ala
 20 25 30
 Pro Gln Val Asp Thr Arg Thr Leu Thr Pro Cys Pro Ser Ser Thr Pro
 35 40 45
 Gln Val Ser Pro Arg Leu Pro Pro Arg Ser Leu Cys Ser Arg Pro Pro
 50 55 60
 Xaa Arg Ser Phe Lys Pro Thr Arg Pro His Trp Cys Val Ser
 65 70 75

<210> 761

<211> 124
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(124)
<223> Xaa = Any amino acid

<400> 761
Thr Phe Arg His Arg Ala Pro Glu Gln Gly His Pro Asn Thr Ser Ser
 5 10 15
Tyr Thr Glu Val Arg Gly Ser Pro Gly Gly His Gln Asp Phe Asp Pro
 20 25 30
Leu Pro Leu Ile His Pro Ala Gly Gln Pro Lys Ala Ala Pro Ser Val
 35 40 45
Thr Leu Phe Pro Pro Ser Xaa Glu Glu Leu Gln Ala Asn Lys Ala Thr
 50 55 60
Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala
 65 70 75 80
Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr
 85 90 95
Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser
 100 105 110
Leu Thr Pro Glu Gln Trp Lys Ser His Lys Ser Tyr
 115 120

<210> 762
<211> 62
<212> PRT
<213> Homo sapiens

<400> 762
Asn Gly Gln Val Val Gly Glu Lys Lys Val Pro Gly Ser Leu Glu Lys
 5 10 15
Asn Val Lys Arg Cys Ser Arg Pro Met Arg Arg Ile Arg Gln Glu Ile
 20 25 30
His Arg Cys Ala Arg Leu Leu Arg Ser Thr Cys Gln Gln Gln Leu Pro
 35 40 45
Ser Leu Ser Leu Gly Glu Gln Asp Ser Gly Val Trp Asp Phe
 50 55 60

<210> 763
<211> 59
<212> PRT
<213> Homo sapiens

<400> 763
Lys Ser Gln Thr Pro Glu Ser Cys Ser Pro Lys Leu Lys Glu Gly Ser
 5 10 15

Cys Cys Trp Gln Val Leu Leu Arg Ser Leu Ala His Leu Cys Ile Ser
 20 25 30
 Cys Leu Ile Leu Leu Ile Gly Leu Glu His Leu Phe Thr Phe Phe Ser
 35 40 45
 Arg Glu Pro Gly Thr Phe Phe Ser Pro Thr Thr
 50 55

<210> 764
 <211> 87
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(87)
 <223> Xaa = Any amino acid

<400> 764
 Val Ser Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
 5 10 15
 Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
 20 25 30
 Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
 35 40 45
 Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Xaa Asn Asn
 50 55 60
 Lys Tyr Xaa Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
 65 70 75 80
 Xaa His Ile Ser Tyr Xaa Pro
 85

<210> 765
 <211> 55
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(55)
 <223> Xaa = Any amino acid

<400> 765
 Ser Thr Leu Thr Ile Asn Arg Xaa Glu Ala Gly Asp Glu Ala Asp Tyr
 5 10 15
 Tyr Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly
 20 25 30
 Gly Thr Lys Leu Ala Val Leu Gly Gln Pro Gln Gly Cys Pro Leu Gly
 35 40 45
 His Ser Val Pro Ala Leu Leu
 50 55

<210> 766
<211> 121
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(121)
<223> Xaa = Any amino acid

<400> 766
Arg Xaa Val Ala Tyr Val Xaa Leu Pro Leu Leu Arg Arg Gln Ala Gln
 5 10 15

Ile Ala Ala Gly Xaa Val Leu Val Val Xaa Leu Phe Gly Gly Cys Gly
 20 25 30

Gly Leu His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His
 35 40 45

Cys His Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly
 50 55 60

Leu Val Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg
 65 70 75 80

Gly Gly Ser Leu Gly Ala Asp Leu Gly Arg Pro Val Trp Ser Leu Arg
 85 90 95

Arg Arg Arg His Gly His Tyr Tyr Asp Pro Thr Leu Asp Ser Asn Ser
 100 105 110

Arg Pro His Arg Arg Leu Xaa Pro Cys
 115 120

<210> 767
<211> 60
<212> PRT
<213> Homo sapiens

<400> 767
Asn Ser Val Met Met Val Phe Lys Asp Ser Arg Lys Gly Val Met Ser
 5 10 15

Gln Asn Leu Pro Glu Cys Pro Ser Ile Val Arg Arg Lys Arg Thr Ser
 20 25 30

Leu Val Asp Val His Val Leu Ile Pro Trp Arg Leu Gly His Gln Thr
 35 40 45

Met Arg Phe Gly Asn Ile Cys Tyr Gln Asp Glu Pro
 50 55 60

<210> 768
<211> 73
<212> PRT
<213> Homo sapiens

<220>
<221> variant

Arg Met Ala Gly Gly Asp Arg Val Arg Ala Leu Arg Val Xaa Cys Arg
20 25 30

Cys Gly Gly Pro Arg Pro Arg Glu Ile Ser Gly Xaa Val Xaa Met Cys
35 40 45

Leu Xaa
50

<210> 771
<211> 62
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(62)
<223> Xaa = Any amino acid

<400> 771
Gln Ile Lys Arg Ala Leu Cys Leu Ser Cys Thr Ala Asn Ser Gly Val
5 10 15

Thr Phe Leu Ala Trp Leu Leu Ser Ser Val Gly Tyr Trp Gly Leu Leu
20 25 30

Val Pro Gln Ala Val Pro Ala Lys Cys Val Phe Trp Ser Pro Cys Met
35 40 45

Gly Gln Gly Pro Gly Gly Ile Gly Glu Pro Xaa Arg Pro Arg
50 55 60

<210> 772
<211> 59
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(59)
<223> Xaa = Any amino acid

<400> 772
Arg Glu Leu Cys Val Ser Pro Ala Gln Arg Thr Leu Gly Leu Leu Phe
5 10 15

Trp Pro Gly Ser Ser Ala Leu Trp Asp Thr Gly Ala Phe Trp Ser Leu
20 25 30

Arg Leu Phe Gln Pro Asn Val Cys Ser Gly Ala Arg Val Trp Gly Lys
35 40 45

Gly Leu Gly Gly Ser Glu Ser His Xaa Asp Arg
50 55

<210> 773
<211> 102
<212> PRT
<213> Homo sapiens

<220>
<221> variant

<222> (1)...(102)

<223> Xaa = Any amino acid

<400> 773

Thr Gly Lys Xaa Phe Tyr Xaa Arg His Met Xaa Xaa Cys Pro Glu Ile
 5 10 15

Ser Arg Gly Leu Gly Pro Pro His Arg His Xaa Thr Leu Ser Ala Leu
 20 25 30

Thr Leu Ser Pro Pro Ala Ile Leu Thr Asp Lys Glu Ser Ser Val Ser
 35 40 45

Leu Leu His Ser Glu Leu Trp Gly Tyr Phe Ser Gly Leu Ala Pro Gln
 50 55 60

Leu Cys Gly Ile Leu Gly Pro Phe Gly Pro Ser Gly Cys Ser Ser Gln
 65 70 75 80

Met Cys Val Leu Glu Pro Val Tyr Gly Ala Arg Ala Trp Gly Asp Arg
 85 90 95

Arg Ala Xaa Ser Thr Ala
 100

<210> 774

<211> 102

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(102)

<223> Xaa = Any amino acid

<400> 774

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
 5 10 15

Leu Pro Gly Ala Lys Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Thr
 20 25 30

Leu Ser Ala Ser Val Gly Asp Thr Val Thr Ile Ser Cys Arg Ala Ser
 35 40 45

Gln Asn Ile Asp Arg Trp Leu Ala Trp His Gln Gln Lys Pro Gly Lys
 50 55 60

Ala Pro Asn Val Leu Ile Tyr Ala Thr Ser Ser Leu Glu Glu Gly Val
 65 70 75 80

Ser Leu Arg Phe Thr Gly Ser Gly Ser Gly Thr Gln Phe Asn Leu Thr
 85 90 95

Xaa Thr Arg Ser Ala Ala
 100

<210> 775

<211> 54

<212> PRT

<213> Homo sapiens

<220>
<221> variant
<222> (1)...(54)
<223> Xaa = Any amino acid

<400> 775
Cys Pro Asn Leu Cys Asp Phe Gln Phe Arg Arg Arg Gly Leu Ile Lys
 5 10 15

Ile Tyr Trp Gln Trp Ile Trp Asp Thr Ile Gln Phe Asn His Xaa Gln
 20 25 30

Val Cys Ser Leu Thr Ile Xaa Gln Leu Ile Ile Xaa Asn Ile Ile Leu
 35 40 45

His Xaa Xaa Xaa Val Leu
 50

<210> 776
<211> 68
<212> PRT
<213> Homo sapiens

<400> 776
Asp Ile Arg Gly Phe Ala Trp Phe Leu Leu Met Pro Gly Gln Pro Pro
 5 10 15

Ile Tyr Ile Leu Arg Gly Pro Thr Thr Tyr Cys Asn Cys Ile Ser Asp
 20 25 30

Arg Cys Arg Gln Gly Gly Arg Arg Leu Gly His Leu Asp Val Thr Phe
 35 40 45

Gly Thr Trp Glu Pro Glu Gln Gln Glu Pro Gln Glu Leu Ser Gly Asp
 50 55 60

Pro His Val His
 65

<210> 777
<211> 50
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(50)
<223> Xaa = Any amino acid

<400> 777
Gln Asn Xaa Xaa Xaa Met Gln Asn Asn Val Xaa Asn Asn Lys Leu Xaa
 5 10 15

Asn Arg Gln Ala Ala Asp Leu Xaa Met Val Lys Leu Asn Cys Val Pro
 20 25 30

Asp Pro Leu Pro Val Asn Leu Asn Glu Thr Pro Ser Ser Lys Leu Glu
 35 40 45

Val Ala

50

<210> 778
 <211> 138
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(138)
 <223> Xaa = Any amino acid

<400> 778
 Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Gln Phe Tyr Val Asp Leu
 5 10 15
 Gly Arg Lys Glu Thr Ala Trp Cys Leu Pro Val Leu Arg Gln Phe Arg
 20 25 30
 Phe Asp Pro Gln Phe Ala Leu Thr Asn Ile Ala Val Leu Lys His Asn
 35 40 45
 Leu Asn Ser Leu Ile Lys Arg Ser Asn Ser Thr Ala Ala Thr Asn Glu
 50 55 60
 Val Pro Glu Val Thr Val Phe Ser Lys Ser Pro Val Thr Leu Gly Gln
 65 70 75 80
 Pro Asn Ile Leu Ile Cys Leu Val Asp Asn Ile Phe Pro Pro Val Xaa
 85 90 95
 Asn Ile Thr Trp Leu Ser Asn Gly His Ser Val Thr Xaa Xaa Val Ser
 100 105 110
 Glu Thr Ser Phe Leu Ser Lys Ser Asp His Xaa Phe Phe Xaa Ile Xaa
 115 120 125
 Tyr Pro Thr Leu Leu Pro Ser Ser Glu Glu
 130 135

<210> 779
 <211> 60
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(60)
 <223> Xaa = Any amino acid

<400> 779
 Val Pro Ile Ala Gln Pro Cys Asp Val Xaa His Arg Arg Lys Asp Val
 5 10 15
 Val His Lys Thr Asp Glu Asp Val Gly Leu Thr Gln Cys His Gly Arg
 20 25 30
 Leu Gly Lys His Cys Asp Leu Arg Asn Leu Ile Gly Ser Ser Gly Arg
 35 40 45
 Val Gly Ala Phe Asn Gln Thr Val Gln Val Met Phe

50

55

60

<210> 780
<211> 66
<212> PRT
<213> Homo sapiens

<400> 780
Pro Ser Val Thr Gly Asp Leu Glu Asn Thr Val Thr Ser Gly Thr Ser
 5 10 15
Leu Val Ala Ala Val Glu Leu Glu Arg Leu Ile Arg Leu Phe Lys Leu
 20 25 30
Cys Phe Arg Thr Ala Met Phe Val Ser Ala Asn Cys Gly Ser Asn Leu
 35 40 45
Asn Cys Leu Arg Thr Gly Lys His Gln Ala Val Ser Phe Leu Pro Arg
 50 55 60
Ser Thr
65

<210> 781
<211> 84
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(84)
<223> Xaa = Any amino acid

<400> 781
Ser Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile
 5 10 15
Ala Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Xaa
 20 25 30
Leu His Ser Arg Leu Asp Gly Xaa Ala Ile Xaa Leu Pro Gly His Cys
 35 40 45
His Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu
 50 55 60
Val Gly Leu Xaa Leu Leu Ile Xaa Gly Arg Glu Gln Ser Asp Arg Xaa
 65 70 75 80
Gly Ser Leu Gly

<210> 782
<211> 84
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(84)

<223> Xaa = Any amino acid

<400> 782

Pro Lys Ala Ala Xaa Ser Val Thr Leu Phe Pro Pro Xaa Tyr Glu Glu
5 10 15
Xaa Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
20 25 30
Pro Gly Ala Val Thr Val Ala Trp Lys Xaa Asp Ser Xaa Pro Val Lys
35 40 45
Ala Gly Val Glu Xaa Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
50 55 60
Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
65 70 75 80
Arg Ser Tyr Arg

<210> 783

<211> 51

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(51)

<223> Xaa = Any amino acid

<400> 783

Asp Thr Phe Lys Trp Ala Gln Cys Gln Pro Thr Gly Leu Leu Thr Gly
5 10 15
Thr Thr Ser Gln Met Pro Phe Ser Ala His Thr Leu Gln Ala Glu Ala
20 25 30
Arg Gly Xaa His Pro Ser Gly Asp Gly Xaa Cys Xaa Cys Val Xaa Val
35 40 45
Cys Ser Ala
50

<210> 784

<211> 59

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(59)

<223> Xaa = Any amino acid

<400> 784

Pro Xaa Xaa Val Gln Met Ser Glu Thr Pro Ser Asn Gly Pro Ser Ala
5 10 15
Ser Gln Leu Gly Ser Ser Leu Ala Pro Arg Pro Arg Cys Pro Ser Leu
20 25 30

Pro Thr Pro Cys Arg Leu Arg Pro Glu Glu Xaa Thr Pro Pro Glu Met
 35 40 45

Gly Xaa Val Xaa Val Cys Xaa Tyr Val Leu Xaa
 50 55

<210> 785
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(59)
 <223> Xaa = Any amino acid

<400> 785
 Arg Arg Thr Tyr Xaa His Thr Xaa Thr Xaa Pro Ile Ser Gly Gly Val
 5 10 15

Xaa Ser Ser Gly Leu Ser Leu Gln Gly Val Gly Arg Glu Gly His Leu
 20 25 30

Gly Arg Gly Ala Ser Glu Glu Pro Ser Trp Leu Ala Leu Gly Pro Phe
 35 40 45

Glu Gly Val Ser Asp Ile Trp Thr Xaa Xaa Gly
 50 55

<210> 786
 <211> 58
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(58)
 <223> Xaa = Any amino acid

<400> 786
 Ala Glu His Xaa His Thr His Xaa His Xaa Pro Ser Pro Glu Gly Xaa
 5 10 15

Pro Pro Leu Ala Ser Ala Cys Arg Val Trp Ala Glu Lys Gly Ile Trp
 20 25 30

Asp Val Val Pro Val Arg Ser Pro Val Gly Trp His Trp Ala His Leu
 35 40 45

Lys Val Ser Gln Thr Phe Gly Pro Xaa Xaa
 50 55

<210> 787
 <211> 52
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(52)

<223> Xaa = Any amino acid

<400> 787

```

Pro Lys Glu Val Arg Gln Leu Ala Glu Asp Phe Leu Lys Asp Tyr Ile
           5                      10                      15

His Ile Asn Ile Gly Ala Leu Glu Leu Xaa Ala Asn His Asn Ile Leu
      20                      25                      30

Xaa Xaa Val Asp Val Cys His Asp Xaa Xaa Lys Asp Glu Lys Leu Ile
      35                      40                      45

Arg Leu Met Glu
      50

```

<210> 788

<211> 55

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(55)

<223> Xaa = Any amino acid

<400> 788

```

Gln His Trp Trp Xaa Xaa Ser His Gly Xaa Gly Arg Ser Pro Leu Arg
           5                      10                      15

Pro Pro Leu Ser Leu His Xaa Leu Cys Xaa Leu Leu Cys Val Asp Ser
      20                      25                      30

Asp Thr Leu Ser Val Ser Gly Pro Arg Lys Gly Gly Gln Asp Tyr Leu
      35                      40                      45

Trp Gly Lys Gln Tyr Trp Glu
      50                      55

```

<210> 789

<211> 95

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(95)

<223> Xaa = Any amino acid

<400> 789

```

Ser Thr Gly Xaa Xaa Ser Ala Met Xaa Trp Ala Val Leu Leu Phe Gly
           5                      10                      15

Leu Leu Ser His Cys Thr Xaa Ser Val Xaa Ser Tyr Val Leu Thr Gln
      20                      25                      30

Thr Pro Ser Val Ser Val Ala Pro Gly Lys Ala Ala Lys Ile Thr Cys
      35                      40                      45

Gly Gly Asn Asn Ile Gly Ser Asn Asn Val Xaa Trp Tyr Tyr Gln Lys
      50                      55                      60

```

Pro Gly Gln Ala Pro Val Leu Ile Ile Ser Phe Asp Asn Asp Arg Pro
65 70 75 80

Ser Gly Ile Ser Glu Arg Phe Ser Gly Phe Asn Ser Gly Asp Met
85 90 95

<210> 790

<211> 90

<212> PRT

<213> Homo sapiens

<400> 790

Val Leu Thr Val Ile Asn Tyr Arg Pro His Asn Met Arg Pro Glu Asp
5 10 15

Arg Met Phe His Ile Arg Ala Val Ile Leu Arg Ala Leu Ser Leu Ala
20 25 30

Phe Leu Leu Ser Leu Arg Gly Ala Gly Ala Ile Lys Ala Asp His Val
35 40 45

Ser Thr Tyr Ala Ala Phe Val Gln Thr His Arg Pro Thr Gly Glu Phe
50 55 60

Met Phe Glu Phe Asp Glu Asp Glu Met Phe Tyr Val Asp Leu Asp Lys
65 70 75 80

Lys Glu Thr Val Trp His Leu Glu Glu Phe
85 90

<210> 791

<211> 55

<212> PRT

<213> Homo sapiens

<400> 791

Val Ser Glu Glu Leu Gly Pro Ser Arg Arg Thr Met Cys Gln Leu Met
5 10 15

Pro Arg Leu Tyr Arg Arg Ile Asp Gln Gln Gly Ser Leu Cys Leu Asn
20 25 30

Leu Met Lys Met Arg Cys Ser Met Trp Ile Trp Thr Arg Arg Arg Pro
35 40 45

Ser Gly Ile Trp Arg Ser Leu
50 55

<210> 792

<211> 56

<212> PRT

<213> Homo sapiens

<400> 792

Leu Ala Cys Cys Ser Gly Pro Trp Ser Cys Pro Val Leu Gln His Gly
5 10 15

Val Ser Glu Ala Pro Trp Arg Leu Leu His Gly Ser Ser Asp Ser Asp
20 25 30

Thr Asp Gly Ala Glu Leu Pro Thr Gly Phe Gly Trp Gly His Gln Thr
35 40 45

Thr Phe Leu Gly Val Leu Tyr Val
50 55

```
<210> 793
<211> 177
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> variant  
<222> (1)...(177)  
<223> Xaa = Any amino acid
```

<400> 793
Leu Pro Ala Ala Leu Ala Pro Gly Pro Val Leu Phe Ser Ser Met Val
5 10 15

Cys Leu Arg Leu Pro Gly Gly Ser Cys Met Ala Val Leu Thr Val Thr
20 25 30

Leu Met Val Leu Ser Ser Pro Leu Ala Leu Ala Gly Asp Thr Arg Pro
35 40 45

Arg Phe Leu Glu Tyr Ser Thr Ser Glu Cys His Phe Phe Asn Gly Thr
50 55 60

Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu Tyr
65 70 75 80

Val Arg Phe Asp Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu Leu
85 90 95

Gly Arg Pro Asp Glu Glu Tyr Trp Asn Ser Gln Lys Asp Phe Leu Glu
100 105 110

Asp Arg Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly Val
115 120 125

Gly Glu Ser Phe Thr Val Gln Arg Arg Val His Pro Lys Val Thr Val
130 135 140

Tyr Pro Ser Lys Thr His Pro Cys Ser Thr Thr Thr Ser Trp Ser Val
145 150 155 160

Leu Xaa Val Val Ser Ile Gln Ala Ala Leu Asn Xaa Val Val Pro Glu
165 170 175

Trp

```
<210> 794
<211> 56
<212> PRT
<213> Homo sapiens
```

<400> 794
Ala Pro His Trp Leu Trp Leu Gly Thr Pro Asp His Val Ser Trp Ser
5 10 15

Thr Leu Arg Leu Ser Val Ile Ser Ser Met Gly Arg Ser Gly Cys Gly
20 25 30
Ser Trp Thr Asp Thr Ser Ile Thr Lys Arg Ser Thr Cys Ala Ser Thr
35 40 45
Ala Thr Trp Gly Ser Ser Gly Arg
50 55

<210> 795
<211> 70
<212> PRT
<213> Homo sapiens

<400> 795
Ser Ser His Gln Pro Arg Ser Cys Val Cys Ser Arg Cys Pro Pro Arg
5 10 15
Pro Ala Cys Leu Pro Gly Ser Pro Ser Gly Cys Ser Ser Thr Pro His
20 25 30
Gln Ala Ala Pro Ala Pro Ser Pro Pro Gly Thr Pro Pro Arg Arg Cys
35 40 45
Arg Ser Ala Arg Thr Pro Leu Gly Tyr Arg Ser Ile Cys Pro Gly Thr
50 55 60
Ala Pro Ala Pro Ser His
65 70

<210> 796
<211> 53
<212> PRT
<213> Homo sapiens

<400> 796
Ser Thr Pro Arg Asn Val Val Trp Cys Pro Gln Pro Lys Pro Val Gly
5 10 15
Ser Ser Ala Pro Ser Val Ser Leu Ser Glu Leu Pro Cys Arg Ser Leu
20 25 30
Gln Gly Ala Ser Asp Thr Pro Cys Trp Arg Thr Gly Gln Asp Gln Gly
35 40 45
Pro Glu Gln Gln Ala
50

<210> 797
<211> 146
<212> PRT
<213> Homo sapiens

<400> 797
Arg Ile His Ser His Leu Arg Met Asp Ser Pro Leu His Cys Glu Ala
5 10 15
Leu Thr Asn Pro Val Val Val Ser Ala Val Gly Val His Arg Gly Pro
20 25 30

Pro Val Phe Gln Glu Val Leu Leu Ala Val Pro Val Leu Leu Ile Arg
 35 40 45
 Pro Pro Gln Leu Arg His Arg Pro Glu Leu Pro His Val Ala Val Glu
 50 55 60
 Ala His Val Leu Leu Leu Val Ile Glu Val Ser Val Gln Glu Pro His
 65 70 75 80
 Pro Leu Arg Pro Ile Glu Glu Met Thr Leu Arg Arg Arg Val Leu Gln
 85 90 95
 Glu Thr Trp Ser Gly Val Pro Ser Gln Ser Gln Trp Gly Ala Gln His
 100 105 110
 His Gln Cys His Cys Gln Asn Cys His Ala Gly Ala Ser Arg Glu Pro
 115 120 125
 Gln Thr His His Ala Gly Glu Gln Asp Arg Thr Arg Gly Gln Ser Ser
 130 135 140
 Arg Gln
 145

<210> 798
 <211> 58
 <212> PRT
 <213> Homo sapiens

<400> 798
 His Ser Asp Val Glu Tyr Ser Lys Lys Arg Gly Leu Val Ser Pro Ala
 5 10 15
 Lys Ala Ser Gly Glu Leu Ser Thr Ile Ser Val Thr Val Arg Thr Ala
 20 25 30
 Met Gln Glu Pro Pro Gly Ser Leu Arg His Thr Met Leu Glu Asn Arg
 35 40 45
 Thr Gly Pro Gly Ala Arg Ala Ala Gly Lys
 50 55

<210> 799
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 799
 Ala Leu Asn Glu Asp Leu Arg Ser Trp Thr Ala Ala Asp Met Ala Ala
 5 10 15
 Gln Ile Thr Lys Arg Lys Trp Glu Ala Ala His Glu Ala Glu Gln Leu
 20 25 30
 Arg Ala Tyr Leu Asp Gly Thr Cys Val Glu Trp Leu Arg Arg Tyr Leu
 35 40 45
 Glu Asn Gly Lys Glu Thr Leu Gln Arg Thr Asp Pro Pro Lys Thr His
 50 55 60

Met Thr His His Pro Ile Ser Asp His Glu Ala Thr Leu Arg Cys Trp
 65 70 75 80
 Ala Leu Gly Phe Tyr Pro Ala Glu Ile Thr Leu Thr Trp Gln Arg Asp
 85 90 95
 Gly Glu Asp Gln Thr Gln Asp Thr Glu Leu Val Glu Thr Arg
 100 105 110

<210> 800
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 800
 Pro Gly Leu His Glu Leu Arg Val Leu Gly Leu Val Leu Pro Ile Pro
 5 10 15
 Leu Pro Gly Gln Cys Asp Leu Arg Arg Val Glu Ala Gln Gly Pro Ala
 20 25 30
 Pro Gln Gly Gly Leu Met Val Arg Asp Gly Val Val Gly His Met Cys
 35 40 45
 Leu Gly Gly Val Arg Ala Leu Gln Arg Leu Leu Pro Val Leu Gln Val
 50 55 60
 Ser Ala Glu Pro Leu His Ala Arg Ala Ile Gln Val Gly Ser Gln Leu
 65 70 75 80
 Leu Arg Leu Met Gly Arg Leu Pro Leu Ala Leu Gly Asp Leu Ser Arg
 85 90 95
 His Val Arg Arg Gly Pro Arg Ala Gln Val Leu Val Gln Gly
 100 105 110

<210> 801
 <211> 70
 <212> PRT
 <213> Homo sapiens

<400> 801
 Ser Pro Gln Gly Arg Ser Pro Gly Pro Ser Thr Ser Gly Trp Pro His
 5 10 15
 Gly Gln Arg Trp Gly Gly Gly Ser Tyr Val Ser Trp Gly Gly Pro Cys
 20 25 30
 Ala Ala Ala Ser Pro Ser Arg Ser Pro Gly Ile Cys Gly Ala Thr Pro
 35 40 45
 Arg Thr Cys His Pro Gly Arg Leu Ser Thr Ala Pro Pro His Gly Pro
 50 55 60
 Pro Pro Thr Cys Ala Trp
 65 70

<210> 802
 <211> 53
 <212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(53)

<223> Xaa = Any amino acid

<400> 802

Pro Arg Gly Gln Xaa Trp Ala Asp Leu Gly Arg Pro Val Trp Ser Leu
5 10 15

Arg Arg Arg Arg His Gly Tyr Tyr Tyr Xaa Pro Xaa Leu Asp Ser Asn
20 25 30

Ser Xaa Pro Ser Ser Pro Ala Ser Asp Pro Phe Asp Gly Xaa Gly Xaa
35 40 45

Asp Leu Trp Pro Xaa
50

<210> 803

<211> 85

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(85)

<223> Xaa = Any amino acid

<400> 803

Xaa Ala Xaa Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Xaa Ile Ala
5 10 15

Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
20 25 30

His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
35 40 45

Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
50 55 60

Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
65 70 75 80

Xaa Leu Gly Leu Thr
85

<210> 804

<211> 129

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(129)

<223> Xaa = Any amino acid

<400> 804

Arg Ala Lys Gly Pro Xaa Leu Xaa His Gln Lys Gly Gln Lys Pro Ala

5

10

15

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<210> 805
<211> 140
<212> PRT
<213> Homo sapiens
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<220>  
<221> variant  
<222> (1)...(140)  
<223> Xaa = Any amino acid
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<400> 805

Thr	Leu	Thr	Ile	Asn	Arg	Val	Glu	Ala	Gly	Asp	Glu	Ala	Asp	Tyr	Tyr	
				5					10					15		
Cys	Gln	Val	Trp	Asp	Leu	Asn	Asn	Asp	His	Val	Val	Phe	Gly	Gly	Gly	
			20					25					30			
Thr	Lys	Leu	Ala	Val	Leu	Gly	Gln	Pro	Lys	Ala	Ala	Pro	Ser	Val	Thr	
		35					40					45				
Leu	Phe	Pro	Pro	Ser	Ser	Glu	Glu	Leu	Gln	Ala	Asn	Lys	Ala	Thr	Leu	
	50					55					60					
Val	Cys	Leu	Ile	Ser	Asp	Phe	Tyr	Pro	Gly	Ala	Val	Thr	Val	Ala	Trp	
	65				70					75					80	
Lys	Ala	Asp	Ser	Ser	Pro	Val	Lys	Xaa	Gly	Val	Glu	Thr	Thr	Thr	Pro	
				85					90					95		
Xaa	Lys	Gln	Ser	Asn	Asn	Lys	Tyr	Ala	Ala	Ser	Ser	Tyr	Xaa	Ser	Leu	
		100						105					110			
Thr	Pro	Glu	Gln	Trp	Lys	Ser	His	Arg	Xaa	Tyr	Arg	Pro	Ala	Arg	Ala	
		115					120					125				
Xaa	Xaa	Gly	Glu	Phe	Gln	His	Thr	Gly	Gly	Arg	Tyr					

130

135

140

<210> 806
 <211> 71
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(71)
 <223> Xaa = Any amino acid

<400> 806
 Glu Thr Ser Tyr Xaa His Asp Xaa Ala Lys Leu Gly Thr Glu Leu Xaa
 5 10 15
 Ser Thr Ser Asn Ala Pro Gln Cys Ala Gly Ile Arg Xaa Xaa Pro Pro
 20 25 30
 Gly Gln Val Cys Xaa Phe Cys Gly Thr Ser Thr Ala Gln Ala Ser Gly
 35 40 45
 Xaa Asp Ser Cys Trp Pro Arg Thr Cys Cys Cys Phe Val Xaa Arg Val
 50 55 60
 Trp Trp Ser Pro Leu Xaa Pro
 65 70

<210> 807
 <211> 120
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(120)
 <223> Xaa = Any amino acid

<400> 807
 Lys Pro Ala Met Xaa Met Ile Xaa Pro Ser Leu Val Pro Ser Ser Xaa
 5 10 15
 Pro Leu Val Thr Pro Pro Ser Val Leu Glu Phe Ala Xaa Xaa Arg Pro
 20 25 30
 Gly Arg Ser Val Xaa Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala
 35 40 45
 Xaa Ile Ala Ala Gly Arg Val Leu Val Val Ala Leu Phe Xaa Gly Cys
 50 55 60
 Gly Gly Leu His Ser Xaa Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly
 65 70 75 80
 His Cys His Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys
 85 90 95
 Gly Leu Val Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp
 100 105 110
 Arg Gly Gly Ser Leu Gly Leu Thr

115

120

<210> 808
<211> 80
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(80)
<223> Xaa = Any amino acid

<400> 808
Thr Xaa Xaa Xaa Asn Arg Gly Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
 5 10 15
Cys Gln Val Trp Asp Leu Asn Asn Asp His Val Val Phe Gly Gly Gly
 20 25 30
Thr Lys Leu Xaa Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
 35 40 45
Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
 50 55 60
Val Cys Leu Ile Ser Asp Xaa Tyr Pro Xaa Ala Val Thr Val Ala Trp
 65 70 75 80

<210> 809
<211> 63
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(63)
<223> Xaa = Any amino acid

<400> 809
Lys Lys Ile Lys Ile Tyr Xaa Val Tyr Xaa Leu Thr Ser Tyr Thr Gln
 5 10 15
Arg Ile Xaa Asp Phe Ser Leu Lys Ile Ile Ile Lys Pro Pro Ile Ser
 20 25 30
Pro Val Glu Lys Glu Ile Leu Arg Phe Xaa Cys Phe Phe Phe Gln His
 35 40 45
Asn Ser Val Thr Tyr Gly Trp Glu Lys Ile Cys Arg Glu Ile Ile
 50 55 60

<210> 810
<211> 123
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(123)
<223> Xaa = Any amino acid

<400> 810

Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
 5 10 15

Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly
 20 25 30

Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
 35 40 45

Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
 50 55 60

Val Cys Leu Ile Ser Asp Xaa Tyr Pro Gly Ala Val Thr Val Ala Trp
 65 70 75 80

Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
 85 90 95

Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu
 100 105 110

Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
 115 120

<210> 811

<211> 50

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(50)

<223> Xaa = Any amino acid

<400> 811

Leu Leu Ala Ala Tyr Leu Leu Leu Leu Cys Leu Glu Gly Val Val Val
 5 10 15

Ser Thr Pro Ala Leu Thr Gly Leu Leu Ser Ala Phe Gln Ala Thr Val
 20 25 30

Thr Ala Pro Gly Xaa Lys Ser Leu Met Arg His Thr Ser Val Ala Leu
 35 40 45

Leu Ala
 50

<210> 812

<211> 85

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(85)

<223> Xaa = Any amino acid

<400> 812

Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala

234

5 10 15
 Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30
 His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45
 Gly Ser Arg Val Xaa Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
 50 55 60
 Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
 65 70 75 80
 Ser Leu Gly Leu Thr
 85

<210> 813
 <211> 71
 <212> PRT
 <213> Homo sapiens

<400> 813
 Asp Ile Arg Gly Phe Ala Trp Phe Leu Leu Met Pro Gly Gln Pro Pro
 5 10 15
 Ile Tyr Ile Leu Arg Gly Pro Thr Thr Tyr Cys Asn Cys Ile Ser Asp
 20 25 30
 Arg Cys Arg Gln Gly Gly Arg Arg Leu Gly His Leu Asp Val Thr Phe
 35 40 45
 Gly Thr Trp Glu Pro Glu Gln Gln Glu Pro Gln Glu Leu Ser Gly Asp
 50 55 60
 Pro His Val His Ala Val Ser
 65 70

<210> 814
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 814
 Ser Gly His Ser Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu
 5 10 15
 Leu Leu Leu Trp Leu Pro Gly Ala Lys Cys Asp Ile Gln Met Thr Gln
 20 25 30
 Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Thr Val Thr Ile Ser
 35 40 45
 Cys Arg Ala Ser Gln Asn Ile Asp Arg Trp Leu Ala Trp His Gln Gln
 50 55 60
 Lys Pro Gly Lys Ala Pro Asn Val Leu Ile Tyr Ala Thr Ser Ser Leu
 65 70 75 80
 Glu Glu Gly Val Ser Leu Arg Phe Thr Gly Ser Gly Ser Gly Thr Gln
 85 90 95

Phe Asn Leu Thr Ile Thr Ser Leu Gln Pro Asp Asp Ser Ala Thr Tyr
 100 105 110

Tyr Cys Gln His Tyr Ser Ala Ser Leu Arg Ser Phe
 115 120

<210> 815
 <211> 114
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(114)
 <223> Xaa = Any amino acid

<400> 815
 Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
 5 10 15
 Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly
 20 25 30
 Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
 35 40 45
 Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
 50 55 60
 Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
 65 70 75 80
 Lys Xaa Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
 85 90 95
 Ser Lys Gln Ser Asn Asn Lys Tyr Arg Gly Gln Gln Leu Ser Glu Pro
 100 105 110
 Asp Ala

<210> 816
 <211> 70
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(70)
 <223> Xaa = Any amino acid

<400> 816
 Leu Leu Pro Ala Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly
 5 10 15
 Leu His Ser Arg Leu Asp Gly Ala Ala Ile Xaa Leu Pro Gly His Cys
 20 25 30
 His Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu
 35 40 45

Val Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly
50 55 60

Gly Ser Leu Gly Leu Thr
65 70

<210> 817
<211> 61
<212> PRT
<213> Homo sapiens

<400> 817
Thr Cys Ile Ser Arg Phe Leu Gly Gln Leu Phe Ile Ile Ser Leu Lys
5 10 15

Ser His Asp Ile Asn Ser Gly Pro His Thr Trp Gly Leu Lys Lys Ser
20 25 30

Gly Thr Tyr Asn Arg Asn His Ile Met Ser Leu Ile Ser Lys Pro Val
35 40 45

Ser Cys Leu Trp Thr Val Cys Val Arg His Ala Tyr Leu
50 55 60

<210> 818
<211> 65
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(65)
<223> Xaa = Any amino acid

<400> 818
Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Gly Ala Asp Tyr Tyr
5 10 15

Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly
20 25 30

Thr Lys Leu Ala Val Leu Ser Gln Pro Lys Ala Ala Pro Ser Xaa Thr
35 40 45

Leu Phe Pro Pro Xaa Ser Xaa Glu Leu Xaa Ala Asn Lys Xaa Thr Leu
50 55 60

Val
65

<210> 819
<211> 61
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(61)
<223> Xaa = Any amino acid

<400> 819

Thr Pro Val Xaa Pro Cys Trp Leu Xaa Ala Xaa Gln Xaa Arg Ala Gly
 5 10 15

Thr Glu Xaa Pro Arg Gly Gln Pro Trp Ala Asp Leu Gly Arg Pro Val
 20 25 30

Trp Ser Leu Arg Arg Arg Arg His Gly His Tyr Tyr Asp Pro Thr Leu
 35 40 45

Asp Asn Asn Ser Arg Pro His Arg Arg Leu Arg Pro Cys
 50 55 60

<210> 820

<211> 141

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(141)

<223> Xaa = Any amino acid

<400> 820

Glu Pro Xaa Asn Pro Ser Glu Lys Asn Ser Pro Ser Thr Gln Tyr Cys
 5 10 15

Tyr Ser Ile Gln Ser Leu Phe Leu Gly Ile Leu Ser Val Met Leu Ile
 20 25 30

Phe Ala Phe Phe Gln Glu Leu Val Ile Ala Gly Ile Val Glu Asn Glu
 35 40 45

Trp Lys Xaa Xaa Cys Ser Xaa Pro Lys Ser Asn Ile Val Leu Leu Ser
 50 55 60

Xaa Glu Glu Lys Lys Glu Gln Thr Ile Glu Ile Lys Glu Glu Val Val
 65 70 75 80

Gly Leu Thr Glu Thr Ser Ser Gln Pro Lys Asn Glu Glu Asp Ile Glu
 85 90 95

Ile Ile Pro Ile Gln Glu Glu Glu Glu Glu Thr Glu Thr Asn Phe
 100 105 110

Xaa Glu Pro Pro Gln Asp Gln Glu Ser Ser Pro Ile Glu Asn Asp Ser
 115 120 125

Ser Pro Xaa Val Ile Ser Ser Xaa Phe Xaa Xaa Leu Phe
 130 135 140

<210> 821

<211> 101

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(101)

<223> Xaa = Any amino acid

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<400> 823
Thr Lys Arg Ser Leu Gln Thr Ala Leu Arg Ser Pro Lys Lys Leu Leu
          5                      10                      15

Pro Arg Gln Pro Arg Arg Ser Tyr Gln Asn Glu Ala Leu Pro Leu Pro
          20                      25                      30

Pro Thr His His Gln Pro Pro Gly Tyr Gly Thr Asp Thr Asn Trp Thr
          35                      40                      45

Leu Arg Thr Lys Arg His Gln Pro Asn Gln Gln Pro Leu Ser Ile Gln
          50                      55                      60

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Gln His Glu Arg Arg His Phe Pro Phe Leu Arg
 65 70 75

<210> 824
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 824
 Thr Lys Lys Arg Lys Met Pro Pro Leu Met Leu Leu Asp Ala Glu Gly
 5 10 15
 Leu Leu Val Trp Leu Val Ser Phe Cys Pro Glu Ser Pro Val Cys Ile
 20 25 30
 Cys Thr Ile Thr Arg Arg Leu Met Val Ser Arg Arg Lys Arg Lys Arg
 35 40 45
 Phe Ile Leu Val Gly Ser Ser Trp Leu Ser Trp
 50 55

<210> 825
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(59)
 <223> Xaa = Any amino acid

<400> 825
 Pro Cys Leu Arg Ser Xaa Xaa Thr Xaa Lys Arg Pro Cys Leu Pro Xaa
 5 10 15
 Met Thr Leu Met Glu Glu Met Leu Arg Glu Ala Phe Xaa Cys Met Thr
 20 25 30
 Gln Gly Lys Thr Ala Lys Asn Leu Val Leu Ala Leu Leu Ile Leu Leu
 35 40 45
 Phe Val Leu Phe Leu Gly Val Leu Arg Ala Lys
 50 55

<210> 826
 <211> 63
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(63)
 <223> Xaa = Any amino acid

<400> 826
 Ser Gly Cys Cys His Phe Ala Leu Lys Thr Pro Lys Asn Lys Thr Asn
 5 10 15
 Asn Lys Met Arg Arg Ala Arg Thr Arg Phe Leu Ala Val Leu Pro Cys

240

20 25 30
 Val Met His Xaa Asn Ala Ser Leu Ser Ile Ser Ser Met Ser Val Ile
 35 40 45
 Xaa Gly Arg His Gly Leu Xaa Arg Val Xaa Leu Asp Leu Arg Gln
 50 55 60

<210> 827
 <211> 85
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(85)
 <223> Xaa = Any amino acid

<400> 827
 Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
 5 10 15
 Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30
 His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Xaa Gly His Cys His
 35 40 45
 Xaa Xaa Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Xaa Leu Val
 50 55 60
 Gly Leu Lys Leu Xaa Xaa Gly Gly Arg Glu Xaa Ser Asp Arg Gly Gly
 65 70 75 80
 Ser Leu Gly Leu Thr
 85

<210> 828
 <211> 85
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(85)
 <223> Xaa = Any amino acid

<400> 828
 Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Xaa Phe Pro Pro Ser Xaa
 5 10 15
 Xaa Glu Leu Gln Ala Asn Lys Xaa Thr Leu Val Cys Leu Ile Ser Asp
 20 25 30
 Phe Tyr Pro Xaa Xaa Val Thr Val Ala Xaa Lys Ala Asp Ser Ser Pro
 35 40 45
 Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
 50 55 60
 Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys

65 70 75 80

Ser His Arg Ser Tyr
85

<210> 829
<211> 61
<212> PRT
<213> Homo sapiens

<400> 829
Ala Leu Asp Arg Lys Ser Leu Asp Cys Pro Glu Glu Val Val Ser Arg
5 10 15
Asn Met Asp Val Lys Gly Ala Pro Ala Glu Val Leu Gly Gly Asn Glu
20 25 30
Gly His Asp Ile Gly Arg Glu Asp Gly Gly Gly Asp Cys Ser Asp Ala
35 40 45
Ser Thr Asp Leu Gly Asp Gln Asp Ala Ala Ala Ile Thr
50 55 60

<210> 830
<211> 103
<212> PRT
<213> Homo sapiens

<400> 830
Val Met Ala Ala Ala Ser Trp Ser Pro Arg Ser Val Asp Ala Ser Leu
5 10 15
Gln Ser Pro Pro Pro Ser Ser Arg Pro Met Ser Cys Pro Ser Phe Pro
20 25 30
Pro Arg Thr Ser Ala Gly Ala Pro Leu Thr Ser Ile Phe Leu Leu Thr
35 40 45
Thr Ser Ser Gly Gln Ser Arg Leu Phe Leu Ser Ser Ala His Cys Pro
50 55 60
Ile Leu Ser Ile Pro Gln Ala Ile Ser Pro Phe Leu Gly Ile Cys Tyr
65 70 75 80
Gly Ser Thr Pro Leu Pro Gly Thr Lys Thr Ser His Met Ile Met Thr
85 90 95
Ala Pro His Cys Ser Gly Leu
100

<210> 831
<211> 83
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(83)
<223> Xaa = Any amino acid

<400> 831

Ser Val Xaa Leu Pro Leu Leu Thr Arg Xaa Ala Gln Ile Ala Ala Gly
 5 10 15

Arg Val Leu Val Val Ala Leu Xaa Gly Gly Cys Gly Gly Leu His Pro
 20 25 30

Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His Gly Ser
 35 40 45

Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val Gly Leu
 50 55 60

Lys Leu Leu Xaa Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly Ser Leu
 65 70 75 80

Gly Leu Thr

<210> 832

<211> 119

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(119)

<223> Xaa = Any amino acid

<400> 832

Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln
 5 10 15

Val Trp Asp Arg Asn Asn Asp His Val Xaa Phe Gly Gly Gly Thr Lys
 20 25 30

Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe
 35 40 45

Pro Pro Ser Xaa Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys
 50 55 60

Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala
 65 70 75 80

Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Xaa
 85 90 95

Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Xaa Thr Arg
 100 105 110

Glu Gln Trp Lys Xaa His Arg
 115

<210> 833

<211> 85

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(85)

<223> Xaa = Any amino acid

<400> 833

Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
 5 10 15

Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30

His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45

Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
 50 55 60

Gly Leu Lys Leu Leu Xaa Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
 65 70 75 80

Xaa Leu Gly Leu Thr
 85

<210> 834

<211> 121

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(121)

<223> Xaa = Any amino acid

<400> 834

Pro Ser Thr Gly Ser Xaa Pro Xaa Met Arg Xaa Thr Xaa Asn Cys Xaa
 5 10 15

Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly Thr Lys
 20 25 30

Leu Ala Val Leu Gly Gln Pro Lys Xaa Ala Pro Ser Val Thr Leu Phe
 35 40 45

Pro Pro Ser Xaa Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys
 50 55 60

Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala
 65 70 75 80

Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys
 85 90 95

Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro
 100 105 110

Glu Gln Trp Lys Ser His Arg Ser Tyr
 115 120

<210> 835

<211> 127

<212> PRT

<213> Homo sapiens

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<400> 836
Arg Pro Arg Ser Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu
          5                      10                      15

Ala Asp Tyr Tyr Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val
          20                      25                      30

Phe Gly Gly Gly Thr Lys Leu Ala Val Xaa Gly Gln Pro Lys Ala Ala
          35                      40                      45

Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn
          50                      55                      60

Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val
          65                      70                      75                      80

Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu
          85                      90                      95

Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser
          100                      105                      110

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Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
 115 120 125

<210> 837
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 837
 Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
 5 10 15
 Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30
 His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45
 Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
 50 55 60
 Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
 65 70 75 80
 Ser Leu Gly Leu Thr
 85

<210> 838
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 838
 Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
 5 10 15
 Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly
 20 25 30
 Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
 35 40 45
 Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
 50 55 60
 Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
 65 70 75 80
 Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
 85 90 95
 Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu
 100 105 110
 Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
 115 120

<210> 839
 <211> 85

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(85)

<223> Xaa = Any amino acid

<400> 839

Val Ala Ser Val Gly Leu Pro Leu Leu Gly Arg Gln Ala Gln Val Ala
5 10 15

Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Phe Gly Gly Leu
20 25 30

His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
35 40 45

Ser Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Xaa Gly Leu Xaa
50 55 60

Gly Leu Xaa Leu Leu Xaa Gly Gly Arg Glu Xaa Xaa Asp Xaa Gly Gly
65 70 75 80

Xaa Leu Gly Leu Thr
85

<210> 840

<211> 54

<212> PRT

<213> Homo sapiens

<400> 840

Leu Leu Pro Gly Ser Cys Asp Ser Gly Leu Glu Gly Arg Trp Gln Pro
5 10 15

Arg Gln Gly Gly Ser Gly Asp His Gln Thr Leu Gln Thr Glu Gln Gln
20 25 30

Gln Val Arg Gly Gln Gln Leu Pro Glu Pro Asp Ala Arg Ala Val Glu
35 40 45

Val Pro Gln Lys Leu Gln
50

<210> 841

<211> 110

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(110)

<223> Xaa = Any amino acid

<400> 841

Asp Tyr Tyr Cys Gln Val Xaa Asp Arg Asn Asn Asp His Val Val Phe
5 10 15

Gly Gly Gly Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Xaa Ala Pro
20 25 30

Xaa Val Xaa Xaa Phe Pro Pro Ser Xaa Glu Glu Xaa Gln Ala Xaa Lys
 35 40 45
 Ala Xaa Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr
 50 55 60
 Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys Ala Gly Val Glu Thr
 65 70 75 80
 Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr
 85 90 95
 Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
 100 105 110

<210> 842
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 842
 Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
 5 10 15
 Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30
 His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45
 Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
 50 55 60
 Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
 65 70 75 80
 Ser Leu Gly Leu Thr
 85

<210> 843
 <211> 125
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(125)
 <223> Xaa = Any amino acid

<400> 843
 Arg Ser Thr Leu Thr Ile Asn Arg Val Glu Ala Asp Asp Glu Xaa Asp
 5 10 15
 Tyr Tyr Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly
 20 25 30
 Gly Gly Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser
 35 40 45
 Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala

50 55 60
 Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val
 65 70 75
 Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr
 85 90 95
 Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu
 100 105 110
 Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
 115 120 125

<210> 844

<211> 94

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(94)

<223> Xaa = Any amino acid

<400> 844

Xaa Leu Ala Cys Cys Ser Gly Pro Trp Ser Cys Pro Val Leu Gln His
 5 10 15

Gly Val Ser Glu Ala Pro Trp Arg Leu Leu His Gly Ser Ser Asp Ser
 20 25 30

Asp Thr Asp Gly Ala Glu Leu Pro Thr Cys Phe Gly Leu Gly Thr Pro
 35 40 45

Asp His Val Ser Trp Ser Thr Leu Arg Leu Ser Val Ile Ser Ser Met
 50 55 60

Gly Arg Ser Gly Cys Gly Ser Trp Thr Asp Thr Ser Ile Thr Lys Arg
 65 70 75 80

Ser Thr Cys Ala Ser Thr Ala Thr Trp Gly Ser Ser Gly Arg
 85 90

<210> 845

<211> 57

<212> PRT

<213> Homo sapiens

<400> 845

Val Leu Pro Ala Ala Leu Ala Pro Gly Pro Val Leu Phe Ser Ser Met
 5 10 15

Val Cys Leu Arg Leu Pro Gly Gly Ser Cys Met Ala Val Leu Thr Val
 20 25 30

Thr Leu Met Val Leu Ser Ser Pro Leu Ala Leu Gly Trp Gly His Gln
 35 40 45

Thr Thr Phe Leu Gly Val Leu Tyr Val
 50 55

Asp Gln Gly Pro Glu Gln Gln Ala Arg
115 120

<210> 848
<211> 54
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(54)
<223> Xaa = Any amino acid

<400> 848
Gln Pro Arg Ser Cys Xaa Cys Ser Arg Cys Pro Pro Xaa Pro Ala Cys
5 10 15

Xaa Pro Gly Ser Pro Xaa Trp Leu Phe Gln Tyr Ser Ser Ser Ala Arg
20 25 30

Pro Ser Xaa Val Thr Ala Arg Asn Ser Pro Thr Ser Leu Ser Lys Arg
35 40 45

Thr Tyr Ser Ser Trp Leu
50

<210> 849
<211> 59
<212> PRT
<213> Homo sapiens

<400> 849
His Ser Asp Val Glu Tyr Ser Lys Lys Arg Gly Leu Val Ser Pro Ala
5 10 15

Gln Ser Lys Trp Gly Ala Gln His His Gln Cys His Cys Gln Asn Cys
20 25 30

His Ala Gly Ala Ser Arg Glu Pro Gln Thr His His Ala Gly Glu Gln
35 40 45

Asp Arg Thr Arg Gly Gln Ser Ser Arg Gln Asp
50 55

<210> 850
<211> 67
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(67)
<223> Xaa = Any amino acid

<400> 850
Asn Pro Val Val Val Xaa Ala Val Gly Val His Arg Xaa Pro Pro Xaa
5 10 15

Phe Gln Glu Val Leu Xaa Gly Cys Ser Ser Thr Pro His Gln Pro Ala
20 25 30

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<400> 852
Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro Tyr Ile Asn
          5                      10                      15

Ile Tyr Asn Cys Glu Pro Pro Asn Pro Ser Glu Lys Asn Ser Pro Ser
          20                      25                      30

Thr Gln Tyr Xaa Tyr Ser Ile Gln Ser Leu Phe Leu Gly Ile Leu Ser
          35                      40                      45

Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile Xaa Gly Ile
          50                      55                      60

Val Asp Asn Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys Ser Asn Ile
          65                      70                      75                      80

Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Xaa Thr Ile Glu Ile Lys
          85                      90                      95

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Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser Gln Pro Lys Asn Glu
 100 105 110
 Glu Xaa Ile Glu Ile Ile Pro Xaa Gln Glu Glu Glu Glu Arg Asn
 115 120 125
 Xaa Arg Arg Thr Phe Gln Asn Xaa Pro Arg Ser Gly Ile Leu Thr Asn
 130 135 140
 Arg Lys
 145

<210> 853
 <211> 137
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(137)
 <223> Xaa = Any amino acid

<400> 853
 Cys His Phe Leu Leu Val Arg Ile Pro Asp Leu Xaa Arg Phe Trp Lys
 5 10 15
 Val Arg Leu Xaa Phe Leu Ser Ser Ser Ser Xaa Ile Gly Ile Ile
 20 25 30
 Ser Met Xaa Ser Ser Phe Phe Gly Trp Glu Asp Val Ser Val Ser Pro
 35 40 45
 Thr Thr Ser Ser Phe Ile Ser Ile Xaa Cys Ser Phe Phe Ser Ser Ala
 50 55 60
 Asp Arg Arg Thr Met Leu Asp Leu Gly Leu Glu His Val Leu Phe His
 65 70 75 80
 Ser Leu Ser Thr Met Pro Xaa Ile Thr Ser Ser Trp Lys Lys Ala Lys
 85 90 95
 Ile Ser Ile Thr Asp Lys Met Pro Lys Asn Arg Asp Cys Met Leu Xaa
 100 105 110
 Gln Tyr Trp Val Asp Gly Glu Phe Phe Ser Glu Gly Leu Gly Gly Ser
 115 120 125
 Gln Leu Tyr Met Leu Ile Tyr Gly Val
 130 135

<210> 854
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(59)
 <223> Xaa = Any amino acid

<400> 854

Ala Ala Thr Ala Ser Ile Ala Gly Ala Pro Thr Gln Tyr Pro Pro Gly
5 10 15
Arg Gly Gly Pro Pro Pro Pro Met Gly Arg Arg Thr Pro Pro Pro Gly
20 25 30
Met Met Gly Pro Pro Pro Xaa Phe Xaa Thr Ser Tyr Gly Cys Pro Gln
35 40 45
Trp Gly Ile Pro Xaa Gly Arg Xaa Leu Gln Trp
50 55

<210> 855

<211> 59

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(59)

<223> Xaa = Any amino acid

<400> 855

Pro Leu Glu Xaa Ser Ser Xaa Gly Asp Pro Pro Leu Gly Ala Pro Ile
5 10 15
Gly Gly Xaa Lys Xaa Gly Arg Trp Ala His His Ala Trp Arg Gly Cys
20 25 30
Ser Ser Ala His Arg Trp Gly Arg Thr Pro Thr Ala Arg Trp Val Leu
35 40 45
Gly Trp Ser Pro Gly Asn Thr Gly Cys Gly Ser
50 55

<210> 856

<211> 50

<212> PRT

<213> Homo sapiens

<400> 856

Lys Leu Leu Glu Gly Thr Cys Tyr Asn Gly Arg Leu Ile Trp Lys Val
5 10 15
Thr Asp Tyr Lys Met Lys Lys Arg Glu Ala Val Asp Gly His Thr Val
20 25 30
Ser Ile Phe Ser Gln Ser Phe Tyr Thr Asn Pro Leu Trp Leu Pro Ala
35 40 45
Leu Cys
50

<210> 857

<211> 61

<212> PRT

<213> Homo sapiens

<400> 857

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<400> 859
Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
          5                      10                      15

Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly
          20                      25                      30

Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
          35                      40                      45

Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
          50                      55                      60

Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
          65                      70                      75                      80

Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
          85                      90                      95

Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu

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100 105 110
 Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
 115 120
 <210> 860
 <211> 123
 <212> PRT
 <213> Homo sapiens
 <400> 860
 Gly His Ser Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu
 5 10 15
 Leu Leu Trp Leu Pro Gly Ala Lys Cys Asp Ile Gln Met Thr Gln Ser
 20 25 30
 Pro Ser Thr Leu Ser Ala Ser Ala Gly Asn Thr Val Thr Ile Ser Cys
 35 40 45
 Arg Ala Ser Gln Asn Ile Asp Arg Trp Leu Ala Trp His Gln Gln Lys
 50 55 60
 Pro Gly Lys Ala Pro Asn Val Leu Ile Tyr Ala Thr Ser Ser Leu Glu
 65 70 75 80
 Glu Gly Val Ser Leu Arg Phe Thr Gly Ser Gly Ser Gly Thr Gln Phe
 85 90 95
 Asn Leu Thr Ile Thr Ser Leu Gln Pro Asp Asp Ser Ala Thr Tyr Tyr
 100 105 110
 Cys Gln His Tyr Ser Ala Ser Leu Arg Ser Phe
 115 120

<210> 861
 <211> 71
 <212> PRT
 <213> Homo sapiens
 <400> 861
 Asp Ile Arg Gly Phe Ala Trp Phe Leu Leu Met Pro Gly Gln Pro Pro
 5 10 15
 Ile Tyr Ile Leu Arg Gly Pro Thr Thr Tyr Cys Asn Cys Ile Ser Gly
 20 25 30
 Arg Cys Arg Gln Gly Gly Arg Arg Leu Gly His Leu Asp Val Thr Phe
 35 40 45
 Gly Thr Trp Glu Pro Glu Gln Gln Glu Pro Gln Glu Leu Ser Gly Asp
 50 55 60
 Pro His Val His Ala Val Ser
 65 70

<210> 862
 <211> 57
 <212> PRT
 <213> Homo sapiens

<400> 862

Gly Ser Ser Thr Gly Gly Ala Ser Ala Met Ala Trp Thr Val Leu Leu
5 10 15

Leu Gly Leu Leu Ser His Cys Thr Asp Ser Val Thr Ser Tyr Val Leu
20 25 30

Thr Gln Thr Pro Ser Val Ser Val Ala Pro Gly Lys Asp Gly Gln Asp
35 40 45

Tyr Leu Trp Gly Lys Gln Tyr Trp Glu
50 55

<210> 863

<211> 65

<212> PRT

<213> Homo sapiens

<400> 863

Leu Arg His Pro Gln Cys Gln Trp Pro Gln Glu Lys Thr Ala Lys Ile
5 10 15

Thr Cys Gly Gly Asn Asn Ile Gly Ser Asn Asn Val His Trp Tyr Tyr
20 25 30

Gln Lys Pro Gly Gln Ala Pro Val Leu Ile Ile Ser Phe Asp Asn Asp
35 40 45

Arg Pro Ser Gly Ile Ser Glu Arg Phe Ser Gly Phe Asn Ser Gly Asp
50 55 60

Met
65

<210> 864

<211> 72

<212> PRT

<213> Homo sapiens

<400> 864

Lys Gln His Trp Trp Cys Leu Ser His Gly Leu Asp Arg Ser Pro Pro
5 10 15

Arg Pro Pro Leu Ser Leu His Arg Leu Cys Asp Leu Leu Cys Val Asp
20 25 30

Ser Asp Thr Leu Ser Val Ser Gly Pro Arg Lys Arg Arg Pro Arg Leu
35 40 45

Pro Val Gly Glu Thr Ile Leu Gly Val Thr Met Tyr Thr Gly Ile Thr
50 55 60

Arg Ser Gln Ala Arg Pro Leu Ser
65 70

<210> 865

<211> 72

<212> PRT

<213> Homo sapiens

<400> 865

Asp Arg Gly Leu Ala Trp Leu Leu Val Ile Pro Val Tyr Ile Val Thr
5 10 15
Pro Asn Ile Val Ser Pro Thr Gly Asn Leu Gly Arg Leu Phe Leu Gly
20 25 30
Pro Leu Thr Leu Arg Val Ser Glu Ser Thr His Arg Arg Ser Gln Ser
35 40 45
Leu Cys Ser Glu Arg Gly Gly Arg Gly Gly Glu Arg Ser Arg Pro Trp
50 55 60
Leu Arg His His Gln Cys Cys Phe
65 70

<210> 866

<211> 69

<212> PRT

<213> Homo sapiens

<400> 866

Ser Ser Thr Gly Gly Ala Ser Ala Met Ala Trp Thr Val Leu Leu Leu
5 10 15
Gly Leu Leu Ser His Cys Thr Gly Asp Pro Pro Arg Val Ser Pro Thr
20 25 30
Cys Pro Ala Gln Gly Phe Trp Val Gln Arg Val Leu Asn Ser Glu Leu
35 40 45
Arg Arg Ala Leu Pro Val Val Gly Arg Met Leu Met Thr Leu Val Gln
50 55 60
Gly Gly Lys Val Gly
65

<210> 867

<211> 59

<212> PRT

<213> Homo sapiens

<400> 867

Ala Ala Leu Val Val Pro Gln Pro Trp Pro Gly Pro Phe Ser Ser Ser
5 10 15
Ala Ser Ser Leu Thr Ala Gln Val Ile Pro Pro Gly Ser His Gln Pro
20 25 30
Ala Gln Pro Lys Ala Ser Gly Ser Ser Val Ser Leu Ile Leu Ser Ser
35 40 45
Gly Gly Pro Phe Leu Trp Trp Ala Gly Cys Ser
50 55

<210> 868

<211> 115

<212> PRT

<213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(115)
 <223> Xaa = Any amino acid

<400> 868
 Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
 5 10 15
 Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30
 His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45
 Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Arg Gly Leu Val
 50 55 60
 Gly Leu Lys Leu Leu Xaa Xaa Arg Arg Glu Thr Glu Xaa Pro Arg Gly
 65 70 75 80
 Xaa Leu Gly Leu Thr Arg Thr Ala Val Trp Ser Ser Ala Lys His Met
 85 90 95
 Ala Leu Leu Arg Ser Thr Leu Asp Ser Asn Ser Xaa Leu Ile Xaa Gly
 100 105 110
 Phe Thr Leu
 115

<210> 869
 <211> 97
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(97)
 <223> Xaa = Any amino acid

<400> 869
 Cys His Val Phe Gly Gly Gly Pro Asn Cys Arg Pro Ser Gln Pro Lys
 5 10 15
 Xaa Ala Pro Arg Xaa Phe Cys Phe Pro Pro Xaa Xaa Glu Glu Phe Gln
 20 25 30
 Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly
 35 40 45
 Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly
 50 55 60
 Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala
 65 70 75 80
 Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser
 85 90 95
 Tyr

<210> 870
<211> 75
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(75)
<223> Xaa = Any amino acid

<400> 870
Xaa Gly Phe Ala Leu Arg Cys Arg Gly Arg Val His Pro Asp His His
 5 10 15
Arg Val Lys Pro Xaa Met Ser Xaa Leu Leu Ser Ser Val Asp Arg
 20 25 30
Asn Asn Ala Met Cys Leu Ala Glu Asp Gln Thr Ala Val Leu Val Ser
 35 40 45
Pro Arg Xaa Pro Leu Gly Xaa Ser Val Ser Arg Leu Xaa Xaa Arg Ser
 50 55 60
Phe Lys Pro Thr Arg Pro Arg Trp Cys Val Ser
 65 70 75

<210> 871
<211> 67
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(67)
<223> Xaa = Any amino acid

<400> 871
Pro Arg Met Met Lys Thr Val Pro Thr Thr Met Pro Thr Arg Pro Thr
 5 10 15
Asp Asn Pro Arg Ala Gln Thr Thr Val Ser Val Ser Ser Asp Ile Gly
 20 25 30
Ala Gly Ile Ser Gly Ser Gln Cys Phe Arg Arg Gly Leu Ser Ser Pro
 35 40 45
Gln Cys Ser Thr Leu Gln Ser Xaa Leu Ser Ser Xaa Glu Gly Arg Arg
 50 55 60
Val Arg Xaa
 65

<210> 872
<211> 66
<212> PRT
<213> Homo sapiens

<220>
<221> variant

<222> (1)...(66)

<223> Xaa = Any amino acid

<400> 872

Xaa Leu Thr Leu Leu Pro Ser Xaa Glu Glu Xaa Tyr Asp Cys Lys Val
5 10 15

Glu His Trp Gly Leu Asp Lys Pro Leu Leu Lys His Trp Glu Pro Glu
20 25 30

Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr Val Val Cys Ala Leu
35 40 45

Gly Leu Ser Val Gly Leu Val Gly Ile Val Val Gly Thr Val Phe Ile
50 55 60

Ile Arg
65

<210> 873

<211> 63

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(63)

<223> Xaa = Any amino acid

<400> 873

Gly Leu Cys Leu Val Ser Val Asp Ala Arg Pro Thr Thr Asp Leu Tyr
5 10 15

Ser Glu Arg Pro Arg Gln Leu Ile Val Thr Gly Ile Ser Asp Arg Cys
20 25 30

Arg Gln Gly Gly Arg Arg Leu Gly His Leu Asp Val Thr Phe Gly Thr
35 40 45

Trp Glu Pro Glu Gln Gln Glu Pro Xaa Glu Leu Ser Gly Asp Pro
50 55 60

<210> 874

<211> 77

<212> PRT

<213> Homo sapiens

<400> 874

Val Val Gly Ala Ser Gln Asn Ile Asp Arg Trp Leu Ala Trp His Gln
5 10 15

Gln Lys Pro Gly Lys Ala Pro Asn Val Leu Ile Tyr Ala Thr Ser Ser
20 25 30

Leu Glu Glu Gly Val Ser Leu Arg Phe Thr Gly Ser Gly Ser Gly Thr
35 40 45

Gln Phe Asn Leu Thr Ile Thr Ser Leu Gln Pro Asp Asp Ser Ala Thr
50 55 60

Tyr Tyr Cys Gln His Tyr Ser Ala Ser Leu Arg Ser Phe

65

70

75

<210> 875

<211> 97

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(97)

<223> Xaa = Any amino acid

<400> 875

Gly Ser Ser Thr Gly Gly Ala Ser Ala Met Ala Trp Thr Val Leu Leu
5 10 15
Leu Gly Leu Leu Ser His Cys Thr Asp Ser Val Thr Ser Tyr Val Leu
20 25 30
Thr Gln Thr Pro Ser Val Ser Val Ala Pro Gly Lys Thr Ala Lys Ile
35 40 45
Thr Cys Gly Gly Asn Asn Ile Gly Ser His Asn Val His Trp Tyr Tyr
50 55 60
Gln Lys Pro Gly Gln Ala Pro Val Leu Ile Ile Ser Phe Asp Asn Asp
65 70 75 80
Arg Xaa Ser Xaa Ile Ser Glu Arg Phe Ser Gly Phe Asn Ser Gly Asp
85 90 95

Met

<210> 876

<211> 76

<212> PRT

<213> Homo sapiens

<400> 876

Lys Gln His Trp Trp Cys Leu Ser His Gly Leu Asp Arg Ser Pro Pro
5 10 15
Arg Pro Pro Leu Ser Leu His Arg Phe Cys Asp Phe Leu Cys Val Asp
20 25 30
Ser Asp Thr Leu Ser Val Ser Gly Pro Arg Lys Asp Gly Gln Asp Tyr
35 40 45
Leu Trp Gly Lys Gln Tyr Trp Glu Ser Gln Cys Thr Leu Val Leu Pro
50 55 60
Glu Ala Arg Pro Gly Pro Cys Pro Asn His Leu Phe
65 70 75

<210> 877

<211> 94

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(94)

<223> Xaa = Any amino acid

<400> 877

Asn Glu Lys Ala Leu Leu Leu Cys Asn Leu Val Gln Asn His Ser Ser
5 10 15

Gly Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met Arg
20 25 30

Glu Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn Gly Leu Phe His
35 40 45

Ile Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly Ile Tyr Ala Pro
50 55 60

Ile Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr Ile
65 70 75 80

Ile Ser Gly Ser Leu Leu Xaa Gln Arg Lys Lys Leu Gln Glu
85 90

<210> 878

<211> 60

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(60)

<223> Xaa = Any amino acid

<400> 878

Asp Phe Gly Gly Cys Pro Asp Tyr Glu Trp Ala Leu Pro His Cys Pro
5 10 15

Gly Gly Ser Ser Asp Asp Pro Ser Arg Asp Leu Cys Thr His Leu Cys
20 25 30

Asp Cys Val Val Pro Ser Leu Gly Arg His Tyr Val Tyr Tyr Phe Arg
35 40 45

Ile Thr Pro Ala Xaa Thr Glu Lys Thr Pro Gly Ser
50 55 60

<210> 879

<211> 60

<212> PRT

<213> Homo sapiens

<400> 879

Ile Pro Ala Gly Ile Ile Arg Arg Pro Pro Arg Ala Met Trp Lys Ser
5 10 15

Pro Phe Ile Ile Trp Thr Ala Pro Lys Val Leu Asp Ser Leu Met Lys
20 25 30

Lys Leu Cys Val Gly Pro Thr Ser Glu Asp Ile Leu Pro Glu Glu Trp
35 40 45

Phe Trp Thr Arg Leu His Ser Asn Arg Ala Phe Ser
 50 55 60

<210> 880
 <211> 62
 <212> PRT
 <213> Homo sapiens

<400> 880
 Ser Gly Asn Asn Ile His Asn Ala Ser Pro Glu Arg Val Pro His Ser
 5 10 15

His Thr Asp Gly Cys Ile Asp Pro Cys Trp Asp His Gln Lys Thr Pro
 20 25 30

Gln Gly Asn Val Glu Glu Pro Ile His Asn Leu Asp Ser Pro Gln Ser
 35 40 45

Leu Arg Phe Pro His Glu Glu Ala Leu Arg Gly Ala His Gln
 50 55 60

<210> 881
 <211> 71
 <212> PRT
 <213> Homo sapiens

<400> 881
 Arg Gly Glu Lys Ala Glu Arg Val Pro Val Ile Phe Lys Arg Gln Asn
 5 10 15

Ile Ser Pro Leu Pro Arg Lys Leu Phe Ser Pro Arg Glu Lys Met Glu
 20 25 30

Val Ile Leu Thr Val His Cys Arg Gly Ile Ser Ser Cys Pro Ile Phe
 35 40 45

Cys Met Thr Cys His Gly Thr Ala Leu Phe Gln Thr Val His Cys Asp
 50 55 60

Leu Trp Val Phe Glu Phe Gln
 65 70

<210> 882
 <211> 73
 <212> PRT
 <213> Homo sapiens

<400> 882
 Thr Lys Ile Ser Leu Asn Ile Glu Val Trp Asn Tyr Phe Phe Asp Ile
 5 10 15

Ser Ala Asn Ser Leu Lys Leu Lys Asp Pro Gln Ile Thr Val Asn Ser
 20 25 30

Leu Lys Gln Gly Cys Thr Met Ala Ser His Ala Lys Asp Gly Thr Arg
 35 40 45

Arg Asn Thr Thr Ala Val Asn Cys Glu Asp Asn Phe His Phe Phe Pro
 50 55 60

Arg Arg Glu Gln Phe Thr Gly Gln Arg
65 70

<210> 883
<211> 118
<212> PRT
<213> Homo sapiens

<400> 883
Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro
5 10 15
Gly Ala Lys Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser
20 25 30
Ala Ser Val Gly Asp Thr Val Thr Ile Ser Cys Arg Ala Ser Gln Asn
35 40 45
Ile Asp Arg Trp Leu Ala Trp His Gln Gln Lys Pro Gly Lys Ala Pro
50 55 60
Asn Val Leu Ile Tyr Ala Thr Ser Ser Leu Glu Glu Gly Val Ser Leu
65 70 75 80
Arg Phe Thr Gly Ser Gly Ser Gly Thr Gln Phe Asn Leu Thr Ile Thr
85 90 95
Ser Leu Gln Pro Asp Asp Ser Ala Thr Tyr Tyr Cys Gln His Tyr Ser
100 105 110
Ala Ser Leu Arg Ser Phe
115

<210> 884
<211> 66
<212> PRT
<213> Homo sapiens

<400> 884
Asp Ile Arg Gly Phe Ala Trp Phe Leu Leu Met Pro Gly Gln Pro Pro
5 10 15
Ile Tyr Ile Leu Arg Gly Pro Thr Thr Tyr Cys Asn Cys Ile Ser Asp
20 25 30
Arg Cys Arg Gln Gly Gly Arg Arg Leu Gly His Leu Asp Val Thr Phe
35 40 45
Gly Thr Trp Glu Pro Glu Gln Gln Glu Pro Gln Glu Leu Ser Gly Asp
50 55 60
Pro His
65

<210> 885
<211> 109
<212> PRT
<213> Homo sapiens

Val	Ala	Ser	Val	Gly	Leu	Pro	Leu	Leu	Arg	Arg	Gln	Ala	Gln	Ile	Ala
				5					10					15	
Ala	Ala	Ala	Tyr	Leu	Leu	Leu	Leu	Cys	Leu	Glu	Gly	Val	Val	Val	Ser
			20					25					30		
Thr	Pro	Ala	Leu	Thr	Gly	Leu	Leu	Ser	Ala	Phe	Gln	Ala	Thr	Val	Thr
		35					40					45			

Ala Pro Gly
50

<210> 888
<211> 118
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(118)
<223> Xaa = Any amino acid

<400> 888
Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
5 10 15
Cys Gln Val Trp Asp Leu Asn Asn Asp His Val Val Phe Gly Gly Gly
20 25 30
Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
35 40 45
Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
50 55 60
Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Xaa Thr Val Ala Trp
65 70 75 80
Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
85 90 95
Xaa Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu
100 105 110
Thr Pro Glu Gln Trp Lys
115

<210> 889
<211> 80
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(80)
<223> Xaa = Any amino acid

<400> 889
Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala Ala Gly Arg Val Leu
5 10 15
Val Val Ala Leu Phe Xaa Gly Cys Gly Gly Leu His Ser Arg Leu Asp
20 25 30
Gly Ala Ala Ile Cys Leu Pro Gly His Cys Xaa Gly Ser Arg Val Glu
35 40 45
Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val Gly Leu Lys Leu Leu
50 55 60

Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly Ser Leu Gly Leu Thr
 65 70 75 80

<210> 890
 <211> 62
 <212> PRT
 <213> Homo sapiens

<400> 890
 Leu Ser Leu Gly Leu Arg Lys Gln His Trp Trp Cys Leu Ser His Gly
 5 10 15

Leu Asp Arg Ser Pro Pro Arg Pro Pro Leu Ser Leu His Arg Leu Cys
 20 25 30

Asp Leu Leu Cys Val Asp Ser Asp Thr Leu Ser Val Ser Gly Pro Arg
 35 40 45

Lys Asp Gly Gln Asp Tyr Leu Trp Gly Lys Gln Tyr Trp Glu
 50 55 60

<210> 891
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 891
 Gly Ser Ser Thr Gly Gly Ala Ser Ala Met Ala Trp Thr Val Leu Leu
 5 10 15

Leu Gly Leu Leu Ser His Cys Thr Asp Ser Val Thr Ser Tyr Val Leu
 20 25 30

Thr Gln Thr Pro Ser Val Ser Val Ala Pro Gly Lys Thr Ala Lys Ile
 35 40 45

Thr Cys Gly Gly Asn Asn Ile Gly Ser Asn Asn Val His Trp Tyr Tyr
 50 55 60

Gln Lys Pro Gly Gln Ala Pro Val Leu Ile Ile Ser Phe Asp Asn Asp
 65 70 75 80

Arg Pro Ser Gly Ile Ser Glu Arg Phe Ser Gly Phe Asn Ser Gly Asp
 85 90 95

Met

<210> 892
 <211> 52
 <212> PRT
 <213> Homo sapiens

<400> 892
 Ser Trp Pro Ser Phe Leu Gly Pro Leu Thr Leu Arg Val Ser Glu Ser
 5 10 15

Thr His Arg Arg Ser Gln Ser Leu Cys Ser Glu Arg Gly Gly Arg Gly
 20 25 30

Gly Glu Arg Ser Arg Pro Trp Leu Arg His His Gln Cys Cys Phe Leu
 35 40 45

Arg Pro Arg Leu
 50

<210> 893
 <211> 68
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(68)
 <223> Xaa = Any amino acid

<400> 893
 Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
 5 10 15

Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly
 20 25 30

Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Xaa Thr
 35 40 45

Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
 50 55 60

Val Cys Leu Ile
 65

<210> 894
 <211> 62
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(62)
 <223> Xaa = Any amino acid

<400> 894
 Asp Thr Pro Val Trp Pro Cys Trp Leu Glu Ala Pro Gln Arg Arg Ala
 5 10 15

Gly Thr Glu Xaa Pro Arg Gly Gln Pro Trp Ala Asp Leu Gly Arg Pro
 20 25 30

Val Trp Ser Leu Arg Arg Arg Arg His Gly His Tyr Tyr Asp Pro Thr
 35 40 45

Leu Asp Ser Asn Ser Arg Pro His Arg Arg Leu Arg Pro Cys
 50 55 60

<210> 895
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 895

Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
 5 10 15

Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30

His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45

Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
 50 55 60

Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
 65 70 75 80

Ser Leu Gly Leu Thr
 85

<210> 896

<211> 123

<212> PRT

<213> Homo sapiens

<400> 896

Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
 5 10 15

Cys Gln Val Trp Asp His Asn Asn Asp His Val Val Phe Gly Gly Gly
 20 25 30

Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
 35 40 45

Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
 50 55 60

Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
 65 70 75 80

Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
 85 90 95

Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu
 100 105 110

Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
 115 120

<210> 897

<211> 115

<212> PRT

<213> Homo sapiens

<400> 897

Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro Gly Ala Lys
 5 10 15

Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val
 20 25 30

Gly Asp Thr Val Thr Ile Ser Cys Arg Ala Ser Gln Asn Ile Asp Arg
 35 40 45

Trp Leu Ala Trp His Gln Gln Lys Pro Gly Lys Ala Pro Asn Val Leu
 50 55 60

Ile Tyr Ala Thr Ser Ser Leu Glu Glu Gly Val Ser Leu Arg Phe Thr
 65 70 75 80

Gly Ser Gly Ser Gly Thr Gln Phe Asn Leu Thr Ile Thr Ser Leu Gln
 85 90 95

Pro Asp Asp Ser Ala Thr Tyr Tyr Cys Gln His Tyr Ser Ala Ser Leu
 100 105 110

Arg Ser Phe
 115

<210> 898
 <211> 63
 <212> PRT
 <213> Homo sapiens

<400> 898
 Asp Ile Arg Gly Phe Ala Arg Phe Leu Leu Met Pro Gly Gln Pro Pro
 5 10 15

Ile Tyr Ile Leu Arg Gly Pro Thr Thr Tyr Cys Asn Cys Ile Ser Asp
 20 25 30

Arg Cys Arg Gln Gly Gly Arg Arg Leu Gly His Leu Asp Val Thr Phe
 35 40 45

Gly Thr Trp Glu Pro Glu Gln Gln Glu Pro Gln Glu Leu Ser Gly
 50 55 60

<210> 899
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 899
 Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
 5 10 15

Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30

His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45

Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
 50 55 60

Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
 65 70 75 80

Ser Leu Gly Leu Thr
 85

<210> 900
<211> 53
<212> PRT
<213> Homo sapiens

<400> 900
Asp Gly Gln Phe Gly Pro Ser Ala Glu Asp Asp Met Val Ile Ile Thr
 5 10 15
Ile Pro His Leu Thr Val Ile Val Gly Leu Ile Ala Gly Phe Asp Pro
 20 25 30
Val Asp Gly Gln Gly Gly His Val Pro Arg Ile Glu Ala Arg Pro Gly
 35 40 45
Pro Cys Pro Asn His
 50

<210> 901
<211> 139
<212> PRT
<213> Homo sapiens

<400> 901
Met Ile Arg Thr Gly Ala Trp Pro Gly Phe Asn Ser Gly Asp Met Ala
 5 10 15
Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
 20 25 30
Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly
 35 40 45
Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
 50 55 60
Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
 65 70 75 80
Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
 85 90 95
Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
 100 105 110
Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu
 115 120 125
Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
 130 135

<210> 902
<211> 85
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(85)
<223> Xaa = Any amino acid

<400> 902

Val Ala Ser Val Xaa Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
 5 10 15

Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30

His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45

Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Xaa Xaa Gly Leu Xaa
 50 55 60

Gly Leu Lys Leu Xaa Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
 65 70 75 80

Ser Leu Gly Leu Thr
 85

<210> 903

<211> 107

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(107)

<223> Xaa = Any amino acid

<400> 903

Val Lys Cys Gly Ile Xaa Asn Asn Asp Xaa Val Xaa Xaa Gly Xaa Gly
 5 10 15

Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
 20 25 30

Leu Phe Pro Pro Ser Ser Xaa Glu Leu Gln Ala Xaa Lys Ala Xaa Xaa
 35 40 45

Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
 50 55 60

Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
 65 70 75 80

Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu
 85 90 95

Thr Pro Glu Gln Trp Lys Xaa His Arg Ser Tyr
 100 105

<210> 904

<211> 55

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(55)

<223> Xaa = Any amino acid

<400> 904

Val Ala Ser Xaa Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
5 10 15Ala Gly Arg Val Leu Val Xaa Ala Leu Phe Gly Gly Cys Gly Xaa Leu
20 25 30His Ser Xaa Leu Asp Gly Ala Xaa Ile Cys Leu Pro Gly His Cys His
35 40 45Xaa Ser Arg Xaa Glu Val Thr
50 55

<210> 905

<211> 55

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(55)

<223> Xaa = Any amino acid

<400> 905

Ser Asp Phe Xaa Pro Gly Xaa Val Thr Val Ala Trp Lys Ala Asp Xaa
5 10 15Ser Pro Val Lys Xaa Gly Val Glu Xaa Thr Thr Pro Ser Lys Gln Ser
20 25 30Xaa Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln
35 40 45Trp Lys Ser Xaa Arg Ser Tyr
50 55

<210> 906

<211> 101

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(101)

<223> Xaa = Any amino acid

<400> 906

Val Ala Ser Val Xaa Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
5 10 15Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
20 25 30His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Xaa His Cys His
35 40 45Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
50 55 60Gly Leu Lys Leu Leu Xaa Gly Xaa Arg Xaa Gln Ser Asp Arg Xaa Gly
65 70 75 80

Asp Met Val Ile Ile
100

```
<210> 907
<211> 101
<212> PRT
<213> Homo sapiens
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<220> /
<221> variant
<222> (1)...(101)
<223> Xaa = Any amino acid
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<400> 907
Asn Asn Asp His Val Xaa Phe Gly Gly Gly Thr Xaa Leu Ala Val Xaa
5 10 15

Gly Gln Pro Lys Xaa Ala Xaa Ser Val Thr Leu Xaa Pro Xaa Ser Xaa
20 25 30

Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
35 40 45

Phe Tyr Pro Gly Ala Val Thr Val Xaa Trp Lys Ala Asp Ser Ser Pro
50 55 60

Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
65 70 75 80

Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
85 90 95

Xaa His Arg Ser Tyr
100

```
<210> 908
<211> 57
<212> PRT
<213> Homo sapiens
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<220>
<221> variant
<222> (1)...(57)
<223> Xaa = Any amino acid
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[illegible]

Ser Gly Ser Gln Leu Cys Asp Ser Arg Ala Ser Ala Pro Arg Ala Leu
20 25 30

Gly Pro Ser Lys Val Ser Xaa Glu Val Pro Pro Ser Asp Pro Leu Phe
35 40 45

Pro Ile Pro Gln Glu Met Glu Pro Thr
50 55

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<220>
<221> variant
<222> (1)...(189)
<223> Xaa = Any amino acid
```

```

<400> 909
Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
          5                      10                      15

Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
          20                      25                      30

His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
          35                      40                      45

Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
          50                      55                      60

Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
          65                      70                      75                      80

Ser Leu Gly Leu Thr Ser Ile Trp Val Trp Ile Leu Ala Leu Gly Pro
          85                      90                      95

Ser Ser Val Ile Pro Glu His Gln Pro Arg Gly His Trp Val Leu Leu
          100                     105                     110

Lys Ser Pro Xaa Arg Cys Leu Pro Gln Thr Pro Cys Ser Gln Phe Pro
          115                     120                     125

Arg Arg Trp Asn Pro Arg Asn Pro Arg Val Asn Leu Phe Arg Gln Glu
          130                     135                     140

Pro Arg Leu Arg Gly Pro Glu Gln Asn Lys Ala Xaa Arg Pro Ser Leu
          145                     150                     155                     160

Arg Leu Ser Asp Thr Gln Arg Asp Lys Gln Arg Glu Arg Asp Arg Gln
          165                     170                     175

Thr Asp Xaa Gln Thr Arg Leu Ser Arg Ser Phe Tyr Leu
          180                     185

```

```
<210> 910
<211> 113
<212> PRT
<213> Homo sapiens
```

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<220>
<221> variant
<222> (1)...(113)
<223> Xaa = Any amino acid
```

<400> 910
Ala Ser Ser Val Xaa Leu Ser Val Cys Leu Ser Leu Ser Val Cys Leu
5 10 15

Phe Val Cys Leu Thr Gly Ala Asp Trp Val Xaa Lys Pro Cys Ser Val
 20 25 30
 Leu Ala Pro Ser Val Trp Val Leu Val Gly Thr Gly Leu Pro Leu Gly
 35 40 45
 Tyr Val Gly Ser Ile Ser Trp Gly Ile Gly Asn Lys Gly Ser Glu Gly
 50 55 60
 Gly Thr Xaa Trp Glu Thr Leu Glu Gly Pro Ser Ala Leu Gly Ala Asp
 65 70 75 80
 Ala Arg Glu Ser Gln Ser Trp Asp Pro Glu Pro Gly Ser Arg Pro Arg
 85 90 95
 Leu Arg Ser Ala Gln Gly Cys Pro Leu Gly His Ser Val Pro Ala Leu
 100 105 110
 Leu

<210> 911
 <211> 50
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(50)
 <223> Xaa = Any amino acid

<400> 911
 Gln Ala Gln Thr Gly Ser Xaa Ser Leu Val Leu Phe Trp Pro Pro Gln
 5 10 15
 Ser Gly Phe Leu Ser Glu Gln Val Tyr Pro Trp Val Thr Trp Val Pro
 20 25 30
 Ser Pro Gly Glu Leu Gly Thr Arg Gly Leu Arg Glu Ala Pro Xaa Gly
 35 40 45
 Arg Leu
 50

<210> 912
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 912
 Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
 5 10 15
 Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
 20 25 30
 Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
 35 40 45
 Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn

50 55 60
 Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
 65 70 75 80

Ser His Arg Ser Tyr
 85

<210> 913
 <211> 85
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(85)
 <223> Xaa = Any amino acid

<400> 913
 Val Ala Ser Val Xaa Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
 5 10 15

Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30

His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45

Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
 50 55 60

Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
 65 70 75 80

Ser Leu Gly Leu Thr
 85

<210> 914
 <211> 111
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(111)
 <223> Xaa = Any amino acid

<400> 914
 Ala Asp Tyr Tyr Cys Xaa Val Trp Asp Xaa Asn Asn Asp His Val Val
 5 10 15

Phe Gly Gly Gly Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala
 20 25 30

Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn
 35 40 45

Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val
 50 55 60

Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu

65		70		75		80
Thr Thr Thr	Pro Ser Lys	Gln Ser Asn	Asn Lys Tyr	Ala Ala Ser	Ser	
	85		90		95	
Tyr Leu Ser	Leu Thr Pro	Glu Gln Trp	Lys Xaa His	Arg Ser Tyr		
	100		105		110	

<210> 915

<211> 75

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(75)

<223> Xaa = Any amino acid

<400> 915

Val Ser Pro	Xaa Leu Pro	Pro Xaa Xaa	Leu Met Xaa	Xaa Pro Ser	Ser
	5		10		15

Glu Glu Leu	Gln Ala Asn	Lys Ala Thr	Leu Val Cys	Leu Ile Xaa	Asp
	20		25		30

Phe Tyr Pro	Gly Ala Val	Thr Val Ala	Trp Lys Ala	Xaa Ser Xaa	Pro
	35		40		45

Val Lys Ala	Xaa Val Xaa	Thr Xaa Thr	Xaa Ser Lys	Gln Ser Asn	Asn
	50		55		60

Lys Tyr Ala	Xaa Xaa Ser	Tyr Leu Ser	Pro Asp
	65		70

<210> 916

<211> 54

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(54)

<223> Xaa = Any amino acid

<400> 916

Thr Leu Thr	Ile Asn Arg	Val Glu Ala	Gly Asp Glu	Ala Asp Tyr	Tyr
	5		10		15

Cys Gln Val	Trp Asp Arg	Asn Asn Asp	His Val Val	Phe Gly Gly	Xaa
	20		25		30

Thr Lys Leu	Ala Xaa Leu	Gly Gln Pro	Xaa Xaa Ala	Pro Xaa Xaa	Thr
	35		40		45

His Xaa Xaa	Ala Leu Leu
	50

<210> 917

<211> 109

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(109)

<223> Xaa = Any amino acid

<400> 917

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Val Arg Thr Gln Ile Ala Xaa Xaa Arg Val Leu Val Val Ala Leu Phe
              5                      10                      15

Gly Xaa Cys Xaa Gly Xaa His Xaa Arg Leu Asp Gly Xaa Ala Xaa Cys
              20                      25                      30

Leu Pro Gly His Cys His Gly Ser Arg Val Glu Val Xaa Tyr Glu Thr
              35                      40                      45

His Gln Cys Gly Leu Val Gly Leu Lys Leu Leu Arg Gly Gly Xaa Xaa
              50                      55                      60

His Glu Xaa Xaa Arg Gly Gln Xaa Trp Ala Asp Leu Xaa Arg Pro Val
              65                      70                      75                      80

Trp Xaa Xaa Arg Arg Arg His Gly His Tyr Tyr Asp Pro Thr Leu
              85                      90                      95

Asp Ser Asn Ser Arg Pro His Arg Arg Leu Arg Pro Cys
              100                      105

```

<210> 918

<211> 85

<212> PRT

<213> Homo sapiens

<400> 918

```

Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
              5                      10                      15

Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
              20                      25                      30

His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
              35                      40                      45

Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
              50                      55                      60

Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
              65                      70                      75                      80

Ser Leu Gly Leu Thr
              85

```

<210> 919

<211> 52

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(52)

<223> Xaa = Any amino acid

<400> 919

Thr Ile Asn Arg Xaa Glu Ala Gly Asp Glu Xaa Xaa Tyr Tyr Cys Gln
5 10 15

Val Trp Asp Arg Asn Asn Asp His Xaa Val Phe Asp Gly Gly Thr Lys
20 25 30

Thr Gly Arg Pro Arg Ser Ala Gln Gly Cys Pro Leu Gly His Ser Val
35 40 45

Pro Ala Leu Leu
50

<210> 920

<211> 121

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(121)

<223> Xaa = Any amino acid

<400> 920

Pro Ser Thr Gly Xaa Lys Pro Ala Met Xaa Pro Xaa Ile Thr Val Lys
5 10 15

Cys Gly Ile Val Ile Met Thr Met Xaa Ser Ser Thr Glu Gly Pro Lys
20 25 30

Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe
35 40 45

Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys
50 55 60

Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala
65 70 75 80

Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys
85 90 95

Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro
100 105 110

Glu Gln Trp Lys Ser His Arg Ser Tyr
115 120

<210> 921

<211> 109

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(109)

<223> Xaa = Any amino acid

<400> 921

Val Ala Ser Val Xaa Leu Pro Leu Leu Arg Arg Xaa Ala Gln Ile Ala
 5 10 15

Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30

His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45

Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
 50 55 60

Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Xaa Ser Asp Arg Gly Gly
 65 70 75 80

Xaa Leu Xaa Leu Thr Xaa Asp Gly Gln Phe Gly Pro Ser Ala Glu Asp
 85 90 95

Asp Met Val Ile Ile Thr Ile Pro His Leu Thr Val Ile
 100 105

<210> 922
 <211> 109
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(109)
 <223> Xaa = Any amino acid

<400> 922
 Tyr Tyr Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly
 5 10 15

Gly Gly Thr Lys Leu Ala Val Xaa Gly Gln Xaa Lys Xaa Ala Pro Ser
 20 25 30

Val Thr Xaa Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala
 35 40 45

Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val
 50 55 60

Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr
 65 70 75 80

Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu
 85 90 95

Ser Xaa Thr Pro Glu Gln Trp Lys Xaa His Arg Ser Tyr
 100 105

<210> 923
 <211> 83
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(83)

<223> Xaa = Any amino acid

<400> 923

Ser Val Gly Leu Pro Leu Leu Arg Arg Xaa Ala Xaa Ile Ala Ala Gly
5 10 15
Arg Val Leu Val Val Ala Xaa Xaa Gly Gly Cys Gly Gly Xaa His Ser
20 25 30
Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His Gly Ser
35 40 45
Arg Val Glu Val Thr Tyr Glu Thr His Xaa Cys Gly Leu Val Gly Leu
50 55 60
Lys Leu Leu Xaa Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly Ser Leu
65 70 75 80
Gly Leu Thr

<210> 924

<211> 122

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(122)

<223> Xaa = Any amino acid

<400> 924

Ala Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr
5 10 15
Tyr Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly
20 25 30
Gly Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val
35 40 45
Thr Leu Phe Pro Pro Ser Xaa Glu Glu Leu Gln Ala Asn Lys Ala Thr
50 55 60
Xaa Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala
65 70 75 80
Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Xaa Thr Thr Thr
85 90 95
Pro Ser Xaa Xaa Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Xaa Ser
100 105 110
Xaa Thr Pro Glu Gln Trp Lys Ser His Arg
115 120

<210> 925

<211> 84

<212> PRT

<213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(84)
 <223> Xaa = Any amino acid

<400> 925
 Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
 5 10 15
 Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Xaa Phe Xaa Gly Gly
 20 25 30
 Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
 35 40 45
 Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
 50 55 60
 Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
 65 70 75 80
 Lys Ala Asp Ser

<210> 926
 <211> 121
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(121)
 <223> Xaa = Any amino acid

<400> 926
 Gly His Ser Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu
 5 10 15
 Leu Leu Trp Leu Pro Gly Ala Lys Cys Asp Ile Gln Met Thr Gln Ser
 20 25 30
 Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Thr Val Thr Ile Ser Xaa
 35 40 45
 Arg Ala Ser Xaa Asn Ile Asp Arg Trp Leu Ala Trp His Gln Gln Lys
 50 55 60
 Pro Gly Lys Ala Pro Asn Val Leu Ile Tyr Ala Thr Ser Ser Leu Glu
 65 70 75 80
 Glu Gly Val Ser Leu Arg Phe Thr Gly Ser Gly Ser Gly Thr Gln Phe
 85 90 95
 Asn Leu Thr Ile Thr Ser Leu Gln Pro Asp Asp Ser Ala Thr Tyr Tyr
 100 105 110
 Cys Gln His Tyr Xaa Ala Ser Leu Xaa
 115 120

<210> 927
 <211> 71

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(71)

<223> Xaa = Any amino acid

<400> 927

```

Asp Ile Arg Gly Phe Ala Trp Phe Leu Leu Met Pro Gly Gln Pro Pro
              5                      10                      15

Ile Tyr Ile Xaa Arg Gly Pro Xaa Thr Tyr Cys Asn Cys Ile Ser Asp
              20                      25                      30

Arg Cys Arg Gln Gly Gly Arg Arg Leu Gly His Leu Asp Val Thr Phe
              35                      40                      45

Gly Thr Trp Glu Pro Glu Gln Gln Glu Pro Gln Glu Leu Ser Gly Asp
              50                      55                      60

Pro His Val His Ala Val Ser
              65                      70

```

<210> 928

<211> 150

<212> PRT

<213> Homo sapiens

<400> 928

```

Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro Tyr Ile Asn
              5                      10                      15

Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser
              20                      25                      30

Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly Ile Leu Ser
              35                      40                      45

Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile Ala Gly Ile
              50                      55                      60

Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys Ser Asn Ile
              65                      70                      75                      80

Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln Thr Ile Glu Ile Lys
              85                      90                      95

Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser Gln Pro Lys Asn Glu
              100                      105                      110

Glu Asp Ile Glu Ile Ile Pro Ile Gln Glu Glu Glu Glu Glu Thr
              115                      120                      125

Glu Thr Asn Phe Pro Glu Pro Pro Gln Asp Gln Glu Ser Ser Pro Ile
              130                      135                      140

Glu Asn Asp Ser Ser Pro
              145                      150

```

<210> 929

<211> 53
<212> PRT
<213> Homo sapiens

<400> 929
Pro Asn His Phe Phe Phe Tyr Phe Asn Ser Leu Phe Phe Phe Phe Phe
 5 10 15
Cys Arg Gln Glu Asn Tyr Val Arg Phe Gly Ser Gly Ala Arg Ser Phe
 20 25 30
Pro Phe Ile Leu Asn Asp Ala Ser Tyr Tyr Lys Phe Leu Glu Glu Gly
 35 40 45
Lys Asp Gln His His
 50

<210> 930
<211> 101
<212> PRT
<213> Homo sapiens

<400> 930
Ser Trp Gly Gly Ser Gly Lys Phe Val Ser Val Ser Ser Ser Ser Ser
 5 10 15
Ser Trp Ile Gly Ile Ile Ser Met Ser Ser Ser Phe Phe Gly Trp Glu
 20 25 30
Asp Val Ser Val Ser Pro Thr Thr Ser Ser Phe Ile Ser Ile Val Cys
 35 40 45
Ser Phe Phe Ser Ser Ala Asp Arg Arg Thr Met Leu Asp Leu Gly Leu
 50 55 60
Glu His Val Leu Phe His Ser Phe Ser Thr Met Pro Ala Ile Thr Ser
 65 70 75 80
Ser Trp Lys Lys Ala Lys Ile Ser Ile Thr Asp Lys Met Pro Lys Asn
 85 90 95
Arg Asp Cys Met Leu
 100

<210> 931
<211> 123
<212> PRT
<213> Homo sapiens

<400> 931
Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
 5 10 15
Cys Gln Val Trp Asp Arg Asn Tyr Asp His Val Val Phe Gly Gly Gly
 20 25 30
Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
 35 40 45
Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
 50 55 60

Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
 65 70 75 80
 Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
 85 90 95
 Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu
 100 105 110
 Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
 115 120

<210> 932
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 932
 Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
 5 10 15
 Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30
 His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45
 Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
 50 55 60
 Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
 65 70 75 80
 Ser Leu Gly Leu Thr
 85

<210> 933
 <211> 150
 <212> PRT
 <213> Homo sapiens

<400> 933
 Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro Tyr Ile Asn
 5 10 15
 Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser
 20 25 30
 Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly Ile Leu Ser
 35 40 45
 Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile Ala Gly Ile
 50 55 60
 Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys Ser Asn Ile
 65 70 75 80
 Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln Thr Ile Glu Ile Lys
 85 90 95

Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser Gln Pro Lys Asn Glu
 100 105 110
 Glu Asp Ile Glu Ile Ile Pro Ile Gln Glu Glu Glu Glu Glu Thr
 115 120 125
 Glu Thr Asn Phe Pro Glu Pro Pro Gln Asp Gln Glu Ser Ser Pro Ile
 130 135 140
 Glu Asn Asp Ser Ser Pro
 145 150

<210> 934
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 934
 Ser Trp Gly Gly Ser Gly Lys Phe Val Ser Val Ser Ser Ser Ser Ser
 5 10 15
 Ser Trp Ile Gly Ile Ile Ser Met Ser Ser Ser Phe Phe Gly Trp Glu
 20 25 30
 Asp Val Ser Val Ser Pro Thr Thr Ser Ser Phe Ile Ser Ile Val Cys
 35 40 45
 Ser Phe Phe Ser Ser Ala Asp Arg Arg Thr Met Leu Asp Leu Gly Leu
 50 55 60
 Glu His Val Leu Phe His Ser Phe Ser Thr Met Pro Ala Ile Thr Ser
 65 70 75 80
 Ser Trp Lys Lys Ala Lys Ile Ser Ile Thr Asp Lys Met Pro Lys Asn
 85 90 95
 Arg Asp Cys Met Leu
 100

<210> 935
 <211> 61
 <212> PRT
 <213> Homo sapiens

<400> 935
 Lys Glu Ala Ala Leu Val Val Pro Gln Pro Trp Pro Gly Pro Phe Ser
 5 10 15
 Ser Ser Ala Ser Ser Leu Thr Ala Gln Val Ile Pro Pro Gly Ser His
 20 25 30
 Gln Pro Ala Gln Pro Lys Ala Ser Gly Ser Ser Val Ser Leu Ile Leu
 35 40 45
 Ser Ser Gly Gly Pro Phe Leu Trp Trp Ala Gly Cys Ser
 50 55 60

<210> 936
 <211> 114
 <212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(114)

<223> Xaa = Any amino acid

<400> 936

```

Ile Pro Pro Lys Leu Cys Ser Arg Thr Cys Glu Asn Leu Arg Asp Cys
      5              10              15

Thr Cys Gln Glu Lys Val Val Ser Phe Gln Phe Glu Val Ser Ile Gln
      20              25              30

Gln Asp Ile Cys Gly Pro Leu Gly Leu Arg Leu Ile Ala Gly Asp Thr
      35              40              45

Leu Arg Val Tyr Arg Leu Ser Gly Phe Cys Leu Gly Gln Gln Asp Lys
      50              55              60

Gly Phe Gln Lys Glu Tyr Leu Ser Leu Gly Arg Gln Pro Leu Xaa His
      65              70              75              80

Leu Phe Phe Xaa Leu Phe Ile Tyr Phe Phe Ile Tyr Ser Tyr Leu Cys
      85              90              95

Arg Leu Cys Asp Leu Leu Cys Val Asp Ser Asp Thr Leu Ser Val Ser
      100             105             110

```

Gly Pro

<210> 937

<211> 64

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(64)

<223> Xaa = Any amino acid

<400> 937

```

Gly Phe Thr Asp Ser Leu Asp Phe Val Trp Asp Ser Arg Thr Arg Asp
      5              10              15

Phe Lys Arg Asn Thr Phe His Leu Glu Gly Asn Leu Ser Xaa Ile Tyr
      20              25              30

Ser Phe Xaa Tyr Leu Phe Ile Phe Leu Phe Ile Leu Ile Phe Ala Asp
      35              40              45

Ser Val Thr Ser Tyr Val Leu Thr Gln Thr Pro Ser Val Ser Val Ala
      50              55              60

```

<210> 938

<211> 82

<212> PRT

<213> Homo sapiens

<400> 938

Gly Ser Ser Thr Gly Gly Ala Ser Ala Met Ala Trp Thr Val Leu Leu
5 10 15
Leu Gly Leu Leu Ser His Cys Thr Gly Asp Pro Pro Arg Val Ser Pro
20 25 30
Thr Cys Pro Ala Gln Gly Phe Trp Val Gln Arg Val Leu Asn Ser Glu
35 40 45
Leu Arg Arg Ala Leu Pro Val Val Gly Arg Met Leu Met Thr Leu Val
50 55 60
Gln Gly Gly Arg Leu Val Gly Leu Asn Ser Pro Gln Thr Val Leu Lys
65 70 75 80
Asp Leu

<210> 939
<211> 88
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(88)
<223> Xaa = Any amino acid

<400> 939
Glu Pro Glu Gly Leu His Leu Pro Arg Glu Ser Ser Glu Phe Ser Val
5 10 15
Arg Ser Leu His Thr Thr Gly His Leu Trp Ala Thr Gly Ala Thr Ala
20 25 30
Asp Cys Arg Gly Tyr Pro Glu Gly Leu Gln Thr Leu Trp Ile Leu Ser
35 40 45
Gly Thr Ala Gly Gln Gly Ile Ser Lys Gly Ile Pro Phe Thr Trp Lys
50 55 60
Ala Thr Ser Leu Xaa Phe Ile Leu Leu Xaa Ile Tyr Leu Phe Phe Tyr
65 70 75 80
Leu Phe Leu Ser Leu Gln Thr Leu
85

<210> 940
<211> 66
<212> PRT
<213> Homo sapiens

<400> 940
Lys Leu Thr Thr Phe Ser Trp Gln Val Gln Ser Leu Arg Phe Ser Gln
5 10 15
Val Leu Glu His Ser Leu Gly Gly Ile Gln Pro His Gln Pro Pro Thr
20 25 30
Leu His Gln Gly His Glu His Pro Ala His His Arg Lys Gly Pro Pro
35 40 45

Glu Leu Arg Ile Lys Asp Thr Leu Asp Pro Glu Ala Leu Gly Trp Ala
 50 55 60

Gly Trp
 65

<210> 941
 <211> 136
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(136)
 <223> Xaa = Any amino acid

<400> 941
 Ile Xaa Lys Arg Ile Asn Xaa Arg Glu Val Ala Phe Gln Val Lys Gly
 5 10 15
 Ile Pro Phe Glu Ile Pro Cys Pro Ala Val Pro Asp Lys Ile Gln Arg
 20 25 30
 Val Cys Lys Pro Ser Gly Tyr Pro Leu Gln Ser Ala Val Ala Pro Val
 35 40 45
 Ala His Lys Cys Pro Val Val Trp Arg Leu Arg Thr Glu Asn Ser Leu
 50 55 60
 Leu Ser Leu Gly Arg Cys Ser Pro Ser Gly Ser His Lys Ser Leu Ser
 65 70 75 80
 Thr Val Trp Gly Glu Phe Ser Pro Thr Ser Leu Pro Pro Cys Thr Arg
 85 90 95
 Val Met Ser Ile Leu Pro Thr Thr Gly Arg Ala Leu Leu Ser Ser Glu
 100 105 110
 Leu Arg Thr Arg Trp Thr Gln Lys Pro Trp Ala Gly Gln Val Gly Glu
 115 120 125
 Thr Leu Gly Gly Ser Pro Val Gln
 130 135

<210> 942
 <211> 84
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(84)
 <223> Xaa = Any amino acid

<400> 942
 Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
 5 10 15
 Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly
 20 25 30

```

<400> 944
Thr Ile Asn Arg Val Glu Ala Gly Xaa Glu Ala Asp Tyr Tyr Cys Gln
          5                      10                      15

Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly Thr Lys
          20                      25                      30

Leu Ala Val Leu Gly Gln Xaa Lys Ala Ala Xaa Ser Val Xaa Leu Xaa
          35                      40                      45

```

Pro Pro Ser Tyr Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys
 50 55 60
 Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala
 65 70 75 80
 Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys
 85 90 95
 Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Xaa Thr Xaa
 100 105 110
 Glu Gln Trp Lys Ser His Arg Ser Tyr
 115 120

<210> 945
 <211> 119
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> variant
 <222> (1)...(119)
 <223> Xaa = Any amino acid

<400> 945
 Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
 5 10 15
 Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30
 His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45
 Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
 50 55 60
 Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
 65 70 75 80
 Ser Leu Gly Leu Thr Xaa Xaa Gly Gln Phe Gly Pro Ser Ala Xaa Asp
 85 90 95
 Asp Met Val His Tyr Tyr Asp Pro Thr Leu Asp Ser Asn Ser Arg Pro
 100 105 110
 His Arg Arg Leu Xaa Pro Cys
 115

<210> 946
 <211> 121
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> variant
 <222> (1)...(121)
 <223> Xaa = Any amino acid

<400> 946

Pro Ser Thr Gly Xaa Lys Pro Ala Met Arg Pro Thr Ile Thr Val Lys
5 10 15
Cys Gly Ile Val Ile Met Asn His Val Val Xaa Gly Gly Gly Thr Lys
20 25 30
Leu Ala Xaa Xaa Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe
35 40 45
Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys
50 55 60
Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala
65 70 75 80
Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys
85 90 95
Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro
100 105 110
Glu Gln Trp Lys Ser His Arg Ser Tyr
115 120

<210> 947

<211> 56

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(56)

<223> Xaa = Any amino acid

<400> 947

Thr Ala Thr Leu Thr Ile Asn Arg Xaa Glu Ala Gly Asp Glu Ala Asp
5 10 15
Tyr Tyr Cys Gln Val Trp Asp Arg Asn Asn Glu Pro Cys Arg Leu Xaa
20 25 30
Arg Arg Asp Gln Thr Gly Arg Xaa Arg Ser Ala Gln Gly Cys Pro Leu
35 40 45
Gly His Ser Val Pro Ala Leu Leu
50 55

<210> 948

<211> 62

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(62)

<223> Xaa = Any amino acid

<400> 948

Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
5 10 15

Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Xaa Gly Gly
20 25 30
Thr Lys Leu Ala Val Leu Gly Xaa Pro Lys Ala Ala Pro Ser Val Thr
35 40 45
Leu Phe Pro Pro Ser Ser Xaa Glu Leu Gln Xaa Asn Lys Ala
50 55 60

<210> 949
<211> 101
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(101)
<223> Xaa = Any amino acid

<400> 949
Val Ala Ser Val Xaa Leu Pro Leu Leu Xaa Arg Gln Ala Gln Ile Ala
5 10 15
Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
20 25 30
His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
35 40 45
Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Xaa Cys Gly Leu Val
50 55 60
Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Xaa Xaa Asp Arg Xaa Gly
65 70 75 80
Ser Leu Gly Leu Thr Xaa Asp Gly Gln Phe Gly Ser Ser Ala Xaa Xaa
85 90 95
Asp Met Val Asn Tyr
100

<210> 950
<211> 102
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(102)
<223> Xaa = Any amino acid

<400> 950
Leu Ile Ile Asp His Val Xaa Xaa Gly Gly Gly Thr Lys Leu Ala Val
5 10 15
Xaa Gly Gln Pro Lys Ala Ala Xaa Ser Val Xaa Xaa Phe Pro Pro Ser
20 25 30
Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Xaa Val Cys Leu Ile Ser
35 40 45

Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser
 50 55 60

Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn
 65 70 75 80

Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Xaa Glu Gln Trp
 85 90 95

Lys Xaa His Arg Ser Tyr
 100

<210> 951
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(67)
 <223> Xaa = Any amino acid

<400> 951
 Val Ala Ser Val Xaa Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
 5 10 15

Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30

His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45

Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Xaa
 50 55 60

Gly Leu Lys
 65

<210> 952
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(67)
 <223> Xaa = Any amino acid

<400> 952
 Leu Gln Ala Xaa Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
 5 10 15

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
 20 25 30

Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
 35 40 45

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Xaa His
 50 55 60

Arg Ser Tyr
65

<210> 953
<211> 83
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(83)
<223> Xaa = Any amino acid

<400> 953
Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
 5 10 15
Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly
 20 25 30
Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
 35 40 45
Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
 50 55 60
Val Cys Leu Ile Ser Asp Phe Leu Pro Gly Ser Arg Asp Xaa Gly Leu
 65 70 75 80
Xaa Gly Xaa

<210> 954
<211> 58
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(58)
<223> Xaa = Any amino acid

<400> 954
Leu Arg Lys Gln His Trp Trp Cys Leu Ser His Gly Leu Asp Arg Ser
 5 10 15
Pro Pro Arg Pro Pro Leu Ser Leu His Arg Leu Cys Asp Leu Leu Cys
 20 25 30
Val Asp Ser Asp Thr Leu Ser Val Ser Gly Pro Xaa Lys Asp Gly Gln
 35 40 45
Asp Tyr Leu Trp Gly Lys Gln Tyr Trp Glu
 50 55

<210> 955
<211> 77
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(77)
<223> Xaa = Any amino acid

<400> 955
Gly Ser Ser Thr Gly Gly Ala Ser Ala Met Ala Trp Thr Val Leu Leu
 5 10 15

Leu Gly Leu Leu Ser His Cys Thr Asp Ser Val Thr Ser Tyr Val Leu
 20 25 30

Thr Gln Thr Pro Ser Val Ser Val Ala Pro Xaa Lys Thr Ala Lys Ile
 35 40 45

Thr Cys Gly Gly Asn Asn Ile Gly Ser Asn Asn Val His Trp Tyr Tyr
 50 55 60

Gln Lys Xaa Gly Xaa Ala Pro Val Pro Asn His Leu Phe
 65 70 75

<210> 956
<211> 55
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(55)
<223> Xaa = Any amino acid

<400> 956
Leu Arg His Pro Gln Cys Gln Trp Pro Xaa Glu Arg Arg Pro Arg Leu
 5 10 15

Pro Val Gly Glu Thr Ile Leu Gly Val Thr Met Tyr Thr Gly Ile Thr
 20 25 30

Arg Ser Xaa Ala Xaa Pro Leu Phe Leu Ile Ile Ser Phe Asp Asn Asp
 35 40 45

Arg Xaa Ser Gly Ile Ser Glu
 50 55

<210> 957
<211> 69
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(69)
<223> Xaa = Any amino acid

<400> 957
Val Ala Ser Xaa Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
 5 10 15

Ala Gly Arg Val Leu Val Val Thr Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30

His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45

Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Xaa Cys Gly Leu Val
 50 55 60

Gly Leu Lys Leu Leu
 65

<210> 958

<211> 69

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(69)

<223> Xaa = Any amino acid

<400> 958

Glu Glu Leu Gln Ala Asn Lys Ala Thr Xaa Val Cys Leu Ile Ser Asp
 5 10 15

Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
 20 25 30

Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
 35 40 45

Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
 50 55 60

Ser Xaa Arg Ser Tyr
 65

<210> 959

<211> 97

<212> PRT

<213> Homo sapiens

<400> 959

Gly Ser Ser Thr Gly Gly Ala Ser Ala Met Ala Trp Thr Val Leu Leu
 5 10 15

Leu Gly Leu Leu Ser His Cys Thr Asp Ser Val Thr Ser Tyr Val Leu
 20 25 30

Thr Gln Thr Pro Ser Val Ser Val Ala Pro Gly Lys Thr Ala Lys Ile
 35 40 45

Thr Cys Gly Gly Asn Asn Ile Gly Ser Asn Asn Val His Trp Tyr Tyr
 50 55 60

Gln Lys Pro Gly Gln Ala Pro Val Leu Ile Ile Ser Phe Asp Asn Asp
 65 70 75 80

Arg Pro Ser Gly Ile Ser Glu Arg Phe Ser Gly Phe Asn Ser Gly Asp
 85 90 95

Met

```
<210> 960
<211> 56
<212> PRT
<213> Homo sapiens
```

```

<400> 960
Lys Gln His Trp Trp Cys Leu Gly His Gly Leu Asp Arg Ser Pro Pro
          5                      10                      15

Arg Pro Pro Leu Ser Leu His Arg Leu Cys Asp Leu Leu Cys Val Asp
          20                      25                      30

Ser Asp Thr Leu Ser Val Ser Gly Pro Arg Lys Asp Gly Gln Asp Tyr
          35                      40                      45

Leu Trp Gly Lys Gln Tyr Trp Glu
          50                      55

```

```
<210> 961
<211> 87
<212> PRT
<213> Homo sapiens
```

```
<400> 961  
Gly Ser Ser Thr Gly Gly Ala Ser Ala Met Ala Trp Thr Val Leu Leu  
          5                      10              15  
  
Pro Gly Leu Leu Ser His Cys Thr Asp Ser Val Thr Ser Tyr Val Leu  
      20                25              30  
  
Thr Gln Thr Pro Ser Val Ser Val Ala Pro Gly Lys Thr Ala Lys Ile  
    35                  40              45  
  
Thr Cys Gly Gly Asn Asn Ile Gly Ser Tyr Ser Val His Trp Tyr Tyr  
    50                55              60  
  
Gln Lys Pro Gly Gln Ala Pro Val Leu Ile Ile Ser Phe Asp Asn Asp  
    65                  70              75              80  
  
Arg Pro Pro Gly Gln Val Gln  
          85
```

```
<210> 962
<211> 63
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> variant  
<222> (1)...(63)  
<223> Xaa = Any amino acid
```

<400> 962
Ser Ser Leu Leu Ile Thr Thr Gly Arg Pro Gly Arg Ser Asn Glu Asp
 5 10 15

Thr Pro Gln Leu Tyr Val Ala Cys Gly Arg Gly Pro Arg Ser Ser Leu
 20 25 30

Arg Val Leu Arg His Gly Leu Glu Val Ser Glu Met Ala Val Ser Glu
35 40 45

Leu Pro Gly Xaa Pro Lys Arg Cys Leu Asp Ser Ala Ser Thr His
50 55 60

<210> 963

<211> 76

<212> PRT

<213> Homo sapiens

<400> 963

Lys Gln His Trp Trp Cys Leu Ser His Gly Leu Asp Arg Ser Pro Pro
5 10 15

Arg Pro Pro Leu Ser Leu His Arg Leu Cys Asp Leu Leu Cys Val Asp
20 25 30

Ser Asp Thr Leu Ser Val Ser Gly Pro Arg Lys Asp Gly Gln Asp Tyr
35 40 45

Leu Trp Gly Lys Gln Tyr Trp Glu Leu Gln Cys Thr Leu Val Leu Pro
50 55 60

Lys Ala Arg Pro Gly Pro Cys Pro Asn His Leu Phe
65 70 75

<210> 964

<211> 71

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(71)

<223> Xaa = Any amino acid

<400> 964

Cys Arg His Gln Thr His Leu Gln Cys Val Asp Ala Leu Ser Arg Gln
5 10 15

Arg Leu Gly Xaa Pro Gly Ser Ser Glu Thr Ala Ile Ser Asp Thr Ser
20 25 30

Ser Pro Cys Leu Arg Thr Leu Arg Asp Asp Arg Gly Pro Leu Pro Gln
35 40 45

Ala Thr Tyr Asn Cys Gly Val Ser Ser Leu Asp Leu Pro Gly Arg Pro
50 55 60

Val Val Ile Lys Arg Asp Asp
65 70

<210> 965

<211> 89

<212> PRT

<213> Homo sapiens

<220>

<221> variant
 <222> (1)...(89)
 <223> Xaa = Any amino acid

<400> 965
 Gly Gly Ile His Glu Arg His Asn Asp Val Gly Ile Lys Leu Ile Phe
 5 10 15
 Asn Val Ser Thr His Cys Pro Asp Ser Val Trp Gly Xaa Gln Val Ala
 20 25 30
 Gln Lys Gln Pro Phe Leu Thr Pro Gln Val His Val Leu Gly Leu Ser
 35 40 45
 Glu Met Ile Gly Val Pro Tyr His Arg Pro His Thr Thr Val Glu Tyr
 50 55 60
 Leu His Trp Thr Cys Pro Gly Gly Arg Ser Leu Ser Lys Glu Met Ile
 65 70 75 80
 Arg Thr Gly Ala Trp Pro Gly Phe Trp
 85

<210> 966
 <211> 66
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(66)
 <223> Xaa = Any amino acid

<400> 966
 Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
 5 10 15
 Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Xaa
 20 25 30
 Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
 35 40 45
 Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
 50 55 60
 Val Cys
 65

<210> 967
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(51)
 <223> Xaa = Any amino acid

<400> 967
 Val Ala Xaa Ala Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala

5 10 15
Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
20 25 30
His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
35 40 45
Gly Ser Arg
50

<210> 968
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(51)
<223> Xaa = Any amino acid

<400> 968
Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
5 10 15
Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
20 25 30
Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser Gly
35 40 45

Xaa Ser Tyr
50

<210> 969
<211> 52
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(52)
<223> Xaa = Any amino acid

<400> 969
Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
5 10 15
Cys Gln Val Trp Asp Leu Asn Asp Asp His Val Val Phe Gly Gly Xaa
20 25 30
Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
35 40 45

Leu Xaa Pro Pro
50

<210> 970
<211> 66
<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(66)

<223> Xaa = Any amino acid

<400> 970

Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
5 10 15

Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Xaa
20 25 30

Thr Lys Leu Ala Val Leu Gly Gln Xaa Lys Ala Xaa Pro Ser Val Thr
35 40 45

Leu Phe Pro Pro Ser Xaa Xaa Glu Leu Gln Ala Asn Lys Ala Thr Leu
50 55 60

Val Cys
65

<210> 971

<211> 56

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(56)

<223> Xaa = Any amino acid

<400> 971

Val Ala Ser Xaa Xaa Leu Pro Leu Leu Arg Arg Gln Ala Xaa Ile Ala
5 10 15

Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
20 25 30

His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
35 40 45

Gly Ser Arg Val Glu Val Thr Leu
50 55

<210> 972

<211> 55

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(55)

<223> Xaa = Any amino acid

<400> 972

Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser
5 10 15

Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser

20	25	30
Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Xaa Ser Leu Thr Pro Glu Gln		
35	40	45

Trp Lys Xaa Xaa Arg Ser Tyr
50 55

```
<210> 973
<211> 101
<212> PRT
<213> Homo sapiens
```

<400> 973
Ser Trp Gly Gly Ser Gly Lys Phe Val Ser Val Ser Ser Ser Ser Ser

5 10 15

Ser Trp Ile Gly Ile Ile Ser Met Ser Ser Ser Phe Phe Gly Trp Glu
20 25 30

Asp Val Ser Val Ser Pro Thr Thr Ser Ser Phe Ile Ser Ile Val Cys
35 40 45

Ser Phe Phe Ser Ser Ala Asp Arg Arg Thr Met Leu Asp Leu Gly Leu
50 55 60

Glu His Val Leu Phe His Ser Phe Ser Thr Met Pro Ala Ile Thr Ser
65 70 75 80

Ser Trp Lys Lys Ala Lys Ile Ser Ile Thr Asp Lys Met Pro Lys Asn
85 90 95

Arg Asp Cys Met Leu
100

```
<210> 974
<211> 150
<212> PRT
<213> Homo sapiens
```

<400> 974
Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro Tyr Ile Asn
 5 10 15

Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser
20 25 30

Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly Ile Leu Ser
35 40 45

Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile Ala Gly Ile
50 55 60

Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys Ser Asn Ile
65 70 75 80

Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln Thr Ile Glu Ile Lys
85 90 95

Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser Gln Pro Lys Asn Glu
100 105 110

Glu Asp Ile Glu Ile Ile Pro Ile Gln Glu Glu Glu Glu Glu Thr
 115 120 125

Glu Thr Asn Phe Pro Glu Pro Pro Gln Asp Gln Glu Ser Ser Pro Ile
 130 135 140

Glu Asn Asp Ser Ser Pro
 145 150

<210> 975
 <211> 53
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(53)
 <223> Xaa = Any amino acid

<400> 975
 Val Ala Ser Xaa Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
 5 10 15

Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30

His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45

Gly Ser Arg Val Glu
 50

<210> 976
 <211> 53
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(53)
 <223> Xaa = Any amino acid

<400> 976
 Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
 5 10 15

Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
 20 25 30

Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
 35 40 45

Ser Xaa Arg Ser Tyr
 50

<210> 977
 <211> 97
 <212> PRT
 <213> Homo sapiens

<220>
<221> variant
<222> (1)...(97)
<223> Xaa = Any amino acid

<400> 977
Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
 5 10 15
Cys Gln Val Trp Asp His Asn Asn Asp His Val Val Phe Gly Gly Gly
 20 25 30
Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
 35 40 45
Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
 50 55 60
Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Xaa Xaa Trp
 65 70 75 80
Lys Ala Xaa Xaa Ser Pro Val Xaa Ala Gly Val Xaa Thr Thr Thr Pro
 85 90 95

Ser

<210> 978
<211> 59
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(59)
<223> Xaa = Any amino acid

<400> 978
Gly Gly Cys Gly Gly Xaa His Ser Arg Xaa Asp Gly Ala Xaa Xaa Cys
 5 10 15
Leu Pro Xaa Xaa Cys His Gly Ser Arg Val Glu Val Thr Tyr Glu Thr
 20 25 30
His Gln Cys Gly Leu Val Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu
 35 40 45
Gln Ser Asp Arg Gly Gly Ser Leu Gly Leu Thr
 50 55

<210> 979
<211> 83
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(83)
<223> Xaa = Any amino acid

<400> 979

Thr Leu Thr Ile Asn Arg Val Xaa Ala Gly Asp Glu Ala Asp Tyr Tyr
 5 10 15

Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly
 20 25 30

Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
 35 40 45

Leu Xaa Pro Xaa Ser Xaa Xaa Glu Leu Gln Ala Asn Lys Ala Thr Leu
 50 55 60

Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
 65 70 75 80

Lys Ala Xaa

<210> 980

<211> 60

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(60)

<223> Xaa = Any amino acid

<400> 980

Leu Glu Gly Val Val Val Ser Thr Pro Ala Leu Thr Gly Leu Leu Xaa
 5 10 15

Cys Leu Pro Gly His Cys His Gly Ser Arg Val Glu Val Thr Tyr Glu
 20 25 30

Thr His Gln Cys Gly Leu Val Gly Leu Lys Leu Xaa Xaa Gly Xaa Arg
 35 40 45

Xaa Gln Ser Asp Arg Gly Gly Ser Leu Gly Leu Thr
 50 55 60

<210> 981

<211> 123

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(123)

<223> Xaa = Any amino acid

<400> 981

Val Ala Ser Val Gly Leu Pro Leu Phe Arg Arg Gln Ala Gln Ile Ala
 5 10 15

Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30

His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45

Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
 50 55 60
 Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
 65 70 75 80
 Ser Leu Gly Leu Thr Xaa Asp Gly Gln Phe Gly Pro Ser Thr Glu Asp
 85 90 95
 Asp Met Val Ile Ile Thr Ile Pro His Leu Thr Val Ile Val Gly Leu
 100 105 110
 Ile Ala Gly Phe Asp Pro Val Asp Gly Gln Gly
 115 120

<210> 982
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(123)
 <223> Xaa = Any amino acid

<400> 982
 Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
 5 10 15
 Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly
 20 25 30
 Thr Lys Leu Ala Val Xaa Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
 35 40 45
 Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
 50 55 60
 Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
 65 70 75 80
 Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
 85 90 95
 Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu
 100 105 110
 Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
 115 120

<210> 983
 <211> 150
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(150)
 <223> Xaa = Any amino acid

<400> 983

Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro Tyr Ile Asn
 5 10 15

 Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser
 20 25 30

 Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly Ile Leu Ser
 35 40 45

 Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile Ala Gly Ile
 50 55 60

 Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys Ser Asn Ile
 65 70 75 80

 Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln Thr Ile Glu Ile Lys
 85 90 95

 Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser Gln Pro Lys Asn Glu
 100 105 110

 Glu Asp Ile Glu Ile Ile Pro Ile Gln Glu Glu Glu Glu Glu Thr
 115 120 125

 Glu Thr Asn Phe Pro Glu Pro Pro Gln Asp Gln Glu Ser Ser Xaa Ile
 130 135 140

 Glu Asn Asp Ser Ser Pro
 145 150

<210> 984

<211> 101

<212> PRT

<213> Homo sapiens

<400> 984

Ser Trp Gly Gly Ser Gly Lys Phe Val Ser Val Ser Ser Ser Ser Ser
 5 10 15

 Ser Trp Ile Gly Ile Ile Ser Met Ser Ser Ser Phe Phe Gly Trp Glu
 20 25 30

 Asp Val Ser Val Ser Pro Thr Thr Ser Ser Phe Ile Ser Ile Val Cys
 35 40 45

 Ser Phe Phe Ser Ser Ala Asp Arg Arg Thr Met Leu Asp Leu Gly Leu
 50 55 60

 Glu His Val Leu Phe His Ser Phe Ser Thr Met Pro Ala Ile Thr Ser
 65 70 75 80

 Ser Trp Lys Lys Ala Lys Ile Ser Ile Thr Asp Lys Met Pro Lys Asn
 85 90 95

 Arg Asp Cys Met Leu
 100

<210> 985

<211> 122

<212> PRT

<213> Homo sapiens

<400> 985

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Ser Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu
              5              10              15

Trp Leu Pro Gly Ala Lys Cys Asp Ile Gln Met Thr Gln Ser Pro Ser
              20              25              30

Thr Leu Ser Ala Ser Val Gly Asp Thr Val Thr Ile Ser Cys Arg Ala
              35              40              45

Ser Gln Asn Ile Asp Arg Trp Leu Ala Trp His Gln Gln Lys Pro Gly
              50              55              60

Lys Ala Pro Asn Val Leu Ile Tyr Ala Thr Ser Ser Leu Glu Glu Gly
              65              70              75              80

Val Ser Leu Arg Phe Thr Gly Ser Gly Ser Gly Thr Gln Phe Asn Leu
              85              90              95

Thr Ile Thr Ser Leu Gln Pro Asp Asp Ser Ala Thr Tyr Tyr Cys Ala
              100             105             110

Thr Leu Phe Cys Ile Ser Ser Gln Phe Trp
              115             120

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<210> 986

<211> 69

<212> PRT

<213> Homo sapiens

<400> 986

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Asp Ile Arg Gly Phe Ala Trp Phe Leu Leu Met Pro Gly Gln Pro Pro
              5              10              15

Ile Tyr Ile Leu Arg Gly Pro Thr Thr Tyr Cys Asn Cys Ile Ser Asp
              20              25              30

Arg Cys Arg Gln Gly Gly Arg Arg Leu Gly His Leu Asp Val Thr Phe
              35              40              45

Gly Thr Trp Glu Pro Glu Gln Gln Glu Pro Gln Glu Leu Ser Gly Asp
              50              55              60

Pro His Val His Ala
              65

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<210> 987

<211> 118

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(118)

<223> Xaa = Any amino acid

<400> 987

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Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
              5              10              15

```

Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly
 20 25 30
 Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
 35 40 45
 Leu Phe Pro Pro Ser Ser Xaa Xaa Leu Xaa Ala Asn Lys Ala Thr Leu
 50 55 60
 Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
 65 70 75 80
 Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
 85 90 95
 Ser Lys Gln Ser Asn Asn Lys Tyr Xaa Ala Ser Xaa Tyr Leu Ser Leu
 100 105 110
 Thr Pro Glu Gln Trp Lys
 115

<210> 988
 <211> 80
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(80)
 <223> Xaa = Any amino acid

<400> 988
 Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Xaa Ala Gly Xaa Val Leu
 5 10 15
 Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu His Ser Arg Leu Asp
 20 25 30
 Gly Ala Ala Ile Cys Leu Pro Gly His Cys His Gly Ser Arg Val Glu
 35 40 45
 Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val Gly Xaa Lys Xaa Xaa
 50 55 60
 Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly Ser Leu Gly Leu Thr
 65 70 75 80

<210> 989
 <211> 63
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(63)
 <223> Xaa = Any amino acid

<400> 989
 Leu Leu Ala Ala Tyr Leu Leu Leu Leu Cys Xaa Glu Gly Val Xaa Val
 5 10 15

Ser Thr Pro Ala Leu Xaa Gly Leu Leu Xaa Xaa Phe Gln Ser His Xaa
 20 25 30
 His Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Xaa Cys Gly Leu
 35 40 45
 Val Xaa Xaa Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg
 50 55 60

<210> 990
 <211> 56
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(56)
 <223> Xaa = Any amino acid

<400> 990
 Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
 5 10 15
 Ala Gly Arg Val Leu Val Val Ala Leu Xaa Xaa Gly Cys Xaa Xaa Leu
 20 25 30
 His Ser Arg Leu Xaa Xaa Ala Ala Ile Xaa Leu Pro Glu Pro Xaa Ser
 35 40 45
 Arg Leu Pro Gly Arg Ser His Leu
 50 55

<210> 991
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 991
 Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asn Tyr Tyr
 5 10 15
 Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly
 20 25 30
 Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
 35 40 45
 Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
 50 55 60
 Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
 65 70 75 80
 Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
 85 90 95
 Ser Lys Gln Ser Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu
 100 105 110
 Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr

115

120

<210> 992
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 992
 Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
 5 10 15
 Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30
 His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45
 Gly Ser Arg Val Glu Val Thr Tyr Glu Ala His Gln Cys Gly Leu Val
 50 55 60
 Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
 65 70 75 80
 Ser Leu Gly Leu Thr
 85

<210> 993
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 993
 Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
 5 10 15
 Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly
 20 25 30
 Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
 35 40 45
 Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
 50 55 60
 Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
 65 70 75 80
 Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
 85 90 95
 Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu
 100 105 110
 Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
 115 120

<210> 994
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 994

Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala

Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
20 25 30

His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
35 40 45

Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
50 55 60

Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
65 70 75 80

Ser Leu Gly Leu Thr
85

<210> 995

<211> 88

<212> PRT

<213> Homo sapiens

<400> 995

Thr Val Ile Asn Tyr Arg Pro His Asn Met Arg Pro Glu Asp Arg Met
5 10 15

Phe His Ile Arg Ala Val Ile Leu Arg Ala Leu Ser Leu Ala Phe Leu
20 25 30

Leu Ser Leu Arg Gly Ala Gly Ala Ile Lys Ala Asp His Val Ser Thr
35 40 45

Tyr Ala Ala Phe Val Gln Thr His Arg Pro Thr Gly Glu Phe Met Phe
50 55 60

Glu Phe Asp Glu Asp Glu Met Phe Tyr Val Asp Leu Asp Lys Lys Glu
65 70 75 80

Thr Val Trp His Leu Glu Glu Phe
85

<210> 996

<211> 55

<212> PRT

<213> Homo sapiens

<400> 996

Val Ser Glu Glu Leu Gly Pro Ser Arg Arg Thr Met Cys Gln Leu Met
5 10 15

Pro Arg Leu Tyr Arg Arg Ile Asp Gln Gln Gly Ser Leu Cys Leu Asn
20 25 30

Leu Met Lys Met Arg Cys Ser Met Trp Ile Trp Thr Arg Arg Arg Pro
35 40 45

Ser Gly Ile Trp Arg Ser Leu
50 55

<210> 997
 <211> 83
 <212> PRT
 <213> Homo sapiens

<400> 997
 Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala Ala Gly
 5 10 15
 Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu His Ser
 20 25 30
 Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His Gly Ser
 35 40 45
 Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val Gly Leu
 50 55 60
 Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly Ser Leu
 65 70 75 80
 Gly Leu Thr

<210> 998
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 998
 Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Lys Ala Asp Tyr Tyr
 5 10 15
 Cys Gln Val Trp Asp Leu Asn Asn Asp His Val Val Phe Gly Gly Gly
 20 25 30
 Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
 35 40 45
 Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
 50 55 60
 Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
 65 70 75 80
 Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
 85 90 95
 Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu
 100 105 110
 Thr Pro Glu Gln Trp Lys Ser His Arg
 115 120

<210> 999
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 999

Lys Gln His Trp Trp Cys Leu Ser His Gly Leu Asp Arg Ser Pro Pro
 5 10 15

Arg Pro Pro Leu Ser Leu His Arg Leu Cys Asp Leu Leu Cys Val Asp
 20 25 30

Ser Asp Thr Leu Ser Val Ser Gly Pro Arg Lys Asp Gly Gln Asp Tyr
 35 40 45

Leu Trp Gly Lys Gln Tyr Trp Glu
 50 55

<210> 1000

<211> 96

<212> PRT

<213> Homo sapiens

<400> 1000

Ser Ser Thr Gly Gly Ala Ser Ala Met Ala Trp Thr Val Leu Leu Leu
 5 10 15

Gly Leu Leu Ser His Cys Thr Asp Ser Val Thr Ser Tyr Val Leu Thr
 20 25 30

Gln Thr Pro Ser Val Ser Val Ala Pro Gly Lys Thr Ala Lys Ile Thr
 35 40 45

Cys Gly Gly Asn Asn Ile Gly Ser Asn Asn Val His Trp Tyr Tyr Gln
 50 55 60

Lys Pro Gly Gln Ala Pro Val Leu Ile Ile Ser Phe Asp Asn Asp Arg
 65 70 75 80

Pro Ser Gly Ile Ser Glu Arg Phe Ser Gly Phe Asn Ser Gly Asp Met
 85 90 95

<210> 1001

<211> 81

<212> PRT

<213> Homo sapiens

<400> 1001

Leu Gly Leu Leu Ser His Cys Thr Asp Ser Val Thr Ser Tyr Val Leu
 5 10 15

Thr Gln Thr Pro Ser Val Ser Val Ala Pro Gly Lys Thr Ala Lys Ile
 20 25 30

Thr Cys Gly Gly Asn Asn Ile Gly Ser Asn Asn Val His Trp Tyr Tyr
 35 40 45

Gln Lys Pro Gly Arg Ala Pro Val Leu Ile Ile Ser Phe Asp Asn Asp
 50 55 60

Trp Pro Ser Gly Ile Ser Glu Arg Phe Ser Gly Phe Asn Ser Gly Asp
 65 70 75 80

Met

<210> 1002
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 1002
 Gln Ala Phe Ser Phe Glu Ala Gln Gly Gly Leu Ala Asn Ile Ala Ile
 5 10 15
 Leu Asn Asn Asn Leu Asn Thr Leu Ile Gln Arg Ser Asn His Thr Gln
 20 25 30
 Ala Thr Asn Asp Pro Pro Glu Val Thr Val Phe Pro Lys Glu Pro Val
 35 40 45
 Glu Leu Gly Gln Pro Asn Thr Leu Ile Cys His Ile Asp Lys Phe Phe
 50 55 60
 Pro Pro Val Leu Asn Val Thr Trp Leu Cys Asn Gly Glu Leu Val Thr
 65 70 75 80
 Glu Gly Val Ala Glu Ser Leu Phe Leu Pro Arg Thr Asp Tyr Ser Phe
 85 90 95
 His Lys Phe His Tyr Leu Thr Phe Val Pro Ser Ala Glu Asp Phe Tyr
 100 105 110
 Asp Cys Arg Val Glu His Trp Gly Leu Asp Gln Pro Leu Leu Lys His
 115 120 125
 Trp Glu Ala Gln Glu Pro Ile Gln Met Pro Glu Thr Thr Glu Thr Val
 130 135 140
 Leu Cys Ala Leu Gly Leu Val Leu Gly Leu Val Gly Ile Ile Val Gly
 145 150 155 160
 Thr Val Leu Ile Ile Lys Ser Leu Arg Ser
 165 170

<210> 1003
 <211> 61
 <212> PRT
 <213> Homo sapiens

<400> 1003
 Pro Cys Phe Pro Arg Ser Leu Trp Ser Trp Ala Ser Pro Thr Pro Ser
 5 10 15
 Ser Ala Thr Leu Thr Ser Ser Ser His Gln Cys Ser Thr Ser Arg Gly
 20 25 30
 Cys Ala Thr Gly Ser Trp Ser Leu Arg Val Ser Leu Arg Ala Ser Ser
 35 40 45
 Cys Pro Glu Gln Ile Thr Ala Ser Thr Ser Ser Ile Thr
 50 55 60

<210> 1004
 <211> 51
 <212> PRT

<213> Homo sapiens

<400> 1004

Pro Leu Cys Pro Gln Gln Arg Thr Ser Met Thr Ala Gly Trp Asn Thr
5 10 15
Gly Ala Trp Thr Ser Arg Ser Ser Ser Thr Gly Arg Pro Lys Ser Gln
20 25 30
Ser Arg Cys Leu Arg Gln Arg Arg Leu Cys Ser Val Pro Trp Ala Trp
35 40 45
Cys Trp Ala
50

<210> 1005

<211> 59

<212> PRT

<213> Homo sapiens

<400> 1005

Pro Glu Arg Arg Asp Phe Met Met Arg Thr Val Pro Thr Met Met Pro
5 10 15
Thr Arg Pro Ser Thr Arg Pro Arg Ala Gln Ser Thr Val Ser Val Val
20 25 30
Ser Gly Ile Trp Ile Gly Ser Trp Ala Ser Gln Cys Leu Arg Ser Gly
35 40 45
Trp Ser Lys Pro Gln Cys Ser Thr Leu Gln Ser
50 55

<210> 1006

<211> 61

<212> PRT

<213> Homo sapiens

<400> 1006

Ser Val Leu Gly Arg Lys Arg Leu Ser Ala Thr Pro Ser Val Thr Ser
5 10 15
Ser Pro Leu His Ser His Val Thr Leu Ser Thr Gly Gly Lys Asn Leu
20 25 30
Ser Met Trp Gln Met Arg Val Leu Gly Trp Pro Ser Ser Thr Gly Ser
35 40 45
Leu Gly Asn Thr Val Thr Ser Gly Gly Ser Leu Val Ala
50 55 60

<210> 1007

<211> 106

<212> PRT

<213> Homo sapiens

<400> 1007

Gly His Lys Gly Gln Val Met Glu Leu Val Glu Ala Val Ile Cys Ser
5 10 15

Gly	Gln	Glu	Glu	Ala	Leu	Ser	Asp	Thr	Leu	Ser	Asp	Gln	Leu	Pro	Val
			20					25					30		
Ala	Gln	Pro	Arg	Asp	Val	Glu	His	Trp	Trp	Glu	Glu	Leu	Val	Asn	Val
		35					40					45			
Ala	Asp	Glu	Gly	Val	Gly	Leu	Ala	Gln	Leu	His	Arg	Leu	Leu	Gly	Lys
	50					55					60				
His	Gly	His	Leu	Arg	Gly	Ile	Val	Gly	Gly	Leu	Ser	Val	Val	Gly	Thr
65					70					75					80
Leu	Asp	Gln	Gly	Ile	Gln	Val	Val	Val	Gln	Tyr	Ser	Asn	Val	Ser	Gln
				85					90					95	
Pro	Ala	Leu	Ser	Leu	Lys	Gly	Lys	Gly	Leu						
			100					105							

```
<210> 1008
<211> 59
<212> PRT
<213> Homo sapiens
```

```

<400> 1008
Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala Ala Gly
          5                      10                      15

Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu His Ser
          20                      25                      30

Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His Gly Ser
          35                      40                      45

Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys
          50                      55

```

```
<210> 1009
<211> 59
<212> PRT
<213> Homo. sapiens
```

```

<400> 1009
Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val
      5                                10                                15

Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr
      20                                25                                30

Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu
      35                                40                                45

Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg
      50                                55

```

```
<210> 1010
<211> 85
<212> PRT
<213> Homo sapiens
```

<400> 1010

Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
 5 10 15
 Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30
 His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45
 Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
 50 55 60
 Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
 65 70 75 80
 Ser Leu Gly Leu Thr
 85

<210> 1011
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 1011
 Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
 5 10 15
 Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly
 20 25 30
 Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
 35 40 45
 Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
 50 55 60
 Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
 65 70 75 80
 Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
 85 90 95
 Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu
 100 105 110
 Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
 115 120

<210> 1012
 <211> 83
 <212> PRT
 <213> Homo sapiens

<400> 1012
 Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala Ala Gly
 5 10 15
 Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu His Ser
 20 25 30
 Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His Gly Ser

Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly Ser Leu
65 70 75 80

Gly Leu Thr

```
<210> 1013
<211> 83
<212> PRT
<213> Homo sapiens
```

<400> 1013
Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
5 10 15

Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
20 25 30

Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
35 40 45

Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
50 55 60

Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
65 70 75 80

Ser His Arg

```
<210> 1014
<211> 55
<212> PRT
<213> Homo sapiens
```

<400> 1014
Pro Arg Met Met Lys Thr Val Pro Thr Thr Met Pro Thr Arg Pro Thr
 5 10 15

Asp Asn Pro Arg Ala Gln Thr Thr Val Ser Val Ser Ser Asp Ile Gly
20 25 30

Ala Gly Ile Ser Gly Ser Gln Cys Phe Arg Arg Gly Leu Ser Ser Pro
35 40 45

Gln Cys Ser Thr Leu Gln' Ser
50 55

```
<210> 1015
<211> 50
<212> PRT
<213> Homo sapiens
```

<220>
<221> variant

<223> Xaa = Any amino acid

Pro Ser Val Thr Gly Asp Leu Glu Asn Thr Val Thr Ser Gly Thr Ser
5 10 15

Leu Val Ala Ala Val Glu Leu Glu Arg Leu Ile Arg Leu Phe Lys Leu
20 25 30

Cys Phe Xaa Thr Ala Met Phe Val Ser Ala Asn Cys Gly Ser Asn Leu
35 40 45

Asn Cys

<211> 59

<213> Homo sapiens

<221> variant

<223> Xaa = Any amino acid

His Arg Gly Trp Asn Leu Arg Leu Pro Val Phe Gln Lys Arg Leu Val
5 10 15

Gln Ser Pro Val Leu His Leu Ala Val Ile Thr Leu Leu Ser Arg Arg
20 25 30

Glu Glu Gly Glu Val Thr Asp Leu Glu Glu Gly Met Ile Thr Leu Gly
35 40 45

Glu Glu Ala Gly Leu Xaa Asn Thr Phe Cys Asp
50 55

<211> 76

<213> Homo sapiens

<221> variant

<223> Xaa = Any amino acid

Val Pro Ile Ala Xaa Pro Cys Asp Val Asp His Arg Arg Lys Asp Val
5 10 15

Val His Lys Thr Asp Glu Asp Val Gly Leu Thr Gln Cys His Gly Arg
20 25 30

Leu Gly Lys His Cys Asp Leu Arg Asn Leu Ile Gly Ser Ser Gly Arg
35 40 45

Val Gly Ala Phe Asn Gln Thr Val Gln Val Met Phe Xaa Asp Ser Asp
50 55 60

Val Cys Gln Cys Lys Leu Arg Val Lys Ser Lys Leu
 65 70 75

<210> 1018
 <211> 52
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(52)
 <223> Xaa = Any amino acid

<400> 1018
 Ala Met Gly Thr Gln Ser Gln Lys Val Phe Xaa Arg Pro Ala Ser Ser
 5 10 15
 Pro Arg Val Ile Ile Pro Ser Ser Arg Ser Val Thr Ser Pro Ser Ser
 20 25 30
 Leu Leu Leu Arg Arg Val Met Thr Ala Arg Trp Ser Thr Gly Asp Trp
 35 40 45
 Thr Ser Leu Phe
 50

<210> 1019
 <211> 165
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(165)
 <223> Xaa = Any amino acid

<400> 1019
 Gln Phe Arg Phe Asp Pro Gln Phe Ala Leu Thr Asn Ile Ala Val Xaa
 5 10 15
 Lys His Asn Leu Asn Ser Leu Ile Lys Arg Ser Asn Ser Thr Ala Ala
 20 25 30
 Thr Asn Glu Val Pro Glu Val Thr Val Phe Ser Lys Ser Pro Val Thr
 35 40 45
 Leu Gly Gln Pro Asn Ile Leu Ile Cys Leu Val Asp Asn Ile Phe Pro
 50 55 60
 Pro Val Val Asn Ile Thr Trp Xaa Ser Asn Gly His Ser Val Thr Glu
 65 70 75 80
 Gly Val Xaa Glu Thr Ser Phe Leu Ser Lys Ser Asp His Ser Phe Phe
 85 90 95
 Lys Ile Ser Tyr Leu Thr Leu Leu Pro Ser Ala Glu Glu Ser Tyr Asp
 100 105 110
 Cys Lys Val Glu His Trp Gly Leu Asp Lys Pro Leu Leu Lys His Trp
 115 120 125

Glu Pro Glu Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr Val Val
 130 135 140
 Cys Ala Leu Gly Leu Ser Val Gly Leu Val Gly Ile Val Val Gly Thr
 145 150 155 160
 Val Phe Ile Ile Arg
 165

<210> 1020
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 1020
 Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
 5 10 15
 Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30
 His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45
 Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
 50 55 60
 Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
 65 70 75 80
 Ser Leu Gly Leu Thr
 85

<210> 1021
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 1021
 Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
 5 10 15
 Cys Gln Val Trp Asp His Asn Asn Asp His Val Val Phe Gly Gly Gly
 20 25 30
 Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
 35 40 45
 Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
 50 55 60
 Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
 65 70 75 80
 Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
 85 90 95
 Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu
 100 105 110

325

Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
 115 120

<210> 1022
 <211> 50
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(50)
 <223> Xaa = Any amino acid

<400> 1022
 Leu Leu Ala Ala Tyr Leu Leu Leu Cys Leu Glu Gly Val Xaa Val
 5 10 15

Ser Thr Pro Ala Leu Thr Gly Leu Leu Ser Ala Phe Gln Ala Thr Val
 20 25 30

Xaa Ala Pro Gly Xaa Lys Ser Leu Xaa Arg His Thr Xaa Val Ala Leu
 35 40 45

Xaa Ala
 50

<210> 1023
 <211> 80
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(80)
 <223> Xaa = Any amino acid

<400> 1023
 Val Ala Ser Xaa Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
 5 10 15

Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Xaa Gly Leu
 20 25 30

His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45

Xaa Ser Arg Val Xaa Val Thr Xaa Glu Thr His Xaa Cys Gly Leu Xaa
 50 55 60

Gly Leu Xaa Leu Leu Ile Gly Gly Arg Glu Gln Xaa Asp Arg Gly Gly
 65 70 75 80

<210> 1024
 <211> 80
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(80)

<223> Xaa = Any amino acid

<400> 1024

Ala Pro Ser Val Xaa Leu Phe Pro Pro Ser Tyr Glu Glu Xaa Gln Ala
5 10 15
Xaa Lys Ala Thr Xaa Val Cys Leu Xaa Ser Asp Xaa Tyr Pro Gly Xaa
20 25 30
Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val
35 40 45
Glu Thr Xaa Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser
50 55 60
Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser Xaa Arg Ser Tyr
65 70 75 80

<210> 1025

<211> 101

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(101)

<223> Xaa = Any amino acid

<400> 1025

Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
5 10 15
Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly
20 25 30
Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
35 40 45
Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
50 55 60
Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
65 70 75 80
Lys Ala Asp Ser Xaa Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
85 90 95
Ser Lys Gln Xaa Asn
100

<210> 1026

<211> 63

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(63)

<223> Xaa = Any amino acid

<400> 1026

Val Xaa Leu Phe Gly Gly Cys Gly Gly Leu His Ser Arg Leu Asp Gly
 5 10 15
 Xaa Ala Ile Cys Leu Pro Gly His Cys His Gly Ser Arg Val Glu Val
 20 25 30
 Thr Tyr Glu Thr His Gln Cys Gly Leu Val Gly Leu Lys Leu Leu Arg
 35 40 45
 Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly Ser Leu Gly Leu Thr
 50 55 60

<210> 1027
 <211> 75
 <212> PRT
 <213> Homo sapiens

<400> 1027
 Gly Cys Leu Ser Gln His Ile Gly Gly His Arg Val Thr Phe Ser Trp
 5 10 15
 Gln Val Gln Ser Leu Arg Phe Ser Gln Val Leu Glu His Ser Leu Gly
 20 25 30
 Gly Ile Gln Pro His Gln Pro Pro Thr Leu His Gln Gly His Glu His
 35 40 45
 Pro Ala His His Arg Lys Gly Pro Pro Glu Leu Arg Ile Lys Asp Thr
 50 55 60
 Leu Asp Pro Glu Ala Leu Gly Trp Ala Gly Trp
 65 70 75

<210> 1028
 <211> 77
 <212> PRT
 <213> Homo sapiens

<400> 1028
 Glu Val Thr Glu Leu Leu Ser Leu Gly Arg Cys Ser Pro Ser Gly Ser
 5 10 15
 His Lys Ser Leu Ser Thr Val Trp Gly Glu Phe Ser Pro Thr Ser Leu
 20 25 30
 Pro Pro Cys Thr Arg Val Met Ser Ile Leu Pro Thr Thr Gly Arg Ala
 35 40 45
 Leu Leu Ser Ser Glu Leu Arg Thr Arg Trp Thr Gln Lys Pro Trp Ala
 50 55 60
 Gly Gln Val Gly Glu Thr Leu Gly Gly Ser Pro Val Gln
 65 70 75

<210> 1029
 <211> 82
 <212> PRT
 <213> Homo sapiens

<400> 1029

Gly Ser Ser Thr Gly Gly Ala Ser Ala Met Ala Trp Thr Val Leu Leu
 5 10 15
 Leu Gly Leu Leu Ser His Cys Thr Gly Asp Pro Pro Arg Val Ser Pro
 20 25 30
 Thr Cys Pro Ala Gln Gly Phe Trp Val Gln Arg Val Leu Asn Ser Glu
 35 40 45
 Leu Arg Arg Ala Leu Pro Val Val Gly Arg Met Leu Met Thr Leu Val
 50 55 60
 Gln Gly Gly Arg Leu Val Gly Leu Asn Ser Pro Gln Thr Val Leu Lys
 65 70 75 80
 Asp Leu

<210> 1030
 <211> 84
 <212> PRT
 <213> Homo sapiens

<400> 1030
 Glu Pro Glu Gly Leu His Leu Pro Arg Glu Ser Asn Ser Val Thr Ser
 5 10 15
 Tyr Val Leu Thr Gln Thr Pro Ser Val Ser Val Ala Pro Gly Lys Thr
 20 25 30
 Ala Lys Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Asn Asn Val His
 35 40 45
 Trp Tyr Tyr Gln Lys Pro Gly Gln Ala Pro Val Leu Ile Ile Ser Phe
 50 55 60
 Asp Asn Asp Arg Pro Ser Gly Ile Ser Glu Arg Phe Ser Gly Phe Asn
 65 70 75 80
 Ser Gly Asp Met

<210> 1031
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 1031
 Glu Ala Ala Leu Val Val Pro Gln Pro Trp Pro Gly Pro Phe Ser Ser
 5 10 15
 Ser Ala Ser Ser Leu Thr Ala Gln Val Ile Pro Pro Gly Ser His Gln
 20 25 30
 Pro Ala Gln Pro Lys Ala Ser Gly Ser Ser Val Ser Leu Ile Leu Ser
 35 40 45
 Ser Gly Gly Pro Phe Leu Trp Trp Ala Gly Cys Ser
 50 55 60

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<210> 1032
<211> 71
<212> PRT
<213> Homo sapiens

<400> 1032
Gly Glu Val Ser Arg Ser Ala Ala Arg Gly Gly Cys Pro Glu Pro Gln
          5                      10                      15

Gly Trp Ser Trp Gly Leu Ser Val Leu Pro Gln Ala Phe Gln Val Gln
          20                      25                      30

Lys Ala Leu Trp Gly Leu Gly Leu Cys Gln Gly Lys Glu Ser Cys Leu
          35                      40                      45

Gly Gly Gly Arg Glu Val Arg Glu Val Thr His Val Ala Leu Glu Pro
          50                      55                      60

Ala Lys Ser Asn Val Ser Met
          65                      70

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<210> 1033
<211> 77
<212> PRT
<213> Homo sapiens

<400> 1033
Cys Pro Lys Arg Ala Ser Pro Gly Ala Leu Gly Leu Gly Leu Arg Glu
          5                      10                      15
Glu Arg Ser Val Gly Gln Arg Pro Gly Val Ala Ala Leu Ser Pro Arg
          20                      25                      30
Ala Gly Pro Gly Val Cys Gln Ser Phe Pro Arg Leu Ser Arg Ser Arg
          35                      40                      45
Arg Leu Cys Gly Val Trp Gly Cys Val Arg Val Arg Lys Ala Ala Leu
          50                      55                      60
Val Glu Glu Glu Lys Ser Glu Arg Ser His Met Trp Pro
          65                      70                      75
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<210> 1034
<211> 54
<212> PRT
<213> Homo sapiens
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<220>  
<221> variant  
<222> (1)...(54)  
<223> Xaa = Any amino acid
```

```

<400> 1034
Pro Glu Ser Ser Arg Tyr Pro Ser Leu Leu Ala Ser Gly Ser Gly Ser
      5              10              15

Arg Gly Gly Gly Ser Ser Gln Ser Xaa Val Ser Ser Met Pro Trp Gly
      20              25              30

Leu Cys Arg Thr Gly Arg Leu Glu Glu Pro Leu Cys Leu Asp Arg Phe
      35              40              45

```


Cys Arg Leu Pro His Leu
50

<210> 1035
<211> 50
<212> PRT
<213> Homo sapiens

<400> 1035
Leu Leu Phe Leu His Gln Gly Ser Phe Pro Tyr Pro Asp Thr Ala Pro
5 10 15

Asp Pro Thr Lys Pro Ser Gly Pro Gly Lys Pro Gly Glu Gly Leu Thr
20 25 30

Asp Pro Arg Thr Ser Pro Gly Ala Gln Gly Ser His Pro Gly Pro Leu
35 40 45

Thr Asp
50

<210> 1036
<211> 69
<212> PRT
<213> Homo sapiens

<400> 1036
Leu Glu Pro Pro Pro Arg Leu Pro Leu Pro Glu Ala Arg Arg Glu Gly
5 10 15

Tyr Leu Glu Asp Ser Gly His Leu Leu Leu Ala Gln Gly Leu Lys Asp
20 25 30

Ala Gly Pro Pro Asn Leu Thr Leu Arg Leu Pro Ala Thr Phe Ser Pro
35 40 45

Gly Phe Cys Arg Leu Ala Ser Leu Pro Leu Leu Ser His Ala Asp Val
50 55 60

Gly Leu Ser Arg Phe
65

<210> 1037
<211> 61
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(61)
<223> Xaa = Any amino acid

<400> 1037
Ser Gly Gly Ala Cys Arg Thr Cys Pro Gly Thr Val Ala Pro Gln Ala
5 10 15

Cys Leu Ser Cys Arg Val Pro Met Ala Trp Ser Leu His Xaa Thr Asp
20 25 30

Trp Ser Pro Leu Pro Asp Ser His Phe Gln Lys Leu Gly Gly Arg Asp
 35 40 45

Thr Trp Lys Thr Pro Val Thr Ser Phe Leu Leu Arg Ala
 50 55 60

<210> 1038
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 1038
 Lys Met Leu Val Leu Pro Thr Ser Leu Ser Asp Ser Leu Pro Pro Phe
 5 10 15

Pro Leu Gly Ser Ala Val Leu Pro His Phe Pro Ser Cys His Met Leu
 20 25 30

Thr Leu Asp Leu Ala Gly Ser Lys Ala Thr Cys Val Thr Ser Leu Thr
 35 40 45

Ser Leu Pro Pro Pro Arg Gln Leu Ser Leu Pro
 50 55

<210> 1039
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 1039
 His Ser Pro Arg Pro His Lys Ala Phe Trp Thr Trp Lys Ala Trp Gly
 5 10 15

Arg Thr Asp Arg Pro Gln Asp Gln Pro Trp Gly Ser Gly Gln Pro Pro
 20 25 30

Arg Ala Ala Asp Arg Leu Thr Ser Pro His Gly Gly Pro Ala Pro Lys
 35 40 45

Pro Gln Gly Trp Pro Val Trp Asp
 50 55

<210> 1040
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 1040
 Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
 5 10 15

Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30

His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45

Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
 50 55 60

Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
 65 70 75 80

Ser Leu Gly Leu Thr
 85

<210> 1041

<211> 123

<212> PRT

<213> Homo sapiens

<400> 1041

Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
 5 10 15

Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly
 20 25 30

Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
 35 40 45

Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
 50 55 60

Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
 65 70 75 80

Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
 85 90 95

Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu
 100 105 110

Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
 115 120

<210> 1042

<211> 96

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(96)

<223> Xaa = Any amino acid

<400> 1042

Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
 5 10 15

Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30

His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45

Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
 50 55 60

Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
 65 70 75 80

Ser Leu Gly Leu Thr Xaa Asp Gly Gln Phe Xaa Pro Ser Ala Glu Asp
 85 90 95

<210> 1043
 <211> 96
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(96)
 <223> Xaa = Any amino acid

<400> 1043
 Val Phe Gly Gly Gly Xaa Lys Leu Ala Val Xaa Gly Gln Pro Lys Ala
 5 10 15

Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala
 20 25 30

Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala
 35 40 45

Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val
 50 55 60

Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser
 65 70 75 80

Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
 85 90 95

<210> 1044
 <211> 85
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(85)
 <223> Xaa = Any amino acid

<400> 1044
 Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
 5 10 15

Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30

His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45

Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Xaa Cys Gly Leu Val
 50 55 60

Gly Leu Lys Leu Leu Xaa Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
 65 70 75 80

Ser Leu Gly Leu Thr
 85

```

<400> 1046
Ser Gly His Ser Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu
      5                                10                                15

Leu Leu Leu Trp Leu Pro Gly Ala Lys Cys Asp Ile Gln Met Thr Gln
      20                                25                                30

Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Thr Val Thr Ile Ser
      35                                40                                45

Cys Arg Ala Ser Gln Asn Ile Asp Arg Trp Leu Ala Trp His Gln Gln
      50                                55                                60

Lys Pro Gly Lys Ala Pro Asn Val Leu Ile Tyr Ala Thr Ser Ser Leu
      65                                70                                75                                80

Glu Glu Gly Val Ser Leu Arg Phe Thr Gly Ser Gly Ser Gly Thr Gln
      85                                90                                95

Phe Asn Leu Thr Ile Thr Ser Leu Gln Pro Asp Asp Ser Ala Thr Tyr
      100                                105                                110

Tyr Cys Gln His Tyr Ser Ala Ser Leu Arg Ser Phe
      115                                120

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<210> 1047
<211> 71
<212> PRT
<213> Homo sapiens

<400> 1047
Asp Ile Arg Gly Phe Ala Trp Phe Leu Leu Met Pro Gly Gln Pro Pro
 5 10 15
Ile Tyr Ile Leu Arg Gly Pro Thr Ala Tyr Cys Asn Cys Ile Ser Asp
 20 25 30
Arg Cys Arg Gln Gly Gly Arg Arg Leu Gly His Leu Asp Val Thr Phe
 35 40 45
Gly Thr Trp Glu Pro Glu Gln Gln Glu Pro Gln Glu Leu Ser Gly Asp
 50 55 60
Pro His Val His Ala Val Ser
 65 70

<210> 1048
<211> 95
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(95)
<223> Xaa = Any amino acid

<400> 1048
Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
 5 10 15
Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly
 20 25 30
Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
 35 40 45
Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
 50 55 60
Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
 65 70 75 80
Lys Ala Xaa Ser Xaa Pro Xaa Lys Ala Gly Val Glu Thr Thr Thr
 85 90 95

<210> 1049
<211> 57
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(57)
<223> Xaa = Any amino acid

<400> 1049

Cys Gly Gly Leu His Ser Arg Leu Xaa Gly Xaa Ala Xaa Cys Leu Pro
5 10 15

Gly His Cys His Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln
20 25 30

Cys Gly Leu Val Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser
35 40 45

Asp Arg Gly Gly Ser Leu Gly Leu Thr
50 55

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<210> 1050
<211> 98
<212> PRT
<213> Homo sapiens
```

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<400> 1050
Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
      5                      10                      15

Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly
      20                      25                      30

Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
      35                      40                      45

Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
      50                      55                      60

Ala Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
      65                      70                      75                      80

Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
      85                      90                      95

Ser Lys

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```
<210> 1051
<211> 60
<212> PRT
<213> Homo sapiens
```

```

<400> 1051
Phe Gly Gly Cys Gly Gly Leu His Ser Arg Leu Asp Gly Ala Ala Ile
          5                      10                      15

Cys Leu Pro Gly His Cys His Gly Ser Arg Val Glu Val Thr Tyr Glu
          20                      25                      30

Thr Arg Gln Cys Gly Leu Val Gly Leu Lys Leu Leu Arg Gly Gly Arg
          35                      40                      45

Glu Gln Ser Asp Arg Gly Gly Ser Leu Gly Leu Thr
          50                      55                      60

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<210> 1052
<211> 60
<212> PRT
```

<213> Homo sapiens

<400> 1052

Ser Trp Pro Ser Phe Leu Gly Pro Leu Thr Leu Arg Val Ser Glu Ser
 5 10 15

Thr His Arg Arg Ser Gln Thr Leu Cys Ser Glu Arg Gly Gly Arg Gly
 20 25 30

Gly Glu Arg Ser Arg Pro Trp Leu Arg His His Gln Cys Cys Phe Leu
 35 40 45

Arg Gln Ser Tyr Pro Cys Leu Lys Trp Tyr Leu Leu
 50 55 60

<210> 1053

<211> 80

<212> PRT

<213> Homo sapiens

<400> 1053

Leu Cys Leu Arg Lys Gln His Trp Trp Cys Leu Ser His Gly Leu Asp
 5 10 15

Arg Ser Pro Pro Arg Pro Pro Leu Ser Leu His Arg Val Cys Asp Leu
 20 25 30

Leu Cys Val Asp Ser Asp Thr Leu Ser Val Ser Gly Pro Arg Lys Asp
 35 40 45

Gly Gln Asp Tyr Leu Trp Gly Lys Gln Tyr Trp Glu Leu Gln Cys Thr
 50 55 60

Leu Val Leu Pro Lys Ala Arg Pro Gly Pro Cys Pro Asn His Leu Phe
 65 70 75 80

<210> 1054

<211> 97

<212> PRT

<213> Homo sapiens

<400> 1054

Gly Ser Ser Thr Gly Gly Ala Ser Ala Met Ala Trp Thr Val Leu Leu
 5 10 15

Leu Gly Leu Leu Ser His Cys Thr Glu Ser Val Thr Ser Tyr Val Leu
 20 25 30

Thr Gln Thr Pro Ser Val Ser Val Ala Pro Gly Lys Thr Ala Lys Ile
 35 40 45

Thr Cys Gly Gly Asn Asn Ile Gly Ser Tyr Ser Val His Trp Tyr Tyr
 50 55 60

Gln Lys Pro Gly Gln Ala Pro Val Leu Ile Ile Ser Phe Asp Asn Asp
 65 70 75 80

Arg Pro Ser Gly Ile Ser Glu Arg Phe Ser Gly Phe Asn Ser Gly Asp
 85 90 95

Met

<210> 1055
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 1055
 Gly Ser Ser Thr Gly Gly Ala Ser Ala Met Ala Trp Thr Val Leu Leu
 5 10 15
 Leu Gly Leu Leu Ser His Cys Thr Asp Ser Val Thr Ser Tyr Val Leu
 20 25 30
 Thr Gln Thr Pro Ser Val Ser Val Ala Pro Gly Lys Thr Ala Lys Ile
 35 40 45
 Thr Cys Gly Gly Asn Asn Ile Gly Ser Asn Asn Val His Trp Tyr Tyr
 50 55 60
 Gln Lys Pro Gly Gln Ala Pro Val Leu Ile Ile Ser Phe Asp Asn Asp
 65 70 75 80
 Arg Pro Ser Gly Ile Ser Glu Arg Phe Ser Gly Phe Asn Ser Gly Asp
 85 90 95
 Met

<210> 1056
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 1056
 Lys Gln His Trp Trp Cys Leu Ser His Gly Leu Asp Arg Ser Pro Pro
 5 10 15
 Arg Pro Pro Leu Ser Leu His Arg Leu Cys Asp Leu Leu Cys Val Asp
 20 25 30
 Ser Asp Thr Leu Ser Val Ser Gly Pro Arg Lys Asp Gly Gln Asp Tyr
 35 40 45
 Leu Trp Gly Lys Gln Tyr Trp Glu
 50 55

<210> 1057
 <211> 64
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(64)
 <223> Xaa = Any amino acid

<400> 1057
 Glu Pro Xaa Pro Leu Arg Pro Ile Glu Glu Met Thr Leu Arg Arg Arg
 5 10 15

Val Leu Gln Glu Thr Trp Xaa Gly Val Pro Ser Gln Ser Gln Trp Gly
 20 25 30
 Ala Xaa His His Xaa Cys His Xaa Gln Asn Xaa His Ala Gly Thr Ser
 35 40 45
 Arg Glu Pro Xaa Thr His His Ala Gly Xaa Gln Asp Arg Thr Arg Gly
 50 55 60

<210> 1058
 <211> 53
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(53)
 <223> Xaa = Any amino acid

<400> 1058
 His Ser Asp Val Glu Tyr Ser Lys Lys Arg Xaa Leu Val Ser Pro Ala
 5 10 15
 Lys Ala Ser Gly Glu Leu Xaa Thr Ile Xaa Val Thr Xaa Arg Thr Xaa
 20 25 30
 Met Gln Glu Pro Pro Gly Ser Xaa Arg His Thr Met Leu Xaa Asn Arg
 35 40 45

Thr Gly Pro Gly Ala
 50

<210> 1059
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(51)
 <223> Xaa = Any amino acid

<400> 1059
 Gly Pro Trp Ser Cys Pro Val Xaa Gln His Gly Val Ser Xaa Ala Pro
 5 10 15
 Trp Arg Phe Leu His Xaa Ser Ser Xaa Ser Asp Xaa Asp Gly Xaa Glu
 20 25 30
 Leu Pro Thr Gly Phe Gly Trp Gly His Gln Xaa Thr Phe Leu Gly Val
 35 40 45

Leu Tyr Val
 50

<210> 1060
 <211> 64
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(64)
 <223> Xaa = Any amino acid

<400> 1060
 Ala Pro Gly Pro Val Leu Xaa Ser Ser Met Val Cys Xaa Arg Leu Pro
 5 10 15
 Gly Gly Ser Cys Met Xaa Val Leu Xaa Val Thr Xaa Met Val Xaa Ser
 20 25 30
 Ser Pro Leu Ala Leu Ala Gly Asp Thr Xaa Pro Arg Phe Leu Glu Tyr
 35 40 45
 Ser Thr Ser Glu Cys His Phe Phe Asn Gly Thr Glu Arg Xaa Arg Phe
 50 55 60

<210> 1061
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 1061
 Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
 5 10 15
 Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30
 His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45
 Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
 50 55 60
 Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
 65 70 75 80
 Ser Leu Gly Leu Thr
 85

<210> 1062
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(123)
 <223> Xaa = Any amino acid

<400> 1062
 Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Xaa Glu Ala Asp Tyr Tyr
 5 10 15
 Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly
 20 25 30
 Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr

35	40	45
Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu		
50	55	60
Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp		
65	70	75
Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro		
85	90	95
Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu		
100	105	110
Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr		
115	120	

<210> 1063
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 1063
Pro Cys Leu Arg Ser Lys Val Thr Arg Lys Arg Pro Cys Leu Pro Ser
5 10 15
Met Thr Leu Met Glu Glu Met Leu Arg Glu Ala Phe Arg Cys Met Thr
20 25 30
Gln Gly Lys Thr Ala Lys Asn Leu Val Leu Ala Leu Leu Ile Leu Leu
35 40 45
Phe Val Ser Phe Leu Gly Val Leu Arg Ala Lys
50 55

<210> 1064
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 1064
Glu Gln Asn Asp Asn Thr Gln Lys Phe Ser Lys Trp Asp Phe Pro Gly
5 10 15
Arg Ala Asn Glu Arg Pro Tyr Cys Tyr Ala Ile Trp Ser Lys Thr Thr
20 25 30
Leu Gln Glu Asp Val Phe Thr Gly Gly Pro His Ala Lys Leu Leu His
35 40 45
Glu Gly Ile
50

<210> 1065
 <211> 120
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant

<222> (1)...(120)

<223> Xaa = Any amino acid

<400> 1065

```

Asp Cys Gln Lys Ser Cys Ser Cys Ser Pro His Phe Val Ile Cys Phe
      5                                10                        15

Ile Phe Arg Ser Phe Glu Ser Lys Met Thr Thr Pro Arg Asn Ser Val
      20                                25                        30

Asn Gly Thr Phe Pro Ala Glu Pro Met Lys Gly Pro Ile Ala Met Gln
      35                                40                        45

Ser Gly Pro Lys Pro Leu Phe Arg Arg Met Ser Ser Leu Val Gly Pro
      50                                55                        60

Thr Gln Ser Phe Phe Met Arg Glu Ser Lys Thr Leu Gly Ala Val Gln
      65                                70                        75                        80

Ile Met Asn Gly Leu Phe His Ile Ala Leu Gly Gly Leu Leu Met Ile
      85                                90                        95

Pro Ala Gly Ile Tyr Ala Pro Ile Cys Val Thr Val Trp Tyr Pro Leu
      100                               105                       110

Trp Gly Xaa Xaa Gly Ser Ile Lys
      115                               120

```

<210> 1066

<211> 89

<212> PRT

<213> Homo sapiens

<400> 1066

```

Ile Pro Ala Gly Ile Ile Arg Arg Pro Pro Arg Ala Met Trp Lys Ser
      5                                10                        15

Pro Phe Ile Ile Trp Thr Ala Pro Lys Val Leu Asp Ser Leu Met Lys
      20                                25                        30

Lys Leu Cys Val Gly Pro Thr Ser Glu Asp Ile Leu Leu Lys Ser Gly
      35                                40                        45

Phe Gly Pro Asp Cys Ile Ala Ile Gly Pro Phe Ile Gly Ser Ala Gly
      50                                55                        60

Lys Val Pro Phe Thr Glu Phe Leu Gly Val Val Ile Leu Leu Ser Lys
      65                                70                        75                        80

Leu Leu Lys Met Lys Gln Ile Thr Lys
      85

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<210> 1067

<211> 60

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(60)

<223> Xaa = Any amino acid

<400> 1067

Leu Tyr Ala Ser Xaa Xaa Ser Pro Glu Arg Val Pro His Ser His Thr
 5 10 15

Asp Gly Cys Ile Asp Pro Cys Trp Asp His Gln Lys Thr Pro Gln Gly
 20 25 30

Asn Val Glu Glu Pro Ile His Asn Leu Asp Ser Pro Gln Ser Leu Arg
 35 40 45

Phe Pro His Glu Glu Ala Leu Arg Gly Ala His Gln
 50 55 60

<210> 1068

<211> 64

<212> PRT

<213> Homo sapiens

<400> 1068

Ile Ser Gly Cys Cys His Phe Ala Leu Lys Thr Pro Lys Asn Glu Thr
 5 10 15

Asn Asn Lys Met Arg Arg Ala Arg Thr Arg Phe Leu Ala Val Leu Pro
 20 25 30

Cys Val Met His Leu Asn Ala Ser Leu Ser Ile Ser Ser Met Ser Val
 35 40 45

Ile Glu Gly Arg His Gly Leu Phe Arg Val Thr Leu Asp Leu Arg Gln
 50 55 60

<210> 1069

<211> 59

<212> PRT

<213> Homo sapiens

<400> 1069

Pro Cys Leu Arg Ser Lys Val Thr Arg Lys Arg Pro Cys Leu Pro Ser
 5 10 15

Met Thr Leu Met Glu Glu Met Leu Arg Glu Ala Phe Arg Cys Met Thr
 20 25 30

Gln Gly Lys Thr Ala Lys Asn Leu Val Leu Ala Leu Leu Ile Leu Leu
 35 40 45

Phe Val Leu Phe Leu Gly Val Leu Arg Ala Lys
 50 55

<210> 1070

<211> 51

<212> PRT

<213> Homo sapiens

<400> 1070

Glu Gln Asn Asp Asn Thr Gln Lys Phe Ser Lys Trp Asp Phe Pro Gly
 5 10 15

Arg Ala Asn Glu Arg Pro Tyr Cys Tyr Ala Ile Trp Ser Lys Thr Thr

20 25 30
 Leu Gln Glu Asp Val Phe Thr Gly Gly Pro His Ala Lys Leu Leu His
 35 40 45

Glu Gly Ile
 50

<210> 1071
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 1071
 Asp Cys Gln Lys Ser Cys Ser Cys Ser Pro His Phe Val Ile Cys Phe
 5 10 15

Ile Phe Arg Ser Phe Glu Ser Lys Met Thr Thr Pro Arg Asn Ser Val
 20 25 30

Asn Gly Thr Phe Pro Ala Glu Pro Met Lys Gly Pro Ile Ala Met Gln
 35 40 45

Ser Gly Pro Lys Pro Leu Phe Arg Arg Met Ser Ser Leu Val Gly Pro
 50 55 60

Thr Gln Ser Phe Phe Met Arg Glu Ser Lys Thr Leu Gly Ala Val Gln
 65 70 75 80

Ile Met Asn Gly Leu Phe His Ile Ala Leu Gly Gly Leu Leu Met Ile
 85 90 95

Pro Ala Gly Ile Tyr Ala Pro Ile Cys Val Thr Val
 100 105

<210> 1072
 <211> 64
 <212> PRT
 <213> Homo sapiens

<400> 1072
 Ile Ser Gly Cys Cys His Phe Ala Leu Lys Thr Pro Lys Asn Lys Thr
 5 10 15

Asn Asn Lys Met Arg Arg Ala Arg Thr Arg Phe Leu Ala Val Leu Pro
 20 25 30

Cys Val Met His Leu Asn Ala Ser Leu Ser Ile Ser Ser Met Ser Val
 35 40 45

Ile Glu Gly Arg His Gly Leu Phe Arg Val Thr Leu Asp Leu Arg Gln
 50 55 60

<210> 1073
 <211> 89
 <212> PRT
 <213> Homo sapiens

<400> 1073
 Ile Pro Ala Gly Ile Ile Arg Arg Pro Pro Arg Ala Met Trp Lys Ser

5 10 15
 Pro Phe Ile Ile Trp Thr Ala Pro Lys Val Leu Asp Ser Leu Met Lys
 20 25 30
 Lys Leu Cys Val Gly Pro Thr Ser Glu Asp Ile Leu Leu Lys Ser Gly
 35 40 45
 Phe Gly Pro Asp Cys Ile Ala Ile Gly Pro Phe Ile Gly Ser Ala Gly
 50 55 60
 Lys Val Pro Phe Thr Glu Phe Leu Gly Val Val Ile Leu Leu Ser Lys
 65 70 75 80
 Leu Leu Lys Ile Lys Gln Ile Thr Lys
 85

<210> 1074
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 1074
 Pro Cys Leu Arg Ser Lys Val Thr Arg Lys Arg Pro Cys Leu Pro Ser
 5 10 15
 Met Thr Leu Met Glu Glu Met Leu Arg Glu Ala Phe Arg Cys Met Thr
 20 25 30
 Gln Gly Lys Thr Ala Lys Asn Leu Val Leu Ala Leu Leu Ile Leu Leu
 35 40 45
 Phe Val Leu Phe Leu Gly Val Leu Arg Ala Lys
 50 55

<210> 1075
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 1075
 Glu Gln Asn Asp Asn Thr Gln Lys Phe Ser Lys Trp Asp Phe Pro Gly
 5 10 15
 Arg Ala Asn Glu Arg Pro Tyr Cys Tyr Ala Ile Trp Ser Lys Thr Thr
 20 25 30
 Leu Gln Glu Asp Val Phe Thr Gly Gly Pro His Ala Arg Leu Leu His
 35 40 45
 Glu Gly Ile
 50

<210> 1076
 <211> 76
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant

<222> (1)...(76)

<223> Xaa = Any amino acid

<400> 1076

Asp Phe Gly Gly Cys Pro Asp Tyr Glu Trp Ala Leu Pro His Cys Pro
 5 10 15

Gly Gly Ser Ser Asp Asp Pro Ser Arg Asp Leu Cys Thr His Leu Cys
 20 25 30

Asp Cys Val Val Pro Ser Leu Gly Arg His Tyr Val Tyr Tyr Phe Arg
 35 40 45

Ile Thr Pro Gly Ser Asn Gly Glu Lys Leu Gln Glu Val Phe Gly Gln
 50 55 60

Arg Lys Asn Asp Asn Glu Phe Ile Xaa Pro Leu Cys
 65 70 75

<210> 1077

<211> 149

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(149)

<223> Xaa = Any amino acid

<400> 1077

Asp Cys Gln Lys Ser Cys Ser Cys Ser Pro His Phe Val Ile Cys Phe
 5 10 15

Ile Phe Arg Ser Phe Glu Ser Lys Met Thr Thr Pro Arg Asn Ser Val
 20 25 30

Asn Gly Thr Phe Pro Ala Glu Pro Met Lys Gly Pro Ile Ala Met Gln
 35 40 45

Ser Gly Pro Lys Pro Leu Phe Arg Arg Met Ser Ser Leu Val Gly Pro
 50 55 60

Thr Gln Gly Phe Phe Met Arg Glu Ser Lys Thr Leu Gly Ala Val Gln
 65 70 75 80

Ile Met Asn Gly Leu Phe His Ile Ala Leu Gly Gly Leu Leu Met Ile
 85 90 95

Pro Ala Gly Ile Tyr Ala Pro Ile Cys Val Thr Val Trp Tyr Pro Leu
 100 105 110

Trp Gly Gly Ile Met Tyr Ile Ile Ser Gly Ser Leu Leu Ala Ala Thr
 115 120 125

Glu Lys Asn Ser Arg Lys Cys Leu Val Lys Gly Lys Met Ile Met Asn
 130 135 140

Ser Xaa Xaa Leu Phe
 145

<210> 1078

<211> 89

<212> PRT

<213> Homo sapiens

<400> 1078

Ile Pro Ala Gly Ile Ile Arg Arg Pro Pro Arg Ala Met Trp Lys Ser
5 10 15
Pro Phe Ile Ile Trp Thr Ala Pro Lys Val Leu Asp Ser Leu Met Lys
20 25 30
Lys Pro Cys Val Gly Pro Thr Ser Glu Asp Ile Leu Leu Lys Ser Gly
35 40 45
Phe Gly Pro Asp Cys Ile Ala Ile Gly Pro Phe Ile Gly Ser Ala Gly
50 55 60
Lys Val Pro Phe Thr Glu Phe Leu Gly Val Val Ile Leu Leu Ser Lys
65 70 75 80
Leu Leu Lys Ile Lys Gln Ile Thr Lys
85

<210> 1079

<211> 62

<212> PRT

<213> Homo sapiens

<400> 1079

Ser Gly Asn Asn Ile His Asn Ala Ser Pro Glu Arg Val Pro His Ser
5 10 15
His Thr Asp Gly Cys Ile Asp Pro Cys Trp Asp His Gln Lys Thr Pro
20 25 30
Gln Gly Asn Val Glu Glu Pro Ile His Asn Leu Asp Ser Pro Gln Ser
35 40 45
Leu Arg Phe Pro His Glu Glu Ala Leu Arg Gly Ala His Gln
50 55 60

<210> 1080

<211> 64

<212> PRT

<213> Homo sapiens

<400> 1080

Ile Ser Gly Cys Cys His Phe Ala Leu Lys Thr Pro Lys Asn Lys Thr
5 10 15
Asn Asn Lys Met Arg Arg Ala Arg Thr Arg Phe Leu Ala Val Leu Pro
20 25 30
Cys Val Met His Leu Asn Ala Ser Leu Ser Ile Ser Ser Met Ser Val
35 40 45
Ile Glu Gly Arg His Gly Leu Phe Arg Val Thr Leu Asp Leu Arg Gln
50 55 60

<210> 1081

```

<400> 1081
Pro Ile Ile Glu Ile Ser Ala Pro Ala Cys Lys Ala Ser Met Asn Ala
          5                      10                      15

Leu Val Pro Asp Leu Ala Ile Val Pro Arg Leu Leu Ile Lys Ser Ala
          20                      25                      30

Leu Val Ile Pro Ile Pro Val Ser Thr Ile Val Arg Val Arg Ser Cys
          35                      40                      45

Leu Phe Gly Ile Arg Leu Ile Cys Ser Ser Phe Ser Glu Ser Asn Leu
          50                      55                      60

Leu Gly Ser Val Lys Leu Ser Tyr Arg Ile Leu Ser Asn Ala Ser Asp
          65                      70                      75                      80

Glu Phe Glu Met Ser Ser Leu Arg Lys Ile Ser Leu Phe Glu
          85                      90

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```
<210> 1082
<211> 61
<212> PRT
<213> Homo sapiens
```

```

<400> 1082
Asn His Arg Asp Ile Cys Thr Ser Leu Gln Ser Phe His Glu Arg Phe
                    5                      10                      15

Gly Pro Arg Leu Gly Asp Ser Thr Lys Val Ile Asp Gln Val Ser Leu
                20                      25                      30

Gly His Ser Asn Ser Ser Ile His Asn Ser Glu Ser Ser Ile Leu Phe
                35                      40                      45

Val Arg Tyr Lys Val Asn Met Gln Leu Phe Leu Arg Val
    50                      55                      60

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<210> 1083
<211> 58
<212> PRT
<213> Homo sapiens
```

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<220>  
<221> variant  
<222> (1)...(58)  
<223> Xaa = Any amino acid
```

<400> 1083
Gly Asn Pro Asp Pro Arg Pro Thr Asp Gly Gly Xaa Gly Gly Xaa Xaa
 5 10 15

Val Arg Leu Ser Gly Arg Asn Cys Pro Val Asp Val Ile Asp His Gln
 20 25 30

Tyr Phe Leu Leu Glu Gln Arg Asp Leu Ser Glu Arg Ala His Phe Lys
 35 40 45

Phe Ile Arg Cys Ile Gly Gln Asn Pro Val
50 55

<210> 1084
<211> 139
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(139)
<223> Xaa = Any amino acid

<400> 1084
Xaa Thr Gly Ala Val Ser Phe Xaa Met Xaa Glu Glu Thr Gln Thr Gln
5 10 15
Asp Gln Pro Met Glu Glu Xaa Glu Val Xaa Thr Phe Ala Phe Gln Ala
20 25 30
Glu Ile Ala Gln Leu Met Ser Leu Ile Ile Asn Thr Phe Tyr Ser Asn
35 40 45
Lys Glu Ile Phe Leu Arg Glu Leu Ile Ser Asn Ser Ser Asp Ala Leu
50 55 60
Asp Lys Ile Arg Tyr Glu Ser Leu Thr Asp Pro Ser Lys Leu Asp Ser
65 70 75 80
Glu Lys Glu Leu His Ile Asn Leu Ile Pro Asn Lys Gln Asp Arg Thr
85 90 95
Leu Thr Ile Val Asp Thr Gly Ile Gly Met Thr Lys Ala Asp Leu Ile
100 105 110
Asn Asn Leu Gly Thr Ile Ala Lys Ser Gly Thr Lys Ala Phe Met Glu
115 120 125
Ala Leu Gln Ala Gly Ala Asp Ile Ser Met Ile
130 135

<210> 1085
<211> 66
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(66)
<223> Xaa = Any amino acid

<400> 1085
Pro Cys Leu Xaa Ser Xaa Val Thr Arg Lys Arg Pro Cys Leu Pro Ser
5 10 15
Met Thr Leu Met Glu Glu Met Leu Xaa Glu Ala Phe Xaa Cys Met Thr
20 25 30
Gln Gly Lys Thr Ala Lys Asn Leu Xaa Leu Ala Leu Leu Ile Leu Leu
35 40 45

Xaa Val Leu Xaa Leu Gly Val Xaa Arg Ala Lys Xaa Xaa His Pro Glu
 50 55 60

Ile Gln
 65

<210> 1086
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(51)
 <223> Xaa = Any amino acid

<400> 1086
 Glu Gln Asn Xaa Xaa Thr Gln Lys Phe Ser Lys Trp Asp Phe Pro Gly
 5 10 15

Arg Xaa Asn Glu Arg Pro Tyr Cys Tyr Ala Ile Trp Ser Lys Thr Thr
 20 25 30

Leu Gln Glu Asp Xaa Phe Thr Gly Gly Pro His Ala Lys Leu Leu His
 35 40 45

Glu Gly Ile
 50

<210> 1087
 <211> 52
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(52)
 <223> Xaa = Any amino acid

<400> 1087
 Asp Phe Gly Gly Cys Pro Asp Tyr Glu Trp Ala Leu Pro His Cys Pro
 5 10 15

Gly Gly Ser Ser Asp Asp Pro Xaa Arg Asp Leu Cys Xaa His Leu Cys
 20 25 30

Asp Cys Val Val Pro Ser Leu Gly Arg His Tyr Val Tyr Tyr Phe Arg
 35 40 45

Ile Thr Pro Gly
 50

<210> 1088
 <211> 125
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(125)

<223> Xaa = Any amino acid

<400> 1088

```

Asp Cys Gln Lys Ser Xaa Ser Cys Ser Pro His Phe Val Ile Xaa Phe
      5                      10                      15

Xaa Phe Arg Ser Xaa Glu Ser Lys Xaa Thr Xaa Pro Arg Asn Ser Val
      20                      25                      30

Asn Gly Thr Phe Pro Ala Xaa Pro Met Lys Gly Pro Ile Ala Met Gln
      35                      40                      45

Ser Gly Pro Lys Pro Leu Phe Arg Arg Met Xaa Ser Leu Val Gly Pro
      50                      55                      60

Thr Gln Ser Phe Phe Met Arg Glu Ser Lys Thr Leu Gly Ala Val Gln
      65                      70                      75                      80

Ile Met Asn Gly Leu Phe His Ile Ala Leu Gly Gly Leu Leu Met Ile
      85                      90                      95

Pro Xaa Gly Ile Tyr Xaa Pro Ile Cys Val Thr Val Trp Tyr Pro Leu
      100                     105                     110

Trp Gly Gly Ile Met Tyr Ile Ile Ser Gly Ser Leu Leu
      115                     120                     125

```

<210> 1089

<211> 89

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(89)

<223> Xaa = Any amino acid

<400> 1089

```

Ile Pro Xaa Gly Ile Ile Arg Arg Pro Pro Arg Ala Met Trp Lys Ser
      5                      10                      15

Pro Phe Ile Ile Trp Thr Ala Pro Lys Val Leu Asp Ser Leu Met Lys
      20                      25                      30

Lys Leu Cys Val Gly Pro Thr Ser Glu Xaa Ile Leu Leu Lys Ser Gly
      35                      40                      45

Phe Gly Pro Asp Cys Ile Ala Ile Gly Pro Phe Ile Xaa Ser Ala Gly
      50                      55                      60

Lys Val Pro Phe Thr Glu Phe Leu Gly Xaa Xaa Ile Leu Leu Ser Xaa
      65                      70                      75                      80

Leu Leu Lys Xaa Lys Xaa Ile Thr Lys
      85

```

<210> 1090

<211> 62

<212> PRT

<213> Homo sapiens

```
<220>  
<221> variant  
<222> (1)...(62)  
<223> Xaa = Any amino acid  
  
<400> 1090  
Ser Gly Asn Asn Ile His Asn Ala Ser Pro Glu Arg Val Pro His Ser  
          5                      10                      15  
His Thr Asp Gly Xaa Ile Asp Pro Xaa Trp Asp His Gln Lys Thr Pro  
      20              25              30  
Gln Gly Asn Val Glu Glu Pro Ile His Asn Leu Asp Ser Pro Gln Ser  
    35              40              45  
Leu Arg Phe Pro His Glu Glu Ala Leu Arg Gly Ala His Gln  
   50              55              60
```

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<210> 1091
<211> 64
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(64)
<223> Xaa = Any amino acid

<400> 1091
Ile Ser Gly Xaa Cys Xaa Phe Ala Leu Xaa Thr Pro Lys Xaa Lys Xaa
      .      5              10              15

Asn Asn Lys Met Arg Arg Ala Arg Xaa Arg Phe Leu Ala Val Leu Pro
      20              25              30

Cys Val Met His Xaa Asn Ala Ser Xaa Ser Ile Ser Ser Met Ser Val
      35              40              45

Ile Glu Gly Arg His Gly Leu Phe Arg Val Thr Xaa Asp Xaa Arg Gln
      50              55              60

```

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<210> 1092
<211> 123
<212> PRT
<213> Homo sapiens

<400> 1092
Gly His Ser Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu
      5                      10                      15
Leu Leu Trp Leu Pro Gly Ala Lys Cys Asp Ile Gln Met Thr Gln Ser
      20                      25                      30
Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Thr Val Thr Ile Ser Cys
      35                      40                      45
Arg Ala Ser Gln Asn Ile Asp Arg Trp Leu Ala Trp His Gln Gln Lys
      50                      55                      60
Pro Gly Lys Ala Pro Asn Val Leu Ile Tyr Ala Thr Ser Ser Leu Glu
      65                      70                      75                      80

```

Glu Gly Val Ser Leu Arg Phe Thr Gly Ser Gly Ser Gly Thr Gln Phe
 85 90 95
 Asn Leu Thr Ile Thr Ser Leu Gln Pro Asp Asp Ser Ala Thr Tyr Tyr
 100 105 110
 Cys Gln His Tyr Ser Ala Ser Leu Arg Ser Phe
 115 120

<210> 1093
 <211> 71
 <212> PRT
 <213> Homo sapiens

<400> 1093
 Asp Ile Arg Gly Phe Ala Trp Phe Leu Leu Met Pro Gly Gln Pro Pro
 5 10 15
 Ile Tyr Ile Leu Arg Gly Pro Thr Thr Tyr Cys Asn Cys Ile Ser Asp
 20 25 30
 Arg Cys Arg Gln Gly Gly Arg Arg Leu Gly His Leu Asp Val Thr Phe
 35 40 45
 Gly Thr Trp Glu Pro Glu Gln Gln Glu Pro Gln Glu Leu Ser Gly Asp
 50 55 60
 Pro His Val His Ala Val Ser
 65 70

<210> 1094
 <211> 85
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(85)
 <223> Xaa = Any amino acid

<400> 1094
 Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
 5 10 15
 Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Xaa Leu
 20 25 30
 His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45
 Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
 50 55 60
 Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
 65 70 75 80
 Ser Leu Gly Leu Thr
 85

<210> 1095
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(123)
 <223> Xaa = Any amino acid

<400> 1095
 Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
 5 10 15
 Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly
 20 25 30
 Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
 35 40 45
 Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
 50 55 60
 Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
 65 70 75 80
 Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Xaa Thr Thr Pro
 85 90 95
 Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu
 100 105 110
 Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
 115 120

<210> 1096
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 1096
 Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
 5 10 15
 Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30
 His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45
 Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
 50 55 60
 Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
 65 70 75 80
 Ser Leu Gly Leu Thr
 85

<210> 1097
 <211> 102

<212> PRT

<213> Homo sapiens

<400> 1097

Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
 5 10 15

Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly
 20 25 30

Thr Lys Leu Ala Val Leu Ser Gln Pro Lys Ala Ala Pro Ser Val Thr
 35 40 45

Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
 50 55 60

Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
 65 70 75 80

Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
 85 90 95

Ser Lys Gln Ser Asn Asn
 100

<210> 1098

<211> 85

<212> PRT

<213> Homo sapiens

<400> 1098

Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
 5 10 15

Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30

His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45

Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
 50 55 60

Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
 65 70 75 80

Ser Leu Gly Leu Thr
 85

<210> 1099

<211> 108

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(108)

<223> Xaa = Any amino acid

<400> 1099

Tyr Xaa Gln Val Trp Asp Arg Asn Tyr Asp His Val Val Phe Gly Gly

5 10 15
 Gly Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val
 20 25 30
 Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr
 35 40 45
 Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala
 50 55 60
 Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr
 65 70 75 80
 Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser
 85 90 95
 Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
 100 105

<210> 1100
 <211> 56
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(56)
 <223> Xaa = Any amino acid

<400> 1100
 Val Ala Ser Val Gly Leu Pro Leu Leu Xaa Arg Gln Ala Gln Ile Ala
 5 10 15
 Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30
 His Ser Xaa Leu Asp Gly Xaa Xaa Tyr Leu Pro Ser Xaa Pro Leu Xaa
 35 40 45
 Arg Leu Xaa Gly Arg Ser His Leu
 50 55

<210> 1101
 <211> 54
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(54)
 <223> Xaa = Any amino acid

<400> 1101
 Lys Ala Thr Xaa Val Cys Leu Ile Ser Asp Phe Tyr Xaa Gly Ala Val
 5 10 15
 Xaa Val Xaa Trp Lys Ala Asp Ser Xaa Pro Arg Gln Xaa Gly Ser Gly
 20 25 30
 Asp His His Thr Leu Gln Thr Lys Gln Gln Gln Val Arg Gly Gln Gln

35 40 45

Leu Ser Glu Pro Asp Xaa
50

<210> 1102
<211> 55
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(55)
<223> Xaa = Any amino acid

<400> 1102
Val Thr Ser Thr Xaa Glu Pro Xaa Gln Trp Xaa Gly Arg Gln Ile Xaa
5 10 15
Xaa Pro Val Lys Xaa Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser
20 25 30
Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Xaa Glu Gln
35 40 45
Trp Lys Ser His Arg Ser Tyr
50 55

<210> 1103
<211> 56
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(56)
<223> Xaa = Any amino acid

<400> 1103
Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
5 10 15
Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Xaa Phe Gly Gly Gly
20 25 30
Thr Lys Leu Ala Val Leu Gly Xaa Pro Lys Ala Ala Pro Ser Val Thr
35 40 45
Leu Phe Xaa Pro Xaa Ser Xaa Glu
50 55

<210> 1104
<211> 85
<212> PRT
<213> Homo sapiens

<400> 1104
Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
5 10 15

Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30
 His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45
 Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
 50 55 60
 Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
 65 70 75 80
 Ser Leu Gly Leu Thr
 85

<210> 1105
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 1105
 Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
 5 10 15
 Cys Gln Val Trp Asp Leu Asn Asn Asp His Val Val Phe Gly Gly Gly
 20 25 30
 Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
 35 40 45
 Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
 50 55 60
 Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
 65 70 75 80
 Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
 85 90 95
 Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu
 100 105 110
 Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
 115 120

<210> 1106
 <211> 194
 <212> PRT
 <213> Homo sapiens

<400> 1106
 Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Gln Phe Tyr Val Asp Leu
 5 10 15
 Gly Arg Lys Glu Thr Val Trp Cys Leu Pro Val Leu Arg Gln Phe Arg
 20 25 30
 Phe Asp Pro Gln Phe Ala Leu Thr Asn Ile Ala Val Leu Lys His Asn
 35 40 45
 Leu Asn Ser Leu Ile Lys Arg Ser Asn Ser Thr Ala Ala Thr Asn Glu

50 55 60
 Val Pro Glu Val Thr Val Phe Ser Lys Ser Pro Val Thr Leu Gly Gln
 65 70 75 80
 Pro Asn Ile Leu Ile Cys Leu Val Asp Asn Ile Phe Pro Pro Val Val
 85 90 95
 Asn Ile Thr Trp Leu Ser Asn Gly His Ser Val Thr Glu Gly Val Ser
 100 105 110
 Glu Thr Ser Phe Leu Ser Lys Ser Asp His Ser Phe Phe Lys Ile Ser
 115 120 125
 Tyr Leu Thr Leu Leu Pro Ser Ala Glu Glu Ser Tyr Asp Cys Lys Val
 130 135 140
 Glu His Trp Gly Leu Asp Lys Pro Leu Leu Lys His Trp Glu Pro Glu
 145 150 155 160
 Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr Val Val Cys Ala Leu
 165 170 175
 Gly Leu Ser Val Gly Leu Val Gly Ile Val Val Gly Thr Val Phe Ile
 180 185 190
 Ile Arg

<210> 1107
 <211> 52
 <212> PRT
 <213> Homo sapiens

<400> 1107
 Ala Met Gly Thr Gln Ser Gln Lys Val Phe Leu Arg Pro Ala Ser Ser
 5 10 15
 Pro Arg Val Ile Ile Pro Ser Ser Arg Ser Val Thr Ser Pro Ser Ser
 20 25 30
 Leu Leu Leu Arg Arg Val Met Thr Ala Arg Trp Ser Thr Gly Asp Trp
 35 40 45
 Thr Ser Leu Phe
 50

<210> 1108
 <211> 55
 <212> PRT
 <213> Homo sapiens

<400> 1108
 Pro Arg Met Met Lys Thr Val Pro Thr Thr Met Pro Thr Arg Pro Thr
 5 10 15
 Asp Asn Pro Arg Ala Gln Thr Thr Val Ser Val Ser Ser Asp Ile Gly
 20 25 30
 Ala Gly Ile Ser Gly Ser Gln Cys Phe Arg Arg Gly Leu Ser Ser Pro
 35 40 45

Gln Cys Ser Thr Leu Gln Ser
50 55

<210> 1109
<211> 66
<212> PRT
<213> Homo sapiens

<400> 1109
Pro Ser Val Thr Gly Asp Leu Glu Asn Thr Val Thr Ser Gly Thr Ser
5 10 15

Leu Val Ala Ala Val Glu Leu Glu Arg Leu Ile Arg Leu Phe Lys Leu
20 25 30

Cys Phe Arg Thr Ala Met Phe Val Ser Ala Asn Cys Gly Ser Asn Leu
35 40 45

Asn Cys Leu Arg Thr Gly Lys His Gln Thr Val Ser Phe Leu Pro Arg
50 55 60

Ser Thr
65

<210> 1110
<211> 59
<212> PRT
<213> Homo sapiens

<400> 1110
His Arg Gly Trp Asn Leu Arg Leu Pro Val Phe Gln Lys Arg Leu Val
5 10 15

Gln Ser Pro Val Leu His Leu Ala Val Ile Thr Leu Leu Ser Arg Arg
20 25 30

Glu Glu Gly Glu Val Thr Asp Leu Glu Glu Gly Met Ile Thr Leu Gly
35 40 45

Glu Glu Ala Gly Leu Arg Asn Thr Phe Cys Asp
50 55

<210> 1111
<211> 60
<212> PRT
<213> Homo sapiens

<400> 1111
Val Pro Ile Ala Gln Pro Cys Asp Val Asp His Arg Arg Lys Asp Val
5 10 15

Val His Lys Thr Asp Glu Asp Val Gly Leu Thr Gln Cys His Gly Arg
20 25 30

Leu Gly Lys His Cys Asp Leu Arg Asn Leu Ile Gly Ser Ser Gly Arg
35 40 45

Val Gly Ala Phe Asn Gln Thr Val Gln Val Met Phe
50 55 60

<210> 1112
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(51)
 <223> Xaa = Any amino acid

<400> 1112
 Lys Gln His Trp Trp Cys Leu Ser His Gly Leu Asp Arg Ser Pro Xaa
 5 10 15
 Arg Xaa Pro Leu Ser Pro Xaa Arg Leu Cys Asp Leu Leu Cys Val Asp
 20 25 30
 Ser Asp Thr Xaa Ser Xaa Xaa Gly Pro Arg Xaa Xaa Gly Gln Asp Tyr
 35 40 45
 Leu Trp Gly
 50

<210> 1113
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(51)
 <223> Xaa = Any amino acid

<400> 1113
 Ser Ser Thr Gly Gly Ala Ser Ala Met Ala Trp Thr Val Leu Xaa Leu
 5 10 15
 Xaa Leu Leu Ser His Xaa Thr Asp Ser Val Thr Ser Tyr Val Leu Thr
 20 25 30
 Gln Thr Pro Xaa Val Xaa Xaa Ala Pro Gly Xaa Thr Ala Lys Ile Thr
 35 40 45
 Cys Gly Gly
 50

<210> 1114
 <211> 79
 <212> PRT
 <213> Homo sapiens

<400> 1114
 Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn
 5 10 15
 Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val
 20 25 30
 Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys Ala Gly Val Glu

Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
65 70 75

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<210> 1115
<211> 54
<212> PRT
<213> Homo sapiens
```

<400> 1115
Leu Leu Pro Gly Ser Cys Asp Ser Gly Leu Glu Gly Arg Trp Gln Pro
5 10 15

Arg Gln Gly Gly Ser Gly Asp His Gln Thr Leu Gln Thr Glu Gln Gln
20 25 30

Gln Val Arg Gly Gln Gln Leu Pro Glu Pro Asp Ala Arg Ala Val Glu
35 40 45

Val Pro Gln Lys Leu Gln
50

```
<210> 1116
<211> 59
<212> PRT
<213> Homo sapiens
```

<400> 1116
Val Ala Ser Val Gly Leu Pro Leu Leu Gly Arg Gln Ala Gln Val Ala
 5 10 15

Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Phe Gly Gly Leu
20 25 30

His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
35 40 45

Ser Ser Arg Val Glu Val Thr Asp Gln Thr His
50 55

```
<210> 1117
<211> 85
<212> PRT
<213> Homo sapiens
```

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<220>
<221> variant
<222> (1)...(85)
<223> Xaa = Any amino acid
```

```
<400> 1117
Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
          5              10              15
```

Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
20 25 30

His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45

Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
 50 55 60

Gly Leu Lys Leu Leu Xaa Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
 65 70 75 80

Ser Leu Gly Leu Thr
 85

<210> 1118
 <211> 93
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(93)
 <223> Xaa = Any amino acid

<400> 1118
 Xaa Gly Thr Lys Xaa Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser
 5 10 15

Val Thr Leu Phe Pro Pro Ser Xaa Glu Glu Leu Gln Ala Asn Lys Ala
 20 25 30

Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val
 35 40 45

Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr
 50 55 60

Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu
 65 70 75 80

Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
 85 90

<210> 1119
 <211> 194
 <212> PRT
 <213> Homo sapiens

<400> 1119
 Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Gln Phe Tyr Val Asp Leu
 5 10 15

Gly Arg Lys Glu Thr Val Trp Cys Leu Pro Val Leu Arg Gln Phe Arg
 20 25 30

Phe Asp Pro Gln Phe Ala Leu Thr Asn Ile Ala Val Leu Lys His Asn
 35 40 45

Leu Asn Ser Leu Ile Lys Arg Ser Asn Ser Thr Ala Ala Thr Asn Glu
 50 55 60

Val Pro Glu Val Thr Val Phe Ser Lys Ser Pro Val Thr Leu Gly Gln

364

[illegible]

```
<210> 1120
<211> 52
<212> PRT
<213> Homo sapiens
```

```

<400> 1120
Ala Met Gly Thr Gln Ser Gln Lys Val Phe Leu Arg Pro Ala Ser Ser
          5                      10                      15

Pro Arg Val Ile Ile Pro Ser Ser Arg Ser Val Thr Ser Pro Ser Ser
          20                      25                      30

Leu Leu Leu Arg Arg Val Met Thr Ala Arg Trp Ser Thr Gly Asp Trp
          35                      40                      45

Thr Ser Leu Phe
          50

```

```
<210> 1121
<211> 55
<212> PRT
<213> Homo sapiens
```

```

<400> 1121
Pro Arg Met Met Lys Thr Val Pro Thr Thr Met Pro Thr Arg Pro Thr
          5                      10                      15

Asp Asn Pro Arg Ala Gln Thr Thr Val Ser Val Ser Ser Asp Ile Gly
          20                      25                      30

Ala Gly Ile Ser Gly Ser Gln Cys Phe Arg Arg Gly Leu Ser Ser Pro
          35                      40                      45

Gln Cys Ser Thr Leu Gln Ser
          50                      55

```

<210> 1122
 <211> 66
 <212> PRT
 <213> Homo sapiens

<400> 1122
 Pro Ser Val Thr Gly Asp Leu Glu Asn Thr Val Thr Ser Gly Thr Ser
 5 10 15
 Leu Val Ala Ala Val Glu Leu Glu Arg Leu Ile Arg Leu Phe Lys Leu
 20 25 30
 Cys Phe Arg Thr Ala Met Phe Val Ser Ala Asn Cys Gly Ser Asn Leu
 35 40 45
 Asn Cys Leu Arg Thr Gly Lys His Gln Thr Val Ser Phe Leu Pro Arg
 50 55 60
 Ser Thr
 65

<210> 1123
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 1123
 His Arg Gly Trp Asn Leu Arg Leu Pro Val Phe Gln Lys Arg Leu Val
 5 10 15
 Gln Ser Pro Val Leu His Leu Ala Val Ile Thr Leu Leu Ser Arg Arg
 20 25 30
 Glu Glu Gly Glu Val Thr Asp Leu Glu Glu Gly Met Ile Thr Leu Gly
 35 40 45
 Glu Glu Ala Gly Leu Arg Asn Thr Phe Cys Asp
 50 55

<210> 1124
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 1124
 Val Pro Ile Ala Gln Pro Cys Asp Val Asp His Arg Arg Lys Asp Val
 5 10 15
 Val His Lys Thr Asp Glu Asp Val Gly Leu Thr Gln Cys His Gly Arg
 20 25 30
 Leu Gly Lys His Cys Asp Leu Arg Asn Leu Ile Gly Ser Ser Gly Arg
 35 40 45
 Val Gly Ala Phe Asn Gln Thr Val Gln Val Met Phe
 50 55 60

<210> 1125

<211> 94
<212> PRT
<213> Homo sapiens

<400> 1125
Thr Gly Gly Ala Ser Ala Met Ala Trp Thr Val Leu Leu Leu Gly Leu
5 10 15
Leu Ser His Cys Thr Asp Ser Val Thr Ser Tyr Val Leu Thr Gln Thr
20 25 30
Pro Ser Val Ser Val Ala Pro Gly Lys Thr Ala Lys Ile Thr Cys Gly
35 40 45
Gly Asn Asn Ile Gly Ser Asn Asn Val His Trp Tyr Tyr Gln Lys Pro
50 55 60
Gly Gln Ala Pro Val Leu Ile Ile Ser Phe Asp Asn Asp Arg Pro Ser
65 70 75 80
Gly Ile Ser Glu Arg Phe Ser Gly Phe Asn Ser Gly Asp Met
85 90

<210> 1126
<211> 53
<212> PRT
<213> Homo sapiens

<400> 1126
Trp Trp Cys Leu Ser His Gly Leu Asp Arg Ser Pro Pro Arg Pro Pro
5 10 15
Leu Ser Leu His Arg Leu Cys Asp Leu Leu Cys Val Asp Ser Asp Thr
20 25 30
Leu Ser Val Ser Gly Pro Arg Lys Asp Gly Gln Asp Tyr Leu Trp Gly
35 40 45
Lys Gln Tyr Trp Glu
50

<210> 1127
<211> 71
<212> PRT
<213> Homo sapiens

<400> 1127
Asp Ile Arg Gly Phe Ala Trp Phe Leu Leu Met Pro Gly Gln Pro Pro
5 10 15
Ile Tyr Ile Leu Arg Gly Pro Thr Thr Tyr Cys Asn Cys Ile Ser Asp
20 25 30
Arg Cys Arg Gln Gly Gly Arg Arg Leu Gly His Leu Asp Val Thr Phe
35 40 45
Gly Thr Trp Glu Pro Glu Gln Gln Glu Pro Gln Glu Leu Ser Gly Asp
50 55 60
Pro His Val His Ala Val Ser
65 70

<210> 1128
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 1128
 Ser Gly His Ser Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu
 5 10 15
 Leu Leu Leu Trp Leu Pro Gly Ala Lys Cys Asp Ile Gln Met Thr Gln
 20 25 30
 Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Thr Val Thr Ile Ser
 35 40 45
 Cys Arg Ala Ser Gln Asn Ile Asp Arg Trp Leu Ala Trp His Gln Gln
 50 55 60
 Lys Pro Gly Lys Ala Pro Asn Val Leu Ile Tyr Ala Thr Ser Ser Leu
 65 70 75 80
 Glu Glu Gly Val Ser Leu Arg Phe Thr Gly Ser Gly Ser Gly Thr Gln
 85 90 95
 Phe Asn Leu Thr Ile Thr Ser Leu Gln Pro Asp Asp Ser Ala Thr Tyr
 100 105 110
 Tyr Cys Gln His Tyr Ser Ala Ser Leu Arg Ser Phe
 115 120

<210> 1129
 <211> 63
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(63)
 <223> Xaa = Any amino acid

<400> 1129
 Asn Asn Asp His Val Val Phe Gly Gly Gly Thr Lys Leu Ala Val Leu
 5 10 15
 Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Xaa Xaa
 20 25 30
 Glu Xaa Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
 35 40 45
 Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Xaa Ser Ser
 50 55 60

<210> 1130
 <211> 73
 <212> PRT
 <213> Homo sapiens

<400> 1130

[illegible]

```
<210> 1131
<211> 57
<212> PRT
<213> Homo sapiens
```

```

<400> 1131
Gly Gly Ala Ser Ala Met Ala Trp Thr Val Leu Leu Leu Gly Leu Leu
      5                      10                      15
Ser His Arg Thr Asp Ser Val Thr Ser Tyr Val Leu Thr Gln Thr Pro
      20                      25                      30
Ser Val Ser Val Ala Pro Gly Lys Thr Ala Lys Ile Thr Cys Gly Gly
      35                      40                      45
Asn Asn Ile Gly Ser His Asn Val His
      50                      55

```

```
<210> 1132
<211> 85
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> variant  
<222> (1)...(85)  
<223> Xaa = Any amino acid
```

```

<400> 1132
Ser Gln Glu Ser Val Gln Glu Pro Phe Leu Thr Pro Val Met Asp Asn
      5              10              15

Lys Ala Xaa Pro Glu Glu Asp Glu Pro Gln His Glu Ala Ser Asn Ala
      20              25              30

Thr Gln His Leu Ala Leu Gly Arg Phe Arg Leu Ser Pro Pro Leu His
      35              40              45

Gly Asp Gly Val Leu Glu Ala Gly Val Leu His Val Ala Gly Val Asp
      50              55              60

Val Ser Met Leu Gly Ser His Phe Gln His His Gln Asp Leu Glu Xaa
      65              70              75              80

Pro Val Thr Xaa Ser
      85

```

<210> 1133
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 1133
 Asp Tyr Phe Asn Trp Asp Trp Leu Ser Leu Phe Cys Asn Ala Cys Leu
 5 10 15
 Ser Leu Pro Arg Ile Pro Asn Cys Leu Cys Gln Pro Val Pro Leu Arg
 20 25 30
 Ser Glu Ser Tyr Ser Gly Cys His Ala Ala Thr Arg Ser Ser Pro Phe
 35 40 45
 Ile Pro Thr Pro Arg Arg Trp Leu
 50 55

<210> 1134
 <211> 70
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(70)
 <223> Xaa = Any amino acid

<400> 1134
 Ile Cys Pro Glu Gln Asp Ala Glu Trp His Trp Arg Leu Arg Ala Gly
 5 10 15
 Ala His Leu Pro Arg Xaa Gly Pro Tyr Tyr Pro Ser Gln Glu Ser Glu
 20 25 30
 Arg Ala Pro Ala Leu Thr Pro Glu Thr Ile Leu Thr Gly Ile Gly Tyr
 35 40 45
 His Phe Ser Val Thr Pro Ala Cys Pro Cys Pro Glu Phe Pro Thr Ala
 50 55 60
 Cys Val Ser Leu Ser Pro
 65 70

<210> 1135
 <211> 82
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(82)
 <223> Xaa = Any amino acid

<400> 1135
 Leu Gly Xaa Gly Asp Trp Xaa Phe Gln Ile Leu Val Met Leu Glu Met
 5 10 15
 Thr Pro Gln His Gly Asp Val Tyr Thr Cys His Val Glu His Pro Ser

20 25 30
 Leu Gln Asn Pro Ile Thr Val Glu Trp Arg Ala Gln Ser Glu Ser Ala
 35 40 45
 Gln Ser Lys Met Leu Ser Gly Ile Gly Gly Phe Val Leu Gly Leu Ile
 50 55 60
 Phe Leu Gly Xaa Gly Leu Ile Ile His His Arg Ser Gln Lys Gly Leu
 65 70 75 80
 Leu His

<210> 1136
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 1136
 Arg Leu Leu Val Pro Ala Gln Asn Ser Gln Leu Pro Val Ser Ala Cys
 5 10 15
 Pro Pro Glu Ile Arg Val Leu Gln Trp Leu Ser Arg Ser His Gln Val
 20 25 30
 Ile Ser Phe His Pro His Pro Lys Ala Leu Ala Val Thr Leu Leu Pro
 35 40 45
 Ala Leu Thr Gln Ser Leu Cys Leu
 50 55

<210> 1137
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 1137
 Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
 5 10 15
 Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
 20 25 30
 His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
 35 40 45
 Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
 50 55 60
 Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
 65 70 75 80
 Ser Leu Gly Leu Thr
 85

<210> 1138
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 1138

```

Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
              5              10              15

Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly
              20              25              30

Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
              35              40              45

Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
              50              55              60

Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
              65              70              75              80

Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
              85              90              95

Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu
              100              105              110

Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
              115              120

```

<210> 1139

<211> 123

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(123)

<223> Xaa = Any amino acid

<400> 1139

```

Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
              5              10              15

Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly
              20              25              30

Thr Lys Leu Xaa Xaa Leu Gly Xaa Xaa Lys Ala Ala Pro Ser Val Thr
              35              40              45

Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
              50              55              60

Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Ala Thr Val Ala Trp
              65              70              75              80

Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
              85              90              95

Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu
              100              105              110

Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
              115              120

```

```
<220>  
<221> variant  
<222> (1)...(85)  
<223> Xaa = Any amino acid
```

```

<400> 1140
Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
                    5                      10                      15
Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
                    20                      25                      30
His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys Arg
                    35                      40                      45
Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
                    50                      55                      60
Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
                    65                      70                      75                      80
Ser Leu Xaa Xaa Thr
                    85

```

```
<210> 1141
<211> 85
<212> PRT
<213> Homo sapiens
```

```

<400> 1141
Val Ala Ser Val Gly Leu Pro Leu Leu Arg Arg Gln Ala Gln Ile Ala
          5                                10                    15

Ala Gly Arg Val Leu Val Val Ala Leu Phe Gly Gly Cys Gly Gly Leu
          20                                25                    30

His Ser Arg Leu Asp Gly Ala Ala Ile Cys Leu Pro Gly His Cys His
          35                                40                    45

Gly Ser Arg Val Glu Val Thr Tyr Glu Thr His Gln Cys Gly Leu Val
          50                                55                    60

Gly Leu Lys Leu Leu Arg Gly Gly Arg Glu Gln Ser Asp Arg Gly Gly
          65                                70                    75                    80

Ser Leu Gly Leu Thr
          85

```

```
<210> 1142
<211> 123
<212> PRT
<213> Homo sapiens
```

<400> 1142
Thr Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr
 5 10 15

Cys Gln Val Trp Asp Arg Asn Asn Asp His Val Val Phe Gly Gly Gly
 20 25 30
 Thr Lys Leu Ala Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr
 35 40 45
 Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
 50 55 60
 Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
 65 70 75 80
 Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
 85 90 95
 Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ser Ser Tyr Leu Ser Leu
 100 105 110
 Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
 115 120

<210> 1143
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 1143
 Thr Leu Pro Pro Asp Arg Met Lys Phe Ile Ser Thr Ser Leu Leu Leu
 5 10 15
 Met Leu Leu Val Ser Ser Leu Ser Pro Val Gln Gly Val Leu Glu Val
 20 25 30
 Tyr Tyr Thr Ser Leu Arg Cys Arg Cys Val Gln Glu Ser Ser Val Phe
 35 40 45
 Ile Pro Arg Arg Phe Ile Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn
 50 55 60
 Gly Cys Pro Arg Lys Glu Ile Ile Val Trp Lys Lys Asn Lys Ser Ile
 65 70 75 80
 Val Cys Val Asp Pro Gln Ala Glu Trp Ile Gln Arg Met Met Glu Val
 85 90 95
 Leu Arg Lys Arg Ser Ser Ser Thr Leu Pro Val Pro Val Phe Lys Arg
 100 105 110
 Lys Ile Pro
 115

<210> 1144
 <211> 55
 <212> PRT
 <213> Homo sapiens

<400> 1144
 Glu Lys Glu Val Leu Gln Leu Tyr Gln Phe Gln Cys Leu Arg Glu Arg
 5 10 15

```
<210> 1145
<211> 51
<212> PRT
<213> Homo sapiens
```

```

<400> 1145
Ser His Ala Tyr Leu Tyr Gly Glu Val Leu Phe Pro Gly Lys Asp Leu
          5                      10                      15

Thr Lys His Lys Thr Lys Ile Gln Ser Arg Asp Lys Gly Arg Met Gln
          20                      25                      30

Val Phe Leu Val Glu Ile Ser Ala Ser Gly Asn Leu Ser Leu Lys His
          35                      40                      45

Trp Asn Trp
          50

```

```
<210> 1146
<211> 60
<212> PRT
<213> Homo sapiens
```

```

<400> 1146
Val Arg Arg Ser Ser Ser Val Ala Gln Val Lys Ala Met Ile Glu Thr
          5              10              15

Lys Thr Gly Ile Ile Pro Glu Thr Gln Ile Val Thr Cys Asn Gly Lys
          20              25              30

Arg Leu Glu Asp Gly Lys Met Met Ala Asp Tyr Gly Ile Arg Lys Gly
          35              40              45

Asn Leu Leu Phe Leu Ala Cys Tyr Cys Ile Gly Gly
          50              55              60

```

```
<210> 1147
<211> 74
<212> PRT
<213> Homo sapiens
```

```

<400> 1147
Asp Pro Asp Cys Asp Leu Gln Trp Lys Glu Thr Gly Arg Trp Glu Asp
          5              10              15

Asp Gly Arg Leu Arg His Gln Lys Gly Gln Leu Thr Leu Pro Gly Met
          20              25              30

Leu Leu Tyr Trp Arg Val Thr Thr Leu Gly Met Gly Cys Trp Gln Gly
          35              40              45

```

Ser Lys Ser Leu Phe Leu Leu Ile Ser Tyr Ser Thr Asn Thr Ser Ser
 50 55 60

Asp Asp Phe Pro Lys Leu Met Arg Met Arg
 65 70

<210> 1148
 <211> 74
 <212> PRT
 <213> Homo sapiens

<400> 1148
 Leu Ile Val Leu Glu Ser Lys Lys His Arg Val Gly Gln Tyr Thr Ser
 5 10 15

Ser Tyr Pro Ser His Pro Asn Leu Thr Leu Leu Ile Ser Phe Ser Leu
 20 25 30

Ile Leu Gly Asn His Gln Lys Met Cys Ser Leu Ser Lys Arg Leu Lys
 35 40 45

Glu Ile Ser Phe Leu Ile Pro Ala Asn Thr Pro Cys Pro Gly Trp Ser
 50 55 60

Pro Ser Asn Thr Ile Thr Cys Gln Glu Glu
 65 70

<210> 1149
 <211> 57
 <212> PRT
 <213> Homo sapiens

<400> 1149
 Ser Ile Pro Gly Gly Tyr Asn Thr Asp Ile Ser Arg Val Phe Asn Gly
 5 10 15

Asn Asn Cys Thr Ser Cys Gln Gln Lys Leu Leu Pro Gly Pro Leu Glu
 20 25 30

Ile Tyr Asp Ile Asp Ala Ile Thr Phe Pro Phe Ile Asp Val Leu Phe
 35 40 45

His Leu Glu Val Lys Ile Gly Ala Thr
 50 55

<210> 1150
 <211> 78
 <212> PRT
 <213> Homo sapiens

<400> 1150
 Leu Asp Val Leu Gln Met Lys Glu Glu Asp Val Leu Lys Phe Leu Ala
 5 10 15

Ala Gly Thr His Leu Gly Gly Thr Asn Leu Asp Phe Gln Met Glu Gln
 20 25 30

Tyr Ile Tyr Lys Arg Lys Ser Asp Gly Ile Tyr Ile Ile Asn Leu Lys
 35 40 45

Arg Thr Trp Glu Lys Leu Leu Leu Ala Ala Arg Ala Ile Val Ala Ile
50 55 60

Glu Asn Pro Ala Asp Val Ser Val Ile Ser Ser Arg Asn Thr
65 70 75

<210> 1151
<211> 115
<212> PRT
<213> Homo sapiens

<400> 1151
Thr Leu Ser Pro Asp Arg Met Lys Phe Ile Ser Thr Ser Leu Leu Leu
5 10 15

Met Leu Leu Val Ser Ser Leu Ser Pro Val Gln Gly Val Leu Glu Val
20 25 30

Tyr Tyr Thr Ser Leu Arg Cys Arg Cys Val Gln Glu Ser Ser Val Phe
35 40 45

Ile Pro Arg Arg Phe Ile Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn
50 55 60

Gly Cys Pro Arg Lys Glu Ile Ile Val Trp Lys Lys Asn Lys Ser Ile
65 70 75 80

Val Cys Val Asp Pro Gln Ala Glu Trp Ile Gln Arg Met Met Glu Val
85 90 95

Leu Arg Lys Arg Ser Ser Ser Thr Leu Pro Val Pro Val Phe Lys Arg
100 105 110

Lys Ile Pro
115

<210> 1152
<211> 55
<212> PRT
<213> Homo sapiens

<400> 1152
Glu Lys Glu Val Leu Gln Leu Tyr Gln Phe Gln Cys Leu Arg Glu Arg
5 10 15

Phe Pro Asp Ala Asp Ile Ser Thr Lys Asn Thr Cys Ile Leu Pro Leu
20 25 30

Ser Leu Leu Trp Ile Leu Val Leu Cys Leu Val Lys Ser Phe Pro Gly
35 40 45

Lys Arg Thr Ser Pro Tyr Lys
50 55

<210> 1153
<211> 51
<212> PRT
<213> Homo sapiens

<400> 1153

Pro His Ala Tyr Leu Tyr Gly Glu Val Leu Phe Pro Gly Lys Asp Leu
 5 10 15
 Thr Lys His Lys Thr Lys Ile Gln Ser Arg Asp Lys Gly Arg Met Gln
 20 25 30
 Val Phe Leu Val Glu Ile Ser Ala Ser Gly Asn Leu Ser Leu Lys His
 35 40 45
 Trp Asn Trp
 50

<210> 1154
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 1154
 Ala Glu Gly Pro Ala His Arg Asp Ser Leu Leu Gly Ser Trp His His
 5 10 15
 Gly Pro Thr Glu Asp Ala Gly Pro Gly Tyr Pro Pro Pro Gly Gly Phe
 20 25 30
 Ser Ala Ala His Pro Arg Ser Ser Arg Asp Gln Cys Gly Pro Gly Val
 35 40 45
 Leu Pro Gly Val Leu Gln Gly Ser His Ser Pro
 50 55

<210> 1155
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 1155
 Glu Gln Arg Asp Leu His Thr Glu Thr Pro Ser Trp Ala Pro Gly Thr
 5 10 15
 Met Ala Pro Leu Lys Met Leu Ala Leu Val Thr Leu Leu Leu Gly Ala
 20 25 30
 Ser Leu Gln His Ile His Ala Ala Arg Gly Thr Asn Val Gly Arg Glu
 35 40 45
 Cys Cys Leu Glu Tyr Phe Lys Gly Ala Ile Pro Leu Arg Lys Leu Lys
 50 55 60
 Thr Trp Tyr Gln Thr Ser Glu Asp Cys Ser Arg Asp Ala Ile Val Phe
 65 70 75 80
 Val Thr Val Gln Gly Arg Ala Ile Cys Ser Asp Pro Asn Asn Lys Arg
 85 90 95
 Val Lys Asn Ala Val Lys Tyr Leu Gln Ser Leu Glu Arg Ser
 100 105 110

<210> 1156
 <211> 145
 <212> PRT

<213> Homo sapiens

<400> 1156

Pro Pro Leu Asp Pro Gly Ala Gln Gly Gly Gly Glu His Arg Arg
5 10 15

Trp Arg Ser Gln Val Val Pro Gly Asp Ser Gln Glu Ser Gly Val Arg
20 25 30

Arg Leu Gln Asp Leu Ser Arg Leu Cys Arg Tyr Leu Thr Ala Phe Phe
35 40 45

Thr Leu Leu Leu Leu Gly Ser Glu Gln Met Ala Leu Pro Cys Thr Val
50 55 60

Thr Lys Thr Met Ala Ser Leu Glu Gln Ser Ser Asp Val Trp Tyr His
65 70 75 80

Val Phe Ser Phe Leu Arg Gly Met Ala Pro Leu Lys Tyr Ser Arg Gln
85 90 95

His Ser Arg Pro Thr Leu Val Pro Arg Ala Ala Trp Met Cys Cys Arg
100 105 110

Glu Ala Pro Arg Arg Arg Val Thr Arg Ala Ser Ile Phe Ser Gly Ala
115 120 125

Met Val Pro Gly Ala Gln Glu Gly Val Ser Val Cys Arg Ser Leu Cys
130 135 140

Ser
145

<210> 1157

<211> 132

<212> PRT

<213> Homo sapiens

<400> 1157

Thr Pro Thr Val Glu Val Pro Gly Ser Pro Gly Arg Gln Ser Gly Val
5 10 15

Trp Gly Glu Glu Ala Ser Arg Pro Leu Lys Ala Leu Gln Val Phe Asn
20 25 30

Cys Ile Leu His Ser Leu Val Val Gly Val Arg Thr Asp Gly Pro Ala
35 40 45

Leu His Ser Tyr Lys Asn Asp Gly Ile Pro Gly Ala Val Leu Arg Cys
50 55 60

Leu Val Pro Arg Leu Gln Leu Ser Lys Gly Asn Gly Ser Leu Glu Val
65 70 75 80

Leu Gln Ala Ala Leu Pro Ala His Ile Gly Pro Ser Ser Cys Val Asp
85 90 95

Val Leu Gln Arg Ser Pro Gln Glu Glu Gly Asn Gln Gly Gln His Leu
100 105 110

Gln Trp Gly His Gly Ala Arg Ser Pro Gly Gly Ser Leu Cys Val Gln
115 120 125

Val Pro Leu Leu
130

<210> 1158
<211> 174
<212> PRT
<213> Homo sapiens

<400> 1158
Ala Leu Ala Pro Gly Pro Val Leu Phe Ser Ser Met Val Cys Leu Arg
5 10 15
Leu Pro Gly Gly Ser Cys Met Ala Val Leu Thr Val Thr Leu Met Val
20 25 30
Leu Ser Ser Pro Leu Ala Leu Ala Gly Asp Thr Arg Pro Arg Phe Leu
35 40 45
Glu Tyr Ser Thr Ser Glu Cys His Phe Phe Asn Gly Thr Glu Arg Val
50 55 60
Arg Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu Tyr Val Arg Phe
65 70 75 80
Asp Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu Leu Gly Arg Pro
85 90 95
Asp Glu Glu Tyr Trp Asn Ser Gln Lys Asp Phe Leu Glu Asp Arg Arg
100 105 110
Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly Val Val Glu Ser
115 120 125
Phe Thr Val Gln Arg Arg Val His Pro Lys Val Thr Val Tyr Pro Ser
130 135 140
Lys Thr Gln Pro Leu Gln His His Asn Leu Leu Val Cys Ser Val Ser
145 150 155 160
Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp Phe Arg Asn
165 170

<210> 1159
<211> 56
<212> PRT
<213> Homo sapiens

<400> 1159
Ala Pro His Trp Leu Trp Leu Gly Thr Pro Asp His Val Ser Trp Ser
5 10 15
Thr Leu Arg Leu Ser Val Ile Ser Ser Met Gly Arg Ser Gly Cys Gly
20 25 30
Ser Trp Thr Asp Thr Ser Ile Thr Lys Arg Ser Thr Cys Ala Ser Thr
35 40 45
Ala Thr Trp Gly Ser Ser Gly Arg
50 55

<210> 1160
<211> 52
<212> PRT
<213> Homo sapiens

<400> 1160
Ser Gly Pro Trp Ser Cys Pro Val Leu Gln His Gly Val Ser Glu Ala
5 10 15
Pro Trp Arg Leu Leu His Gly Ser Ser Asp Ser Asp Thr Asp Gly Ala
20 25 30
Glu Leu Pro Thr Gly Phe Gly Trp Gly His Gln Thr Thr Phe Leu Gly
35 40 45
Val Leu Tyr Val
50

<210> 1161
<211> 54
<212> PRT
<213> Homo sapiens

<400> 1161
His Ser Asp Val Glu Tyr Ser Lys Lys Arg Gly Leu Val Ser Pro Ala
5 10 15
Lys Ala Ser Gly Glu Leu Ser Thr Ile Ser Val Thr Val Arg Thr Ala
20 25 30
Met Gln Glu Pro Pro Gly Ser Leu Arg His Thr Met Leu Glu Asn Arg
35 40 45
Thr Gly Pro Gly Ala Arg
50

<210> 1162
<211> 70
<212> PRT
<213> Homo sapiens

<400> 1162
Ser Ser Pro Gln Pro Arg Ser Cys Val Cys Ser Arg Cys Pro Pro Arg
5 10 15
Pro Ala Cys Leu Pro Gly Ser Pro Ser Gly Cys Ser Ser Thr Pro His
20 25 30
Gln Ala Ala Pro Ala Pro Ser Pro Pro Gly Thr Pro Pro Arg Arg Cys
35 40 45
Arg Ser Ala Arg Thr Pro Leu Gly Tyr Arg Ser Ile Cys Pro Gly Thr
50 55 60
Ala Pro Ala Pro Ser His
65 70

<210> 1163
<211> 50

<212> PRT

<213> Homo sapiens

<400> 1163

Ser Thr Pro Arg Asn Val Val Trp Cys Pro Gln Pro Lys Pro Val Gly
5 10 15

Ser Ser Ala Pro Ser Val Ser Leu Ser Glu Leu Pro Cys Arg Ser Leu
20 25 30

Gln Gly Ala Ser Asp Thr Pro Cys Trp Arg Thr Gly Gln Asp Gln Gly
35 40 45

Pro Glu
50

<210> 1164

<211> 143

<212> PRT

<213> Homo sapiens

<400> 1164

Arg Ile His Ser His Leu Arg Met Asp Ser Pro Leu His Cys Glu Ala
5 10 15

Leu His Asn Pro Val Val Val Ser Ala Val Gly Val His Arg Gly Pro
20 25 30

Pro Val Phe Gln Glu Val Leu Leu Ala Val Pro Val Leu Leu Ile Arg
35 40 45

Pro Pro Gln Leu Arg His Arg Pro Glu Leu Pro His Val Ala Val Glu
50 55 60

Ala His Val Leu Leu Leu Val Ile Glu Val Ser Val Gln Glu Pro His
65 70 75 80

Pro Leu Arg Pro Ile Glu Glu Met Thr Leu Arg Arg Arg Val Leu Gln
85 90 95

Glu Thr Trp Ser Gly Val Pro Ser Gln Ser Gln Trp Gly Ala Gln His
100 105 110

His Gln Cys His Cys Gln Asn Cys His Ala Gly Ala Ser Arg Glu Pro
115 120 125

Gln Thr His His Ala Gly Glu Gln Asp Arg Thr Arg Gly Gln Ser
130 135 140

<210> 1165

<211> 63

<212> PRT

<213> Homo sapiens

<400> 1165

Cys Phe Leu Ala Asn Asn Ile Val Ile Lys Glu Thr Leu Thr Ile Arg
5 10 15

Asn Arg Asn Gly Ser His Lys Arg Lys Gln Gln Asn Pro Gln Thr Lys
20 25 30

Lys Gln Arg Arg Leu Phe Leu Ser Ser Leu Leu Leu Gly Thr His
 35 40 45

Glu Met Leu Gly Val Glu Val Ser Gln Leu Lys Lys Arg Gly Gly
 50 55 60

<210> 1166

<211> 50

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(50)

<223> Xaa = Any amino acid

<400> 1166

Tyr Ile Cys Glu Tyr Gly Leu Ser Phe Leu Ala Asp Gln Ile Ser Arg
 5 10 15

Arg Leu Leu Tyr Thr Xaa Glu Val His Ser Tyr Arg Lys Phe Lys Lys
 20 25 30

Ser Thr Leu Ser Phe Leu Ser Asn Ser Ser Glu Val Met Gly Ser Cys
 35 40 45

Ser Ser
 50

<210> 1167

<211> 115

<212> PRT

<213> Homo sapiens

<400> 1167

Thr Leu Pro Pro Asp Arg Met Lys Phe Ile Ser Thr Ser Leu Leu Leu
 5 10 15

Met Leu Leu Val Ser Ser Leu Ser Pro Val Gln Gly Val Leu Glu Val
 20 25 30

Tyr Tyr Thr Ser Leu Arg Cys Arg Cys Val Gln Glu Ser Ser Val Phe
 35 40 45

Ile Pro Arg Arg Phe Ile Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn
 50 55 60

Gly Cys Pro Arg Lys Glu Ile Ile Val Trp Lys Lys Asn Lys Ser Ile
 65 70 75 80

Val Cys Val Asp Pro Gln Ala Glu Trp Ile Gln Arg Met Met Glu Val
 85 90 95

Leu Arg Lys Arg Ser Ser Ser Thr Leu Pro Val Pro Val Phe Lys Arg
 100 105 110

Lys Ile Pro
 115

<210> 1168

```

<400> 1168
Glu Lys Glu Val Leu Gln Leu Tyr Gln Phe Gln Cys Leu Arg Glu Arg
      5                      10                      15

Phe Pro Asp Ala Asp Ile Ser Thr Lys Asn Thr Cys Ile Leu Pro Leu
      20                      25                      30

Ser Leu Leu Trp Ile Leu Val Leu Cys Leu Val Lys Ser Phe Pro Gly
      35                      40                      45

Lys Arg Thr Ser Pro Tyr Lys
      50                      55

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```
<210> 1169
<211> 51
<212> PRT
<213> Homo sapiens
```

```

<400> 1169
Ser His Ala Tyr Leu Tyr Gly Glu Val Leu Phe Pro Gly Lys Asp Leu
          5                      10                      15

Thr Lys His Lys Thr Lys Ile Gln Ser Arg Asp Lys Gly Arg Met Gln
          20                      25                      30

Val Phe Leu Val Glu Ile Ser Ala Ser Gly Asn Leu Ser Leu Lys His
          35                      40                      45

Trp Asn Trp
          50

```

```
<210> 1170
<211> 117
<212> PRT
<213> Homo sapiens
```

<400> 1170

Ala Ala Met Ala Arg Gly Pro Lys Lys His Leu Lys Arg Val Ala Ala
5 10 15

Pro Lys His Trp Met Leu Asp Lys Leu Thr Gly Val Phe Ala Pro Arg
20 25 30

Pro Ser Thr Gly Pro His Lys Leu Arg Glu Cys Leu Pro Leu Ile Ile
35 40 45

Phe Leu Arg Asn Arg Leu Lys Tyr Ala Leu Thr Gly Asp Glu Val Lys
50 55 60

Lys Ile Cys Met Gln Arg Phe Ile Lys Ile Asp Gly Lys Val Arg Thr
65 70 75 80

Asp Ile Thr Tyr Pro Ala Gly Phe Met Asp Val Ile Ser Ile Asp Lys
85 90 95

Thr Gly Glu Asn Phe Arg Leu Ile Tyr Asp Thr Lys Gly Arg Phe Ala
100 105 110

Val His Arg Ile Thr
115

<210> 1171

<211> 117

<212> PRT

<213> Homo sapiens

<400> 1171

Cys Asn Thr Met Tyr Ser Lys Ala Thr Leu Gly Val Ile Asp Gln Thr
5 10 15

Glu Ile Leu Ser Arg Leu Val Asn Ala Asp Asp Ile His Glu Ser Ser
20 25 30

Arg Val Gly Tyr Ile Ser Ser Asp Leu Ala Ile Asp Phe Asn Glu Pro
35 40 45

Leu His Ala Asn Leu Leu Tyr Phe Ile Ser Cys Gln Gly Ile Leu Lys
50 55 60

Ser Val Pro Gln Glu Asn Asp Glu Gly Glu Thr Leu Ser Gln Leu Val
65 70 75 80

Gly Thr Gly Gly Trp Thr Arg Ser Lys His Thr Gly Gln Phe Ile Gln
85 90 95

His Pro Met Leu Trp Ser Cys His Pro Leu Gln Met Leu Leu Gly Thr
100 105 110

Thr Ser His Gly Cys
115

<210> 1172

<211> 83

<212> PRT

<213> Homo sapiens

<400> 1172

Val Ile Ser Val Arg Thr Leu Pro Ser Ile Leu Met Asn Arg Cys Met
5 10 15

Gln Ile Phe Phe Thr Ser Ser Pro Val Arg Ala Tyr Leu Ser Leu Phe
20 25 30

Leu Arg Lys Met Met Arg Gly Arg His Ser Leu Asn Leu Trp Gly Pro
35 40 45

Val Asp Gly Arg Gly Ala Asn Thr Pro Val Asn Leu Ser Ser Ile Gln
50 55 60

Cys Phe Gly Ala Ala Thr Arg Phe Arg Cys Phe Leu Gly Pro Arg Ala
65 70 75 80

Met Ala Ala

<210> 1173

<211> 170

<212> PRT

<213> Homo sapiens

<400> 1173

Cys Tyr Ser Phe Ala Ser Met Gly Met Leu Glu Ala Arg Ile Arg Ile
 5 10 15

 Leu Thr Asn Asn Ser Gln Thr Pro Ile Leu Ser Pro Gln Glu Val Val
 20 25 30

 Ser Cys Ser Gln Tyr Ala Gln Gly Cys Asp Gly Gly Phe Pro Tyr Leu
 35 40 45

 Ile Ala Gly Lys Tyr Ala Gln Asp Phe Gly Leu Val Glu Glu Ala Cys
 50 55 60

 Phe Pro Tyr Thr Gly Thr Asp Ser Pro Cys Lys Met Lys Glu Asp Cys
 65 70 75 80

 Phe Arg Tyr Tyr Ser Ser Glu Tyr His Tyr Val Gly Gly Phe Tyr Gly
 85 90 95

 Gly Cys Asn Glu Ala Leu Met Lys Leu Glu Leu Val His His Gly Pro
 100 105 110

 Met Ala Val Ala Phe Glu Val Tyr Asp Asp Phe Leu His Tyr Lys Lys
 115 120 125

 Gly Ile Tyr His His Thr Gly Leu Arg Asp Pro Phe Asn Pro Phe Glu
 130 135 140

 Leu Thr Asn His Ala Val Leu Leu Val Gly Tyr Gly Thr Asp Ser Ala
 145 150 155 160

 Ser Gly Met Asp Tyr Trp Ile Val Lys Asn
 165 170

<210> 1174

<211> 91

<212> PRT

<213> Homo sapiens

<400> 1174

Lys Gly Leu Leu Asp Gln Cys Gly Gly Arg Ser Pro Phe Cys Ser Gly
 5 10 15

 Gly Ser His His Ile Leu Gln Lys Gln Leu Pro Trp Ala His Asp Gly
 20 25 30

 Pro Thr Gln Ala Ser Ser Gly Leu His Cys Ser Leu His Arg Asn Leu
 35 40 45

 Leu His Ser Gly Thr Gln Arg Ser Asn Asn Glu Ser Ser Leu Pro Ser
 50 55 60

 Phe Cys Met Glu Asn Gln Cys Leu Cys Arg Gly Ser Lys Leu Leu Pro
 65 70 75 80

 Pro Ala Gln Asn Leu Gly Arg Thr Phe Leu Gln
 85 90

<210> 1175
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 1175
 Thr Ser Val Val Val Asp Pro Leu Phe Val Val Glu Glu Val Ile Ile
 5 10 15
 Tyr Phe Lys Ser Asn Cys His Gly Pro Met Met Asp Gln Leu Lys Leu
 20 25 30
 His Gln Gly Phe Ile Ala Ala Ser Ile Glu Thr Ser Tyr Ile Val Val
 35 40 45
 Leu Arg Gly Val Ile Thr Lys Ala Val Phe Leu His Phe Ala Trp Arg
 50 55 60
 Ile Ser Ala Cys Val Gly Glu Ala Ser Phe Phe His Gln Pro Lys Ile
 65 70 75 80
 Leu Gly Val Leu Ser Cys Asn Lys Val Trp Glu Ala Ala Ile Thr Ala
 85 90 95
 Leu Ser Ile Leu Ala Thr Arg His Asn Leu Leu Arg Ala
 100 105

<210> 1176
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 1176
 Ser His Ala Tyr Leu Tyr Gly Glu Val Leu Phe Pro Gly Lys Asp Leu
 5 10 15
 Thr Lys His Lys Thr Lys Ile Gln Ser Arg Asp Lys Gly Arg Met Gln
 20 25 30
 Val Phe Leu Val Glu Ile Ser Ala Ser Gly Asn Leu Ser Leu Lys His
 35 40 45
 Trp Asn Trp
 50

<210> 1177
 <211> 78
 <212> PRT
 <213> Homo sapiens

<400> 1177
 Arg Cys Arg Cys Val Gln Glu Ser Ser Val Phe Ile Pro Arg Arg Phe
 5 10 15
 Ile Asp Arg Ile Gln Ile Leu Pro Arg Gly Ser Gly Cys Pro Arg Lys
 20 25 30
 Glu Ile Ile Val Trp Lys Lys Asn Lys Ser Ile Val Cys Val Gly Pro
 35 40 45
 Gln Ala Glu Trp Ile Gln Arg Met Met Glu Val Leu Arg Lys Arg Ser

50 55 60
 Ser Ser Thr Leu Pro Val Pro Val Phe Lys Arg Lys Ile Pro
 65 70 75

 <210> 1178
 <211> 53
 <212> PRT
 <213> Homo sapiens

 <400> 1178
 Ile Phe Ser Arg Lys Lys Asn Phe Pro Ile Gln Ile Ser Met Arg Leu
 5 10 15
 Cys Lys Asn Asn Leu Val Glu Ala Asp Gly Ala Asn Ser Ser Phe Phe
 20 25 30
 Thr His Ser Thr Leu Tyr Thr Leu Gly Val Cys Ile Leu Ile His Gln
 35 40 45
 Gly Gly Lys Phe Leu
 50

 <210> 1179
 <211> 55
 <212> PRT
 <213> Homo sapiens

 <400> 1179
 Glu Lys Glu Val Leu Gln Leu Tyr Gln Phe Gln Cys Leu Arg Glu Arg
 5 10 15
 Phe Pro Asp Ala Asp Ile Ser Thr Lys Asn Thr Cys Ile Leu Pro Leu
 20 25 30
 Ser Leu Leu Trp Ile Leu Val Leu Cys Leu Val Lys Ser Phe Pro Gly
 35 40 45
 Lys Arg Thr Ser Pro Tyr Lys
 50 55

 <210> 1180
 <211> 99
 <212> PRT
 <213> Homo sapiens

 <400> 1180
 Leu Ser Phe Leu Glu Val Leu Cys Thr Tyr Ala Pro His Leu Tyr Leu
 5 10 15
 Ala Phe Ala Trp Ser Asp His Ser Ser Phe Ser Leu Thr Leu Asn Val
 20 25 30
 Glu Asn Val Ala Ile Val Ala Ala Cys Val Val Thr Leu Leu Leu Leu
 35 40 45
 Ser Asn Phe Leu Thr Leu Lys Lys Gly Arg Met Ser Ala Ser Glu Cys
 50 55 60
 Asp Phe Leu Leu Thr Cys Ser Leu Asp Arg Leu Phe Ser Ile Val Phe

65		70		75		80									
Phe	Leu	Ser	Phe	Ser	Pro	Ser	Thr	Thr	Arg	Glu	Thr	Ala	Pro	Asp	Gly
				85					90					95	

Lys Asp Ile

<210> 1181
 <211> 57
 <212> PRT
 <213> Homo sapiens

<400> 1181															
Tyr	Phe	Phe	Cys	His	Phe	Leu	His	Gln	Gln	Pro	Gly	Arg	Leu	His	Leu
				5					10					15	

Met	Glu	Lys	Ile	Tyr	Asp	Cys	Phe	Met	Thr	Phe	Leu	Asn	Tyr	Leu	Phe
			20					25					30		

Phe	Ile	Pro	His	Leu	Arg	Phe	Trp	Trp	Ser	Pro	Phe	Cys	Ile	Ile	Val
		35				40						45			

Leu	Arg	Met	Ile	Lys	Lys	Asn	Asn	Asn
	50					55		

<210> 1182
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 1182															
Ser	Ser	His	Ile	Ser	Phe	Pro	Ser	Gly	Ala	Val	Ser	Leu	Val	Val	Asp
				5					10					15	

Gly	Glu	Asn	Asp	Lys	Lys	Asn	Thr	Ile	Leu	Lys	Ser	Leu	Ser	Lys	Glu
		20					25					30			

Gln	Val	Ser	Arg	Lys	Ser	His	Ser	Glu	Ala	Leu	Ile	Leu	Pro	Phe	Phe
		35				40					45				

Ser	Val	Arg	Lys	Leu	Leu	Lys	Arg	Arg	Ser	Val	Thr	Thr	Gln	Ala	Ala
	50					55				60					

Thr	Met	Ala	Thr	Phe	Ser	Thr	Phe	Asn	Val	Arg	Glu	Lys	Glu	Leu	Trp
65					70				75					80	

Ser	Leu	His	Ala	Lys	Ala	Arg
				85		

<210> 1183
 <211> 53
 <212> PRT
 <213> Homo sapiens

<400> 1183															
Ala	Met	Leu	Phe	Leu	Gln	Lys	Thr	Asp	Gly	Cys	Trp	Leu	Phe	Arg	Ala
				5					10					15	

Ser	Leu	Met	Gly	Cys	Gly	Asn	Ser	Lys	Asn	Val	Pro	Gln	Cys	Gln	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

20 25 30
 Cys Arg Lys Ile Asn Gly Met Gly Ser Val Leu Ser Leu Val Val Ile
 35 40 45

Phe Phe Tyr His Pro
 50

<210> 1184
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 1184
 Ser Thr His Ser Ala Phe Leu Gln Cys Lys Lys Val Ala Gln Lys Lys
 5 10 15

Lys Arg Asp Asn Thr Ser Cys Tyr Asn Gly Tyr Ile Leu Tyr Ile Gln
 20 25 30

Cys Lys Arg Glu Gly Ala Met Val Thr Pro Cys Lys Gly Gln Ile Glu
 35 40 45

Met Trp Cys Val Cys Ala Glu Tyr Leu Lys Lys
 50 55

<210> 1185
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 1185
 Thr Leu Pro Pro Asp Arg Met Lys Phe Ile Ser Thr Ser Leu Leu Leu
 5 10 15

Met Leu Leu Val Ser Ser Leu Ser Pro Val Gln Gly Val Leu Glu Val
 20 25 30

Tyr Tyr Thr Ser Leu Arg Cys Arg Cys Val Gln Glu Ser Ser Val Phe
 35 40 45

Ile Pro Arg Arg Phe Ile Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn
 50 55 60

Gly Cys Pro Arg Lys Glu Ile Ile Val Trp Lys Lys Asn Lys Ser Ile
 65 70 75 80

Val Cys Val Asp Pro Gln Ala Glu Trp Ile Gln Arg Met Met Glu Val
 85 90 95

Leu Arg Lys Arg Ser Ser Ser Thr Leu Pro Val Pro Val Phe Lys Arg
 100 105 110

Lys Ile Pro
 115

<210> 1186
 <211> 55
 <212> PRT
 <213> Homo sapiens

<400> 1186

Glu Lys Glu Val Leu Gln Leu Tyr Gln Phe Gln Cys Leu Arg Glu Arg
5 10 15

Phe Pro Asp Ala Asp Ile Ser Thr Lys Asn Thr Cys Ile Leu Pro Leu
20 25 30

Ser Leu Leu Trp Ile Leu Val Leu Cys Leu Val Lys Ser Phe Pro Gly
35 40 45

Lys Arg Thr Ser Pro Tyr Lys
50 55

<210> 1187

<211> 51

<212> PRT

<213> Homo sapiens

<400> 1187

Ser His Ala Tyr Leu Tyr Gly Glu Val Leu Phe Pro Gly Lys Asp Leu
5 10 15

Thr Lys His Lys Thr Lys Ile Gln Ser Arg Asp Lys Gly Arg Met Gln
20 25 30

Val Phe Leu Val Glu Ile Ser Ala Ser Gly Asn Leu Ser Leu Lys His
35 40 45

Trp Asn Trp
50

<210> 1188

<211> 98

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1) . . . (98)

<223> Xaa = Any amino acid

<400> 1188

Pro Asn Cys Leu Ser Asn Val Cys Ile Asn Cys Glu Ser Gln Xaa Xaa
5 10 15

Gln Leu Leu Ser Arg Ile Tyr Ser Leu Thr Ser Asn Lys Gln Ala Leu
20 25 30

Arg Asp Thr Glu Ser Gln Ile Gln Ile Leu Pro Met Gly Ile Lys Arg
35 40 45

Leu Arg Leu Ser Pro His Leu Glu Asn Tyr Leu His His Lys Tyr Ile
50 55 60

Ile Thr Gly Ser Leu Tyr Glu Ala Asp Thr Lys Cys Tyr Arg His Ser
65 70 75 80

Gln Asn Ile Ile Leu Gly Asn Asn Val Ile Lys Met Pro Asn Leu Ser
85 90 95

Gln Gln

<210> 1189
 <211> 142
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(142)
 <223> Xaa = Any amino acid

<400> 1189
 Trp Thr Xaa Leu Glu Gly Val Glu Val Gln Thr Asp Tyr Val Pro Leu
 5 10 15
 Leu Asn Ser Leu Ala Ala Tyr Gly Trp Gln Leu Thr Cys Val Leu Pro
 20 25 30
 Thr Pro Val Val Lys Thr Thr Ser Glu Gly Ser Val Ser Thr Lys Gln
 35 40 45
 Ile Val Phe Leu Gln Arg Pro Cys Leu Pro Gln Lys Ile Lys Lys Lys
 50 55 60
 Glu Ser Lys Phe Gln Trp Arg Phe Ser Arg Glu Glu Met His Asn Arg
 65 70 75 80
 Gln Met Arg Lys Ser Lys Gly Lys Leu Ser Ala Arg Asp Lys Gln Gln
 85 90 95
 Ala Glu Glu Asn Glu Lys Asn Leu Glu Asp Gln Ser Ser Lys Ala Gly
 100 105 110
 Asp Met Gly Asn Cys Val Ser Gly Gln Gln Gln Glu Gly Gly Val Ser
 115 120 125
 Glu Glu Met Lys Gly Pro Val Gln Glu Asp Lys Gly Glu Gln
 130 135 140

<210> 1190
 <211> 64
 <212> PRT
 <213> Homo sapiens

<400> 1190
 Thr Arg Trp Arg Pro Met Ala Gly Ser Ser Pro Val Cys Tyr Gln Leu
 5 10 15
 Pro Ser Ser Arg Leu Pro Ala Arg Gly Val Tyr Pro Pro Ser Arg Leu
 20 25 30
 Ser Phe Phe Arg Asp Leu Val Tyr Leu Arg Lys Ser Arg Arg Arg Asn
 35 40 45
 Arg Ser Phe Ser Gly Asp Ser Pro Glu Lys Lys Cys Thr Thr Gly Arg
 50 55 60

<210> 1191

```
<211> 86
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> variant  
<222> (1)...(86)  
<223> Xaa = Any amino acid
```

```
<400> 1191
Asp Xaa Pro Gly Arg Cys Arg Ser Ala Asp Arg Leu Arg Ala Pro Ala
           5                      10                  15

Glu Leu Ala Gly Gly Leu Trp Leu Ala Ala His Leu Cys Ala Thr Asn
          20                25              30

Ser Arg Arg Gln Asp Tyr Gln Arg Gly Glu Cys Ile His Gln Ala Asp
      35                 40             45

Cys Leu Ser Ser Glu Thr Leu Ser Thr Ser Glu Asn Gln Glu Glu Gly
    50                   55               60

Ile Glu Val Ser Val Ala Ile Leu Gln Arg Arg Asn Ala Gln Gln Ala
   65                     70             75                    80

Asp Glu Glu Ile Lys Arg
        85
```

```
<210> 1192
<211> 73
<212> PRT
<213> Homo sapiens
```

```

<400> 1192
Cys Ser Pro Leu Ser Ser Trp Thr Gly Pro Phe Ile Ser Ser Glu Thr
          5                      10                      15

Pro Pro Ser Cys Cys Cys Pro Glu Thr Gln Phe Pro Met Ser Pro Ala
          20                      25                      30

Leu Glu Asp Trp Ser Ser Lys Phe Phe Ser Phe Ser Ser Ala Cys Cys
          35                      40                      45

Leu Ser Leu Ala Leu Ser Leu Pro Phe Asp Phe Leu Ile Cys Leu Leu
          50                      55                      60

Cys Ile Ser Ser Leu Glu Asn Arg His
          65                      70

```

```
<210> 1193
<211> 52
<212> PRT
<213> Homo sapiens
```

```

<400> 1193
Val Leu Pro Cys Pro Leu Gly Gln Gly Pro Ser Ser Pro Arg Arg Leu
          5          10          15

His Pro Pro Ala Val Leu Lys His Ser Phe Pro Cys Leu Gln Leu
      20          25          30

```

Trp Lys Thr Gly Leu Leu Ser Ser Ser His Phe Leu Leu Leu Val Val
35 40 45

Cys Leu Trp His
50

```
<210> 1194
<211> 115
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> variant  
<222> (1)...(115)  
<223> Xaa = Any amino acid
```

<400> 1194
Thr Leu Pro Pro Asp Arg Met Lys Phe Ile Ser Thr Ser Leu Leu Leu
 5 10 15

Met Leu Leu Val Ser Ser Leu Ser Pro Val Gln Gly Val Leu Glu Val
20 25 30

Tyr Tyr Thr Ser Leu Arg Cys Arg Cys Val Gln Xaa Ser Ser Val Phe
35 40 45

Ile Pro Xaa Arg Phe Ile Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn
50 55 60

Gly Cys Pro Arg Lys Glu Ile Ile Val Trp Lys Lys Asn Lys Ser Ile
65 70 75 80

Val Cys Val Asp Pro Gln Ala Glu Trp Ile Gln Arg Met Met Glu Val
85 90 95

Leu Arg Lys Arg Ser Ser Ser Thr Leu Pro Val Pro Val Phe Lys Arg
100 105 110

Lys Ile Pro
115

```
<210> 1195
<211> 70
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> variant
<222> (1)...(70)
<223> Xaa = Any amino acid
```

<400> 1195
Leu Pro Pro Phe Leu Ser Glu Leu Phe Leu Leu His Ile Thr Ala Ala
5 10 15

Thr Thr Ala Pro Val Ile Thr Ala Pro Arg Arg Thr Arg Pro Ala Met
20 25 30

Met Pro Thr Met Gly Met Val Gly Trp Glu Asp Ser Ser His Leu Xaa
35 40 45

Val Arg Gly Leu Gly Arg Pro Ser Cys Cys Thr Trp Gln Val Tyr Leu
 50 55 60

Cys Ser Ser Pro Glu Gly
 65 70

<210> 1196
 <211> 63
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(63)
 <223> Xaa = Any amino acid

<400> 1196
 Ala Leu Pro Pro Pro His His Gly Ser Asp His Ser Ser Ser Asp His
 5 10 15

Ser Ser Lys Glu Asn Gln Ala Ser Asn Asp Ala His Asp Gly Asp Gly
 20 25 30

Gly Leu Gly Arg Gln Leu Pro Ser Xaa Gly Glu Gly Leu Gly Gln Thr
 35 40 45

Leu Met Leu His Met Ala Gly Val Ser Leu Leu Leu Ser Arg Arg
 50 55 60

<210> 1197
 <211> 50
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(50)
 <223> Xaa = Any amino acid

<400> 1197
 Gly Ser Ala Gln Ala Pro His Xaa Glu Met Gly Ala Val Phe Pro Ala
 5 10 15

His His Pro His Arg Gly His His Cys Trp Pro Gly Ser Pro Trp Ser
 20 25 30

Cys Asp His Trp Ser Cys Gly Arg Cys Arg Asp Val Glu Glu Glu Glu
 35 40 45

Leu Arg
 50

<210> 1198
 <211> 92
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(92)

<223> Xaa = Any amino acid

<400> 1198

```

Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys His Val Gln His Glu Gly
           5                      10                      15

Leu Pro Lys Pro Leu Thr Xaa Arg Trp Glu Leu Ser Ser Gln Pro Thr
           20                      25                      30

Ile Pro Ile Val Gly Ile Ile Ala Gly Leu Val Leu Leu Gly Ala Val
           35                      40                      45

Ile Thr Gly Ala Val Val Ala Ala Val Met Trp Arg Arg Lys Ser Ser
           50                      55                      60

Asp Arg Lys Gly Gly Ser Tyr Thr Gln Ala Ala Ser Ser Asp Ser Ala
           65                      70                      75                      80

Gln Gly Ser Asp Val Ser Leu Thr Ala Cys Lys Val
           85                      90

```

<210> 1199

<211> 55

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(55)

<223> Xaa = Any amino acid

<400> 1199

```

Glu Lys Glu Val Leu Gln Leu Tyr Gln Phe Gln Cys Leu Arg Glu Arg
           5                      10                      15

Phe Pro Asp Ala Asp Ile Ser Thr Lys Asn Thr Cys Ile Leu Pro Leu
           20                      25                      30

Ser Leu Leu Trp Ile Leu Val Leu Xaa Leu Val Lys Ser Phe Pro Gly
           35                      40                      45

Lys Arg Thr Ser Pro Tyr Lys
           50                      55

```

<210> 1200

<211> 115

<212> PRT

<213> Homo sapiens

<400> 1200

```

Thr Leu Pro Pro Asp Arg Met Lys Phe Ile Ser Thr Ser Leu Leu Leu
           5                      10                      15

Met Leu Leu Val Ser Ser Leu Ser Pro Val Gln Gly Val Leu Glu Val
           20                      25                      30

Tyr Tyr Thr Ser Leu Arg Cys Arg Cys Val Gln Glu Ser Ser Val Phe
           35                      40                      45

Ile Pro Arg Arg Phe Ile Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn
           50                      55                      60

```

Gly Cys Pro Arg Lys Glu Ile Ile Val Trp Lys Lys Asn Lys Ser Ile
 65 70 75 80
 Val Cys Val Asp Pro Gln Ala Glu Trp Ile Gln Arg Met Met Glu Val
 85 90 95
 Leu Arg Lys Arg Ser Ser Ser Thr Leu Pro Val Pro Val Phe Lys Arg
 100 105 110
 Lys Ile Pro
 115

<210> 1201
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(51)
 <223> Xaa = Any amino acid

<400> 1201
 Ser His Ala Tyr Leu Tyr Gly Glu Val Leu Phe Pro Gly Lys Asp Leu
 5 10 15
 Thr Lys Xaa Lys Thr Lys Ile Gln Ser Arg Asp Lys Gly Arg Met Gln
 20 25 30
 Val Phe Leu Val Glu Ile Ser Ala Ser Gly Asn Leu Ser Leu Lys His
 35 40 45
 Trp Asn Trp
 50

<210> 1202
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 1202
 Thr Leu Pro Pro Asp Arg Met Lys Phe Ile Ser Thr Ser Leu Leu Leu
 5 10 15
 Met. Leu Leu Val Ser Ser Leu Ser Pro Val Gln Gly Val Leu Glu Val
 20 25 30
 Tyr Tyr Thr Ser Leu Arg Cys Arg Cys Val Gln Glu Ser Ser Val Phe
 35 40 45
 Ile Pro Arg Arg Phe Ile Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn
 50 55 60
 Gly Cys Pro Arg Lys Glu Ile Ile Val Trp Lys Lys Asn Lys Ser Ile
 65 70 75 80
 Val Cys Val Asp Pro Gln Ala Glu Trp Ile Gln Arg Met Met Glu Val
 85 90 95
 Leu Arg Lys Arg Ser Ser Ser Thr Leu Pro Val Pro Val Phe Lys Arg

100 105 110

Lys Ile Pro
115

<210> 1203
<211> 55
<212> PRT
<213> Homo sapiens

<400> 1203
Glu Lys Glu Val Leu Gln Leu Tyr Gln Phe Gln Cys Leu Arg Glu Arg
5 10 15
Phe Pro Asp Ala Asp Ile Ser Thr Lys Asn Thr Cys Ile Leu Pro Leu
20 25 30
Ser Leu Leu Trp Ile Leu Val Leu Cys Leu Val Lys Ser Phe Pro Gly
35 40 45
Lys Arg Thr Ser Pro Tyr Lys
50 55

<210> 1204
<211> 51
<212> PRT
<213> Homo sapiens

<400> 1204
Ser His Ala Tyr Leu Tyr Gly Glu Val Leu Phe Pro Gly Lys Asp Leu
5 10 15
Thr Lys His Lys Thr Lys Ile Gln Ser Arg Asp Lys Gly Arg Met Gln
20 25 30
Val Phe Leu Val Glu Ile Ser Ala Ser Gly Asn Leu Ser Leu Lys His
35 40 45
Trp Asn Trp
50

<210> 1205
<211> 50
<212> PRT
<213> Homo sapiens

<400> 1205
Arg Ile Gly Phe Ser His Gln Gly Tyr Asn Cys Trp Trp Trp Cys His
5 10 15
Ser Thr His Pro Gln Ile Ser Asp Trp Glu Glu Arg Thr Thr Glu Asp
20 25 30
Cys Leu Lys Asp Ala Trp Ile Pro Cys Tyr Leu Arg Thr Leu Asn Thr
35 40 45
Leu Thr
50

<210> 1206
<211> 134
<212> PRT
<213> Homo sapiens

<400> 1206
Ala Ser Ala Glu Phe Glu Met Ala Gly Gly Lys Ala Gly Lys Asp Ser
5 10 15
Gly Lys Ala Lys Thr Lys Ala Val Ser Arg Ser Gln Arg Ala Gly Leu
20 25 30
Gln Phe Pro Val Gly Arg Ile His Arg His Leu Lys Ser Arg Thr Thr
35 40 45
Ser His Gly Arg Val Gly Ala Thr Ala Ala Val Tyr Ser Ala Ala Ile
50 55 60
Leu Glu Tyr Leu Thr Ala Glu Val Leu Glu Leu Ala Gly Asn Ala Ser
65 70 75 80
Lys Asp Leu Lys Val Lys Arg Ile Thr Pro Arg His Leu Gln Leu Ala
85 90 95
Ile Arg Gly Asp Glu Glu Leu Asp Ser Leu Ile Lys Ala Thr Ile Ala
100 105 110
Gly Gly Gly Val Ile Pro His Ile His Lys Ser Leu Ile Gly Lys Lys
115 120 125

Gly Gln Gln Lys Thr Val
130

<210> 1207
<211> 67
<212> PRT
<213> Homo sapiens

<400> 1207
Arg Cys Asp Glu Gly Val Gly Gly Gly Ile Ser Pro Trp Val Arg Leu
5 10 15
Ala Phe Ser Leu Pro Cys Leu Leu Glu Leu Gln Arg Asn Ser Lys Trp
20 25 30
Leu Ala Val Arg Leu Glu Arg Thr Pro Glu Arg Pro Arg Gln Arg Arg
35 40 45
Phe Pro Ala Arg Arg Glu Pro Ala Cys Ser Ser Gln Trp Ala Val Phe
50 55 60

Ile Asp Thr
65

<210> 1208
<211> 60
<212> PRT
<213> Homo sapiens

<400> 1208
Asp Asn Lys Glu Ser Arg His Pro Leu Asp Ser Leu Leu Leu Ser Phe

399

	5		10		15										
Leu	Pro	Asn	Gln	Arg	Phe	Val	Asp	Val	Trp	Asn	Asp	Thr	Thr	Thr	Ser
		20						25					30		
Asn	Cys	Ser	Leu	Asp	Glu	Arg	Ile	Gln	Phe	Phe	Ile	Ser	Thr	Asn	Ser
		35					40					45			
Lys	Leu	Gln	Val	Thr	Arg	Gly	Asn	Thr	Leu	Tyr	Leu				
	50					55					60				

<210> 1209
 <211> 64
 <212> PRT
 <213> Homo sapiens

	5		10		15										
Ile	Arg	Pro	Thr	Gly	Asn	Cys	Lys	Pro	Ala	Leu	Cys	Glu	Arg	Glu	Thr
				5					10					15	
Ala	Phe	Val	Leu	Ala	Phe	Pro	Glu	Ser	Phe	Pro	Ala	Leu	Pro	Pro	Ala
		20					25						30		
Ile	Ser	Asn	Ser	Ala	Glu	Ala	Gln	Ala	Ser	Lys	Ala	Glu	Lys	Arg	Leu
		35					40					45			
Ile	Gly	Pro	Thr	Val	Arg	Ser	His	His	Leu	Leu	Leu	Arg	Arg	Thr	Ala
	50					55						60			

<210> 1210
 <211> 53
 <212> PRT
 <213> Homo sapiens

	5		10		15										
Ile	Leu	Gly	Val	Asp	Glu	Tyr	Gly	Pro	Leu	Gly	Thr	Ala	Ser	Arg	Leu
				5					10					15	
Ser	Ala	Ser	Gly	Lys	Pro	Pro	Leu	Ser	Trp	Pro	Phe	Arg	Ser	Pro	Phe
		20					25						30		
Gln	Pro	Tyr	Arg	Gln	Pro	Phe	Arg	Ile	Pro	Leu	Lys	Leu	Lys	Gln	Ala
		35					40					45			
Arg	Gln	Arg	Lys	Gly											
	50														

<210> 1211
 <211> 99
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(99)
 <223> Xaa = Any amino acid

	5		10		15										
Pro	Pro	Leu	Asp	Pro	Gly	Ala	Gln	Gly	Gly	Gly	Gly	Glu	His	Gln	Arg
				5					10					15	

Trp Arg Ser Gln Val Val Pro Gly Asp Ser Gln Glu Ser Gly Val Arg
 20 25 30
 Arg Leu Gln Asp Leu Ser Arg Leu Cys Arg Tyr Leu Thr Ala Phe Phe
 35 40 45
 Thr Leu Leu Leu Leu Gly Ser Glu Gln Met Ala Leu Pro Cys Thr Val
 50 55 60
 Thr Lys Thr Met Xaa Ser Leu Glu Gln Xaa Xaa Asp Xaa Trp Xaa His
 65 70 75 80
 Val Phe Ser Phe Leu Xaa Gly Met Ala Pro Leu Lys Tyr Ser Arg Xaa
 85 90 95
 Ala Leu Pro

<210> 1212
 <211> 86
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(86)
 <223> Xaa = Any amino acid

<400> 1212
 Thr Pro Thr Val Glu Val Pro Gly Ser Pro Gly Arg Gln Ser Gly Val
 5 10 15
 Trp Gly Glu Glu Ala Ser Arg Pro Leu Lys Ala Leu Gln Val Phe Asn
 20 25 30
 Cys Ile Leu His Ser Leu Val Val Gly Val Arg Thr Asp Gly Pro Ala
 35 40 45
 Leu His Ser Tyr Lys Asn Asp Gly Xaa Pro Gly Ala Xaa Xaa Arg Xaa
 50 55 60
 Leu Xaa Pro Arg Leu Gln Leu Ser Xaa Gly Asn Gly Ser Leu Glu Val
 65 70 75 80
 Leu Gln Ala Xaa Thr Pro
 85

<210> 1213
 <211> 64
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(64)
 <223> Xaa = Any amino acid

<400> 1213
 Gly Ser Xaa Cys Leu Glu Tyr Phe Lys Gly Ala Ile Pro Xaa Arg Lys
 5 10 15

Leu Lys Thr Trp Xaa Gln Xaa Ser Xaa Xaa Cys Ser Arg Xaa Ala Ile
 20 25 30
 Val Phe Val Thr Val Gln Gly Arg Ala Ile Cys Ser Asp Pro Asn Asn
 35 40 45
 Lys Arg Val Lys Asn Ala Val Lys Tyr Leu Gln Ser Leu Glu Arg Ser
 50 55 60

<210> 1214
 <211> 84
 <212> PRT
 <213> Homo sapiens

<400> 1214
 Pro Pro Leu Asp Pro Gly Ala Gln Gly Gly Gly Glu His Gln Arg
 5 10 15
 Trp Arg Ser Gln Val Val Pro Gly Asp Ser Gln Glu Ser Gly Val Arg
 20 25 30
 Arg Leu Gln Asp Leu Ser Arg Leu Cys Arg Tyr Leu Thr Ala Phe Phe
 35 40 45
 Thr Leu Leu Leu Leu Gly Ser Glu Gln Met Ala Leu Pro Cys Thr Val
 50 55 60
 Thr Lys Thr Met Ala Ser Leu Glu Gln Ser Ser Asp Val Trp Tyr His
 65 70 75 80
 Val Phe Ser Phe

<210> 1215
 <211> 71
 <212> PRT
 <213> Homo sapiens

<400> 1215
 Thr Pro Thr Val Glu Val Pro Gly Ser Pro Gly Arg Gln Ser Gly Val
 5 10 15
 Trp Gly Glu Glu Ala Ser Arg Pro Leu Lys Ala Leu Gln Val Phe Asn
 20 25 30
 Cys Ile Leu His Ser Leu Val Val Gly Val Arg Thr Asp Gly Pro Ala
 35 40 45
 Leu His Ser Tyr Lys Asn Asp Gly Ile Pro Gly Ala Val Leu Arg Cys
 50 55 60
 Leu Val Pro Arg Leu Gln Leu
 65 70

<210> 1216
 <211> 199
 <212> PRT
 <213> Homo sapiens

<400> 1216

His Leu Ile Tyr Lys Cys Gly Gly Ile Asp Lys Arg Thr Ile Glu Lys
 5 10 15

 Phe Gly Lys Glu Ala Ala Glu Met Gly Lys Gly Ser Phe Lys Tyr Ala
 20 25 30

 Trp Val Leu Asp Lys Leu Lys Ala Glu Arg Glu Arg Gly Ile Thr Ile
 35 40 45

 Asp Ile Ser Leu Trp Lys Phe Glu Thr Ser Lys Tyr Tyr Val Thr Ile
 50 55 60

 Ile Asp Ala Pro Gly His Arg Asp Phe Ile Lys Asn Met Ile Thr Gly
 65 70 75 80

 Thr Ser Gln Ala Asp Cys Ala Val Leu Ile Val Ala Ala Gly Val Gly
 85 90 95

 Glu Phe Glu Ala Gly Ile Ser Lys Asn Gly Gln Thr Arg Glu His Ala
 100 105 110

 Leu Leu Ala Tyr Thr Leu Gly Val Lys Gln Leu Ile Val Gly Val Asn
 115 120 125

 Lys Met Asp Ser Thr Glu Pro Pro Tyr Ser Gln Lys Arg Tyr Glu Glu
 130 135 140

 Ile Val Lys Glu Val Ser Thr Tyr Ile Lys Lys Ile Gly Tyr Asn Pro
 145 150 155 160

 Asp Thr Val Ala Phe Val Pro Ile Ser Gly Trp Asn Gly Asp Asn Met
 165 170 175

 Leu Glu Pro Ser Ala Asn Met Pro Trp Phe Lys Gly Trp Lys Val Thr
 180 185 190

 Arg Lys Asp Gly Asn Ala Ser
 195

<210> 1217

<211> 76

<212> PRT

<213> Homo sapiens

<400> 1217

Thr Gly Ile Ala Ile Leu Thr Gly Asp Phe Pro Ser Leu Glu Pro Arg
 5 10 15

 His Val Ser Thr Trp Leu Gln His Val Val Thr Ile Pro Thr Arg Asn
 20 25 30

 Trp His Lys Cys Tyr Cys Val Gly Val Val Ala Asn Phe Leu Asn Val
 35 40 45

 Ser Ala Asp Phe Leu Asn Asn Phe Leu Ile Ser Leu Leu Ala Val Gly
 50 55 60

 Trp Leu Ser Gly Ile His Phe Val Asn Thr Asp Asn
 65 70 75

<210> 1218
 <211> 122
 <212> PRT
 <213> Homo sapiens

<400> 1218
 Leu Phe His Thr Gln Cys Val Ser Gln Lys Gly Met Leu Ser Gly Leu
 5 10 15
 Pro Ile Leu Gly Asp Thr Ser Phe Lys Phe Thr Asn Thr Ser Ser Asn
 20 25 30
 Asn Gln Asp Ser Thr Val Ser Leu Arg Cys Pro Cys Asn His Val Phe
 35 40 45
 Asp Lys Val Ser Val Ser Trp Gly Ile Asn Asp Ser His Ile Val Leu
 50 55 60
 Ala Gly Leu Lys Phe Pro Gln Gly Asp Ile Asn Gly Asp Thr Thr Phe
 65 70 75 80
 Thr Leu Ser Phe Gln Phe Ile Gln Asp Pro Gly Ile Leu Glu Gly Ala
 85 90 95
 Leu Ser His Leu Ser Ser Leu Leu Pro Lys Phe Phe Asn Gly Ser Phe
 100 105 110
 Val Asp Ala Thr Ala Phe Ile Asp Gln Met
 115 120

<210> 1219
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 1219
 Tyr Leu Leu Val Ser Asn Phe His Lys Glu Ile Ser Met Val Ile Pro
 5 10 15
 Arg Ser Arg Ser Ala Phe Ser Leu Ser Lys Thr Gln Ala Tyr Leu Lys
 20 25 30
 Glu Pro Phe Pro Ile Ser Ala Ala Ser Phe Pro Asn Phe Ser Met Val
 35 40 45
 Leu Leu Ser Met Pro Pro His Leu
 50 55

<210> 1220
 <211> 62
 <212> PRT
 <213> Homo sapiens

<400> 1220
 Val Phe Leu Ser Pro Trp Val Lys Ser Glu Ser Gly Ser Leu Cys Leu
 5 10 15
 Ser Val Leu Val Tyr Cys Trp Ser Glu Ser Lys Phe Leu Ile Lys Ala
 20 25 30
 Val Asp Leu Ala Leu Thr Val Tyr Ala Asp Ile Gly Glu Thr Ile Trp

35 40 45
 Leu Phe Gln Thr Ser Gln Asp Leu Ser Lys Lys Thr Trp Leu
 50 55 60

<210> 1221
 <211> 86
 <212> PRT
 <213> Homo sapiens

<400> 1221
 Glu Pro Ser Gln Gln Leu Leu Ser Arg Ile Tyr Ser Leu Thr Ser Asn
 5 10 15
 Lys Gln Ala Leu Arg Asp Thr Glu Ser Gln Ile Gln Ile Leu Pro Met
 20 25 30
 Gly Ile Lys Arg Leu Arg Leu Ser Pro His Leu Glu Asn Tyr Leu His
 35 40 45
 His Lys Tyr Ile Ile Thr Gly Ser Leu Tyr Glu Ala Asp Thr Lys Cys
 50 55 60
 Tyr Arg His Ser Gln Asn Ile Ile Leu Gly Asn Asn Val Ile Lys Met
 65 70 75 80
 Pro Asn Leu Ser Gln Gln
 85

<210> 1222
 <211> 95
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(95)
 <223> Xaa = Any amino acid

<400> 1222.
 Pro Leu Xaa Val Ala Leu Ala Gln Arg Lys Glu Glu Arg Gln Ala His
 5 10 15
 Leu Thr Asn Gln Tyr Met Gln Arg Met Ala Ser Val Arg Ala Val Pro
 20 25 30
 Asn Pro Val Ile Asn Pro Tyr Gln Pro Ala Pro Pro Ser Gly Tyr Phe
 35 40 45
 Met Ala Ala Ile Pro Gln Thr Gln Asn Xaa Ala Ala Tyr Tyr Pro Pro
 50 55 60
 Ser Gln Ile Ala Gln Leu Arg Pro Ser Pro Arg Trp Thr Ala Gln Gly
 65 70 75 80
 Ala Arg Pro His Pro Phe Gln Asn Met Pro Gly Ala Ile Arg Pro
 85 90 95

<210> 1223
 <211> 115

<212> PRT

<213> Homo sapiens

<400> 1223

Thr Leu Pro Pro Asp Arg Met Lys Phe Ile Ser Thr Ser Leu Leu Leu
5 10 15
Met Leu Leu Val Ser Ser Leu Ser Pro Val Gln Gly Val Leu Glu Val
20 25 30
Tyr Tyr Thr Ser Leu Gly Cys Arg Cys Val Gln Glu Ser Ser Val Phe
35 40 45
Ile Pro Arg Arg Phe Ile Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn
50 55 60
Gly Cys Pro Arg Lys Glu Ile Ile Val Trp Lys Lys Asn Lys Ser Ile
65 70 75 80
Val Cys Val Asp Pro Gln Ala Glu Trp Ile Gln Arg Met Met Glu Val
85 90 95
Leu Arg Lys Arg Ser Phe Ser Thr Leu Pro Val Pro Val Phe Lys Arg
100 105 110
Lys Ile Pro
115

<210> 1224

<211> 51

<212> PRT

<213> Homo sapiens

<400> 1224

Ile Phe Ser Arg Lys Lys Asn Phe Pro Ile Gln Ile Ser Met Arg Leu
5 10 15
Cys Lys Asn Asn Leu Ala Glu Ala Asp Gly Ala Asn Ser Ser Phe Phe
20 25 30
Thr His Ser Thr Leu Tyr Thr Leu Gly Val Cys Ile Leu Ile His Gln
35 40 45
Gly Gly Lys
50

<210> 1225

<211> 64

<212> PRT

<213> Homo sapiens

<400> 1225

Ser Ser Ser Arg His Leu Cys Phe Ser Cys Cys Trp Ser Ala Ala Ser
5 10 15
Leu Gln Ser Lys Val Phe Trp Arg Ser Ile Thr Gln Ala Trp Gly Val
20 25 30
Asp Val Ser Lys Arg Ala Gln Ser Leu Ser Leu Asp Ala Ser Leu Ile
35 40 45

Glu Phe Lys Ser Cys Pro Val Gly Met Val Val Gln Glu Lys Lys Ser
 50 55 60

<210> 1226
 <211> 55
 <212> PRT
 <213> Homo sapiens

<400> 1226
 Glu Lys Glu Val Phe Gln Leu Tyr Gln Phe Gln Cys Leu Arg Glu Arg
 5 10 15

Phe Pro Asp Ala Asp Ile Ser Thr Lys Asn Thr Cys Ile Leu Pro Leu
 20 25 30

Ser Leu Leu Trp Ile Leu Val Leu Cys Leu Val Lys Ser Phe Pro Gly
 35 40 45

Lys Arg Thr Ser Pro Tyr Lys
 50 55

<210> 1227
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 1227
 Ser His Ala Tyr Leu Tyr Gly Glu Val Leu Phe Pro Gly Lys Asp Leu
 5 10 15

Thr Lys His Lys Thr Lys Ile Gln Ser Arg Asp Lys Gly Arg Met Gln
 20 25 30

Val Phe Leu Val Glu Ile Ser Ala Ser Gly Asn Leu Ser Leu Lys His
 35 40 45

Trp Asn Trp
 50

<210> 1228
 <211> 73
 <212> PRT
 <213> Homo sapiens

<400> 1228
 Tyr Ser Ile Phe Phe Cys His Phe Leu His Gln Gln Pro Gly Arg Leu
 5 10 15

His Leu Met Glu Lys Ile Tyr Asp Cys Phe Met Thr Phe Leu Asn Tyr
 20 25 30

Leu Phe Phe Ile Pro His Leu Arg Phe Trp Trp Ser Pro Phe Cys Ile
 35 40 45

Ile Val Leu Arg Met Ile Lys Lys Ile Thr Thr Arg Asp Asn Thr Glu
 50 55 60

Pro Ile Pro Phe Ile Phe Leu Gln Gly
 65 70

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<210> 1229
<211> 70
<212> PRT
<213> Homo sapiens
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<400> 1229
Ser Phe Ser Leu Thr Leu Asn Val Glu Asn Val Ala Ile Val Ala Ala
      5              10              15

Cys Val Val Thr Leu Leu Leu Leu Ser Asn Phe Leu Thr Leu Lys Lys
      20              25              30

Gly Arg Met Ser Ala Ser Glu Cys Asp Phe Leu Leu Thr Cys Ser Leu
      35              40              45

Asp Arg Leu Phe Ser Ile Val Phe Phe Phe Val Ile Phe Ser Ile Asn
      50              55              60

Asn Gln Gly Asp Cys Thr
      65              70

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<210> 1230
<211> 82
<212> PRT
<213> Homo sapiens
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<400> 1230
Glu Cys His Glu Ala Val Ile Tyr Leu Phe His Gln Val Gln Ser Pro
      5                                10                                15

Trp Leu Leu Met Glu Lys Met Thr Lys Lys Asn Thr Ile Leu Lys Ser
      20                                25                                30

Leu Ser Lys Glu Gln Val Ser Arg Lys Ser His Ser Glu Ala Leu Ile
      35                                40                                45

Leu Pro Phe Phe Ser Val Arg Lys Leu Leu Lys Arg Arg Ser Val Thr
      50                                55                                60

Thr Gln Ala Ala Thr Met Ala Thr Phe Ser Thr Phe Asn Val Arg Glu
      65                                70                                75                                80

Lys Glu

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<210> 1231
<211> 72
<212> PRT
<213> Homo sapiens
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<400> 1231
Ala Met Leu Phe Leu Gln Lys Thr Asp Gly Cys Trp Leu Phe Arg Ala
          5                      10                      15

Ser Leu Met Gly Cys Gly Asn Ser Lys Asn Val Pro Gln Cys Gln Pro
          20                      25                      30

Cys Arg Lys Ile Asn Gly Met Gly Ser Val Leu Ser Leu Val Val Ile
          35                      40                      45

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Phe Phe Ile Ile Leu Lys Thr Met Met Gln Lys Gly Leu His Gln Lys
 50 55 60

Arg Arg Cys Gly Ile Lys Lys Arg
 65 70

<210> 1232
 <211> 50
 <212> PRT
 <213> Homo sapiens

<400> 1232
 Tyr Ser Ile Phe Phe Cys His Phe Leu His Gln Gln Pro Gly Arg Leu
 5 10 15

His Leu Met Glu Lys Ile Tyr Asp Cys Phe Met Thr Phe Leu Asn Tyr
 20 25 30

Ile Phe Leu Phe His Ile Tyr Val Phe Gly Gly Val Pro Phe Ala Ser
 35 40 45

Leu Phe
 50

<210> 1233
 <211> 94
 <212> PRT
 <213> Homo sapiens

<400> 1233
 Leu Ser Phe Leu Glu Val Leu Cys Thr Tyr Ala Pro His Leu Tyr Leu
 5 10 15

Ala Phe Ala Trp Ser Asp His Ser Ser Phe Ser Leu Thr Leu Asn Val
 20 25 30

Glu Asn Val Ala Ile Val Ala Ala Cys Val Val Thr Ile Leu Leu Leu
 35 40 45

Ser Asn Phe Leu Thr Leu Lys Lys Gly Arg Met Ser Ala Ser Glu Cys
 50 55 60

Asp Phe Leu Leu Thr Cys Ser Leu Asp Arg Leu Phe Ser Ile Val Phe
 65 70 75 80

Phe Phe Val Ile Phe Ser Ile Asn Asn Gln Gly Asp Cys Thr
 85 90

<210> 1234
 <211> 53
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(53)
 <223> Xaa = Any amino acid

<400> 1234
 Xaa Met Leu Phe Leu Gln Lys Thr Asp Gly Cys Trp Leu Phe Arg Ala

5 10 15
 Ser Leu Met Gly Cys Gly Asn Ser Lys Asn Val Pro Gln Cys Gln Pro
 20 25 30
 Cys Arg Lys Ile Asn Gly Met Gly Ser Val Leu Ser Leu Val Val Ile
 35 40 45
 Phe Phe Tyr His Pro
 50

<210> 1235
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 1235
 Ser Thr His Ser Ala Phe Leu Gln Cys Lys Lys Val Ala Gln Lys Lys
 5 10 15
 Lys Arg Asp Asn Thr Ser Cys Tyr Asn Gly Tyr Ile Leu Tyr Ile Gln
 20 25 30
 Cys Lys Arg Glu Gly Ala Met Val Thr Pro Cys Lys Gly Gln Ile Glu
 35 40 45
 Met Trp Cys Val Cys Ala Glu Tyr Leu Lys Lys
 50 55

<210> 1236
 <211> 91
 <212> PRT
 <213> Homo sapiens

<400> 1236
 Glu Cys His Glu Ala Val Ile Tyr Leu Phe His Gln Val Gln Ser Pro
 5 10 15
 Trp Leu Leu Met Glu Lys Met Thr Lys Lys Asn Thr Ile Leu Lys Ser
 20 25 30
 Leu Ser Lys Glu Gln Val Ser Arg Lys Ser His Ser Glu Ala Leu Ile
 35 40 45
 Leu Pro Phe Phe Ser Val Arg Lys Leu Leu Lys Arg Arg Ser Val Thr
 50 55 60
 Thr Gln Ala Ala Thr Met Ala Thr Phe Ser Thr Phe Asn Val Arg Glu
 65 70 75 80
 Lys Glu Leu Trp Ser Leu His Ala Lys Ala Arg
 85 90

<210> 1237
 <211> 55
 <212> PRT
 <213> Homo sapiens

<400> 1237
 Pro Arg Leu Leu Pro Ala Pro Pro Trp Arg Arg Ala Thr Ser Cys Leu

410

5 10 15
 Thr Ala Arg Ser Ser Pro Leu Ala Met Ser Gly Ser Ala Ala Leu Arg
 20 25 30
 His Ser Ser Ser Leu Pro Ser Trp Ala Trp Ser Pro Val Ala Ser Thr
 35 40 45
 Lys Leu Pro Ser Thr Pro Ser
 50 55

<210> 1238
 <211> 54
 <212> PRT
 <213> Homo sapiens

<400> 1238
 Arg Ser Arg Ser Leu Leu Leu Leu Ser Ala Ser Thr Pro Cys Gly Ser
 5 10 15
 Ala Ala Pro Ser Trp Pro Arg Cys Pro Pro Ser Ser Arg Cys Gly Ser
 20 25 30
 Ala Ser Arg Ser Met Thr Ser Pro Ala Pro Pro Ser Ser Thr Ala Asn
 35 40 45
 Ala Ser Arg Arg Thr Met
 50

<210> 1239
 <211> 147
 <212> PRT
 <213> Homo sapiens

<400> 1239
 Thr Ala Ala Ser Ser Ser Ser Leu Glu Lys Ser Tyr Glu Leu Pro Asp
 5 10 15
 Gly Gln Val Ile Thr Ile Gly Asn Glu Arg Phe Arg Cys Pro Glu Ala
 20 25 30
 Leu Phe Gln Pro Ser Phe Leu Gly Met Glu Ser Cys Gly Ile His Glu
 35 40 45
 Thr Thr Phe Asn Ser Ile Met Lys Cys Asp Val Asp Ile Arg Lys Asp
 50 55 60
 Leu Tyr Ala Asn Thr Val Leu Ser Gly Gly Thr Thr Met Tyr Pro Gly
 65 70 75 80
 Ile Ala Asp Arg Met Gln Lys Glu Ile Thr Ala Leu Ala Pro Ser Thr
 85 90 95
 Met Lys Ile Lys Ile Ile Ala Pro Pro Glu Arg Lys Tyr Ser Val Trp
 100 105 110
 Ile Gly Gly Ser Ile Leu Ala Ser Leu Ser Thr Phe Gln Gln Met Trp
 115 120 125
 Ile Ser Lys Gln Glu Tyr Asp Glu Ser Gly Pro Ser Ile Val His Arg
 130 135 140

Lys Cys Phe
145

<210> 1240
<211> 135
<212> PRT
<213> Homo sapiens

<400> 1240
Lys His Leu Arg Trp Thr Met Glu Gly Pro Asp Ser Ser Tyr Ser Cys
5 10 15
Leu Leu Ile His Ile Cys Trp Lys Val Asp Ser Glu Ala Arg Met Glu
20 25 30
Pro Pro Ile His Thr Glu Tyr Leu Arg Ser Gly Gly Ala Met Ile Leu
35 40 45
Ile Phe Ile Val Leu Gly Ala Arg Ala Val Ile Ser Phe Cys Ile Leu
50 55 60
Ser Ala Met Pro Gly Tyr Met Val Val Pro Pro Asp Ser Thr Val Leu
65 70 75 80
Ala Tyr Arg Ser Leu Arg Met Ser Thr Ser His Phe Met Met Glu Leu
85 90 95
Lys Val Val Ser Trp Met Pro Gln Asp Ser Met Pro Arg Lys Glu Gly
100 105 110
Trp Lys Ser Ala Ser Gly Gln Arg Asn Arg Ser Leu Pro Met Val Met
115 120 125
Thr Trp Pro Ser Gly Ser Ser
130 135

<210> 1241
<211> 151
<212> PRT
<213> Homo sapiens

<400> 1241
Ile Val Arg Leu Glu Ala Phe Ala Val Asp Asp Gly Gly Ala Gly Leu
5 10 15
Val Ile Leu Leu Leu Ala Asp Pro His Leu Leu Glu Gly Gly Gln Arg
20 25 30
Gly Gln Asp Gly Ala Ala Asp Pro His Gly Val Leu Ala Leu Arg Arg
35 40 45
Ser Asn Asp Leu Asp Leu His Cys Ala Gly Cys Gln Gly Ser Asp Leu
50 55 60
Leu Leu His Pro Val Gly Asn Ala Arg Val His Gly Gly Ala Ala Arg
65 70 75 80
Gln His Cys Val Gly Val Gln Val Phe Ala Asp Val His Val Thr Leu
85 90 95

His Asp Gly Val Glu Gly Ser Phe Val Asp Ala Thr Gly Leu His Ala
 100 105 110

Gln Glu Gly Arg Leu Glu Glu Cys Leu Arg Ala Ala Glu Pro Leu Ile
 115 120 125

Ala Asn Gly Asp Asp Leu Ala Val Arg Gln Leu Val Ala Leu Leu Gln
 130 135 140

Gly Gly Ala Gly Ser Ser Arg
 145 150

<210> 1242
 <211> 85
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(85)
 <223> Xaa = Any amino acid

<400> 1242
 Pro Pro Leu Asp Pro Gly Ala Gln Gly Gly Gly Glu His Gln Arg
 5 10 15

Trp Arg Ser Gln Val Val Pro Gly Asp Ser Gln Glu Ser Gly Val Arg
 20 25 30

Arg Leu Gln Asp Leu Ser Arg Leu Cys Arg Tyr Leu Thr Ala Phe Phe
 35 40 45

Thr Leu Leu Leu Xaa Gly Ser Glu Gln Met Ala Leu Pro Cys Xaa Val
 50 55 60

Thr Lys Thr Met Ala Ser Leu Glu Gln Ser Ser Asp Val Trp Tyr His
 65 70 75 80

Val Phe Ser Phe Leu
 85

<210> 1243
 <211> 72
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(72)
 <223> Xaa = Any amino acid

<400> 1243
 Thr Pro Thr Val Glu Val Pro Gly Ser Pro Gly Arg Gln Ser Gly Val
 5 10 15

Trp Gly Glu Glu Ala Ser Arg Pro Leu Lys Ala Leu Gln Val Phe Asn
 20 25 30

Cys Ile Leu His Ser Leu Val Xaa Gly Val Arg Thr Asp Gly Pro Ala
 35 40 45

Leu Xaa Ser Tyr Lys Asn Asp Gly Ile Pro Gly Ala Val Leu Arg Cys
 50 55 60

Leu Val Pro Arg Leu Gln Leu Ser
 65 70

<210> 1244

<211> 50

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(50)

<223> Xaa = Any amino acid

<400> 1244

Arg Lys Leu Lys Thr Trp Tyr Gln Thr Ser Glu Asp Cys Ser Arg Asp
 5 10 15

Ala Ile Val Phe Val Thr Xaa Gln Gly Arg Ala Ile Cys Ser Asp Pro
 20 25 30

Xaa Asn Lys Arg Val Lys Asn Ala Val Lys Tyr Leu Gln Ser Leu Glu
 35 40 45

Arg Ser
 50

<210> 1245

<211> 115

<212> PRT

<213> Homo sapiens

<400> 1245

Thr Leu Pro Pro Asp Arg Met Lys Phe Ile Ser Thr Ser Leu Leu Leu
 5 10 15

Met Leu Leu Val Ser Ser Leu Ser Pro Val Gln Gly Val Leu Glu Val
 20 25 30

Tyr Tyr Thr Ser Leu Arg Cys Arg Cys Val Gln Glu Ser Ser Val Phe
 35 40 45

Ile Pro Arg Arg Phe Ile Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn
 50 55 60

Gly Cys Pro Arg Lys Glu Ile Ile Val Trp Lys Lys Asn Lys Ser Ile
 65 70 75 80

Val Cys Val Asp Pro Gln Ala Glu Trp Ile Gln Arg Met Met Glu Val
 85 90 95

Leu Arg Lys Arg Ser Ser Ser Thr Leu Pro Val Pro Val Phe Lys Arg
 100 105 110

Lys Ile Pro
 115

<210> 1246

<211> 55
 <212> PRT
 <213> Homo sapiens

<400> 1246
 Glu Lys Glu Val Leu Gln Leu Tyr Gln Phe Gln Cys Leu Arg Glu Arg
 5 10 15
 Phe Pro Asp Ala Asp Ile Ser Thr Lys Asn Thr Cys Ile Leu Pro Leu
 20 25 30
 Ser Leu Leu Trp Ile Leu Val Leu Cys Leu Val Lys Ser Phe Pro Gly
 35 40 45
 Lys Arg Thr Ser Pro Tyr Lys
 50 55

<210> 1247
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(51)
 <223> Xaa = Any amino acid

<400> 1247
 Xaa His Ala Tyr Leu Tyr Gly Glu Val Leu Phe Pro Gly Lys Asp Leu
 5 10 15
 Thr Lys His Lys Thr Lys Ile Gln Ser Arg Asp Lys Gly Arg Met Gln
 20 25 30
 Val Phe Leu Val Glu Ile Ser Ala Ser Gly Asn Leu Ser Leu Lys His
 35 40 45
 Trp Asn Trp
 50

<210> 1248
 <211> 62
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(62)
 <223> Xaa = Any amino acid

<400> 1248
 Val Phe Leu Ser Pro Trp Val Lys Ser Glu Ser Gly Ser Leu Cys Xaa
 5 10 15
 Ser Val Leu Val Tyr Cys Trp Ser Glu Ser Lys Phe Leu Ile Lys Ala
 20 25 30
 Val Asp Leu Ala Leu Thr Val Tyr Ala Xaa Ile Gly Glu Thr Ile Trp
 35 40 45
 Leu Phe Gln Thr Ser Gln Asp Xaa Ser Lys Xaa Thr Trp Leu

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<210> 1250
<211> 69
<212> PRT
<213> Homo sapiens
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<210> 1251
<211> 102
<212> PRT
<213> Homo sapiens
```

<400> 1251
Leu Pro Thr Ser Pro Ser Ala Leu Ala Ser Tyr Ser Pro Ser Thr Thr
5 10 15

Asp Met Ala Gln Ser Leu Ala Leu Ser Leu Leu Ile Leu Val Leu Ala
 20 25 30
 Phe Gly Ile Pro Arg Thr Gln Gly Ser Asp Gly Gly Ala Gln Asp Cys
 35 40 45
 Cys Leu Lys Tyr Ser Gln Arg Lys Ile Pro Ala Lys Val Val Arg Ser
 50 55 60
 Tyr Arg Lys Gln Glu Pro Ser Leu Gly Cys Ser Ile Pro Ala Ile Leu
 65 70 75 80
 Phe Leu Pro Arg Lys Arg Ser Gln Ala Glu Leu Cys Ala Asp Pro Lys
 85 90 95
 Glu Leu Trp Val Gln Gln
 100

<210> 1252
 <211> 77
 <212> PRT
 <213> Homo sapiens

<400> 1252
 Ala Ser Leu Ser Trp Phe Trp Pro Leu Ala Ser Pro Gly Pro Lys Ala
 5 10 15
 Val Met Glu Gly Leu Arg Thr Val Ala Ser Ser Thr Ala Lys Gly Arg
 20 25 30
 Phe Pro Pro Arg Leu Ser Ala Ala Thr Gly Ser Arg Asn Gln Ala Trp
 35 40 45
 Ala Ala Pro Ser Gln Leu Ser Cys Ser Cys Pro Ala Ser Ala Leu Arg
 50 55 60
 Gln Ser Tyr Val Gln Thr Gln Arg Ser Ser Gly Cys Ser
 65 70 75

<210> 1253
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 1253
 Trp Arg Gly Ser Gly Leu Leu Pro Gln Val Gln Pro Lys Glu Asp Ser
 5 10 15
 Arg Gln Gly Cys Pro Gln Leu Pro Glu Ala Gly Thr Lys Leu Gly Leu
 20 25 30
 Leu His Pro Ser Tyr Pro Val Leu Ala Pro Gln Ala Leu Ser Gly Arg
 35 40 45
 Ala Met Cys Arg Pro Lys Gly Ala Leu Gly Ala Ala
 50 55 60

<210> 1254
 <211> 115

<212> PRT

<213> Homo sapiens

<400> 1254

Thr Leu Pro Pro Asp Arg Met Lys Phe Ile Ser Thr Ser Leu Leu Leu
 5 10 15

Met Leu Leu Val Ser Ser Leu Ser Pro Val Gln Gly Val Leu Glu Val
 20 25 30

Tyr Tyr Thr Ser Leu Arg Cys Arg Cys Val Gln Glu Ser Ser Val Phe
 35 40 45

Ile Pro Arg Arg Phe Ile Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn
 50 55 60

Gly Cys Pro Arg Lys Glu Ile Ile Val Trp Lys Lys Asn Lys Ser Ile
 65 70 75 80

Val Cys Val Asp Pro Gln Ala Glu Trp Ile Gln Arg Met Met Glu Val
 85 90 95

Leu Arg Lys Arg Ser Ser Ser Thr Leu Pro Val Pro Val Phe Lys Arg
 100 105 110

Lys Ile Pro
 115

<210> 1255

<211> 55

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(55)

<223> Xaa = Any amino acid

<400> 1255

Glu Lys Glu Val Leu Gln Leu Tyr Gln Phe Gln Cys Leu Arg Glu Arg
 5 10 15

Phe Pro Asp Ala Asp Ile Ser Thr Lys Asn Thr Cys Ile Leu Pro Leu
 20 25 30

Ser Leu Leu Trp Ile Leu Val Leu Cys Leu Val Lys Ser Phe Pro Gly
 35 40 45

Lys Arg Xaa Ser Pro Tyr Lys
 50 55

<210> 1256

<211> 51

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(51)

<223> Xaa = Any amino acid


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<400> 1256
Ser His Ala Tyr Leu Tyr Gly Glu Xaa Leu Phe Pro Gly Lys Asp Leu
          5                      10                      15

Thr Lys His Lys Thr Lys Ile Gln Ser Arg Asp Lys Gly Arg Met Gln
          20                      25                      30

Val Phe Leu Val Glu Ile Ser Ala Ser Gly Asn Leu Ser Leu Lys His
          35                      40                      45

Trp Asn Trp
          50

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<210> 1257
<211> 64
<212> PRT
<213> Homo sapiens
```

```

<400> 1257
Pro Asn His Phe Phe Phe Tyr Phe Asn Ser Leu Phe Phe Phe Ser Ser
          5                      10                      15

Ala Asp Arg Arg Thr Met Leu Asp Leu Gly Leu Glu His Val Leu Phe
          20                      25                      30

His Ser Phe Ser Thr Met Pro Ala Ile Thr Ser Ser Trp Lys Lys Ala
          35                      40                      45

Lys Ile Ser Ile Thr Asp Lys Met Pro Lys Asn Arg Asp Cys Met Leu
          50                      55                      60

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<210> 1258
<211> 59
<212> PRT
<213> Homo sapiens
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```

<400> 1258
Ser Trp Gly Gly Ser Gly Lys Phe Val Ser Val Ser Ser Ser Ser Ser
          5                      10                      15

Ser Trp Ile Gly Ile Ile Ser Met Ser Ser Ser Phe Phe Gly Trp Glu
          20                      25                      30

Asp Val Ser Val Ser Pro Thr Thr Ser Ser Phe Ile Ser Ile Val Cys
          35                      40                      45

Ser Phe Phe Leu Leu Leu Thr Gly Glu Leu Cys
          50                      55

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<210> 1259
<211> 71
<212> PRT
<213> Homo sapiens
```

<400> 1259
His Ser Ser Pro Val Ser Arg Arg Lys Lys Glu Gln Thr Ile Glu Ile
 5 10 15
Lys Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser Gln Pro Lys Asn
 20 25 30

Glu Glu Asp Ile Glu Ile Ile Pro Ile Gln Glu Glu Glu Glu Glu
 35 40 45
 Thr Glu Thr Asn Phe Pro Glu Pro Pro Gln Asp Gln Glu Ser Ser Pro
 50 55 60
 Ile Glu Asn Asp Ser Ser Pro
 65 70

<210> 1260
 <211> 94
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(94)
 <223> Xaa = Any amino acid

<400> 1260
 Lys Met Glu Ser Xaa Asn Phe Ile Arg Ala His Thr Pro Tyr Ile Asn
 5 10 15
 Ile Xaa Asn Tyr Glu Pro Ala Asn Pro Xaa Glu Lys Asn Ser Pro Ser
 20 25 30
 Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly Ile Leu Ser
 35 40 45
 Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile Ala Gly Ile
 50 55 60
 Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys Ser Asn Ile
 65 70 75 80
 Val Leu Leu Ser Ala Glu Glu Lys Lys Asn Arg Leu Leu Lys
 85 90

<210> 1261
 <211> 164
 <212> PRT
 <213> Homo sapiens

<400> 1261
 Leu Asn Met Leu Gly Glu Lys Leu Leu Gly Pro Asn Ala Ser Pro Asp
 5 10 15
 Gly Leu Ile Pro Trp Thr Arg Phe Cys Lys Glu Asn Ile Asn Asp Lys
 20 25 30
 Asn Phe Pro Phe Trp Leu Trp Ile Glu Ser Ile Leu Glu Leu Ile Lys
 35 40 45
 Lys His Leu Leu Pro Leu Trp Asn Asp Gly Cys Ile Met Gly Phe Ile
 50 55 60
 Ser Lys Glu Arg Glu Arg Ala Leu Leu Lys Asp Gln Gln Pro Gly Thr
 65 70 75 80
 Phe Leu Leu Arg Phe Ser Glu Ser Ser Arg Glu Gly Ala Ile Thr Phe

420

85

90

95

Thr Trp Val Glu Arg Ser Gln Asn Gly Gly Glu Pro Asp Phe His Ala
100 105 110

Val Glu Pro Tyr Thr Lys Lys Glu Leu Ser Ala Val Thr Phe Pro Asp
115 120 125

Ile Ile Arg Asn Tyr Lys Val Met Ala Ala Glu Asn Ile Pro Glu Asn
130 135 140

Pro Leu Lys Tyr Leu Tyr Pro Asn Ile Asp Lys Asp His Ala Phe Gly
145 150 155 160

Lys Tyr Tyr Ser

<210> 1262

<211> 72

<212> PRT

<213> Homo sapiens

<400> 1262

Arg Thr Ser Ser Arg Gly Pro Ser Cys Cys Gly Ser Val Arg Ala Pro
5 10 15

Gly Lys Gly Pro Ser His Ser His Gly Trp Ser Gly Pro Arg Thr Glu
20 25 30

Ala Asn Leu Thr Ser Met Arg Leu Asn Pro Thr Arg Arg Lys Asn Phe
35 40 45

Leu Leu Leu Leu Ser Leu Thr Ser Phe Ala Ile Thr Lys Ser Trp Leu
50 55 60

Leu Arg Ile Phe Leu Arg Ile Pro
65 70

<210> 1263

<211> 120

<212> PRT

<213> Homo sapiens

<400> 1263

Gly Val Ile Leu Ser Lys Gly Met Val Phe Val Asn Ile Trp Ile Gln
5 10 15

Ile Leu Gln Gly Ile Leu Arg Asn Ile Leu Ser Ser His Asp Phe Val
20 25 30

Ile Ala Asn Asp Val Arg Glu Ser Asn Ser Arg Lys Phe Phe Leu Arg
35 40 45

Val Gly Phe Asn Arg Met Glu Val Arg Phe Ala Ser Val Leu Gly Pro
50 55 60

Leu His Pro Cys Glu Cys Asp Gly Pro Phe Pro Gly Ala Leu Thr Glu
65 70 75 80

Pro Gln Gln Glu Gly Pro Arg Leu Leu Val Leu Gln Gln Gly Thr Leu
85 90 95

Ser Leu Leu Ala Asp Glu Ala His Asp Ala Pro Ile Ile Pro Glu Arg
 100 105 110

Glu Gln Val Phe Phe Asn Glu Phe
 115 120

<210> 1264

<211> 114

<212> PRT

<213> Homo sapiens

<400> 1264

Gly Ser Thr Ala Trp Lys Ser Gly Ser Pro Pro Phe Trp Asp Arg Ser
 5 10 15

Thr His Val Asn Val Met Ala Pro Ser Arg Glu Leu Ser Leu Asn Arg
 20 25 30

Ser Arg Lys Val Pro Gly Cys Trp Ser Phe Asn Arg Ala Arg Ser Arg
 35 40 45

Ser Leu Leu Met Lys Pro Met Met His Pro Ser Phe Gln Arg Gly Ser
 50 55 60

Arg Cys Phe Leu Met Ser Ser Arg Met Leu Ser Ile Gln Ser Gln Lys
 65 70 75 80

Gly Lys Phe Leu Ser Phe Ile Phe Ser Leu Gln Asn Leu Val His Gly
 85 90 95

Met Arg Pro Ser Gly Leu Ala Leu Gly Pro Arg Ser Phe Ser Pro Asn
 100 105 110

Met Phe

<210> 1265

<211> 88

<212> PRT

<213> Homo sapiens

<400> 1265

Thr Leu Pro Pro Asp Arg Met Lys Phe Ile Ser Thr Ser Leu Leu Leu
 5 10 15

Met Leu Leu Val Ser Ser Leu Ser Pro Val Gln Gly Val Leu Glu Val
 20 25 30

Tyr Tyr Thr Ser Leu Arg Cys Arg Cys Val Gln Glu Ser Ser Val Phe
 35 40 45

Ile Pro Arg Arg Phe Ile Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn
 50 55 60

Gly Cys Pro Arg Lys Glu Ile Ile Val Trp Lys Lys Asn Lys Ser Ile
 65 70 75 80

Val Cys Val Asp Pro Gln Ala Glu
 85

<210> 1266
<211> 75
<212> PRT
<213> Homo sapiens

<400> 1266
Cys Val Gln Glu Ser Ser Val Phe Ile Pro Arg Arg Phe Ile Asp Arg
5 10 15
Ile Gln Ile Leu Pro Arg Gly Asn Gly Cys Pro Arg Lys Glu Ile Ile
20 25 30
Val Trp Lys Lys Asn Lys Ser Ile Val Cys Val Asp Pro Gln Ala Glu
35 40 45
Trp Ile Gln Arg Met Met Glu Val Leu Arg Lys Arg Ser Ser Ser Thr
50 55 60
Leu Pro Val Pro Val Phe Lys Arg Lys Ile Pro
65 70 75

<210> 1267
<211> 53
<212> PRT
<213> Homo sapiens

<400> 1267
Ile Phe Ser Arg Lys Lys Asn Phe Pro Ile Gln Ile Ser Met Arg Leu
5 10 15
Cys Lys Asn Asn Leu Ala Glu Ala Asp Gly Ala Asn Ser Ser Phe Phe
20 25 30
Thr His Ser Thr Leu Tyr Thr Leu Gly Val Cys Ile Leu Ile His Gln
35 40 45
Gly Gly Lys Phe Leu
50

<210> 1268
<211> 55
<212> PRT
<213> Homo sapiens

<400> 1268
Glu Lys Glu Val Leu Gln Leu Tyr Gln Phe Gln Cys Leu Arg Glu Arg
5 10 15
Phe Pro Asp Ala Asp Ile Ser Thr Lys Asn Thr Cys Ile Leu Pro Leu
20 25 30
Ser Leu Leu Trp Ile Leu Val Leu Cys Leu Val Lys Ser Phe Pro Gly
35 40 45
Lys Arg Thr Ser Pro Tyr Lys
50 55

<210> 1269
<211> 52

<212> PRT

<213> Homo sapiens

<400> 1269

Asp Tyr Val Lys Ile Thr Leu Gln Lys Leu Met Gly Gln Thr Gln Ala
 5 10 15

Ser Ser Leu Thr Ala Pro Tyr Ile His Leu Glu Phe Ala Phe Leu Phe
 20 25 30

Ile Arg Glu Glu Ser Phe Phe Glu Asn Ser Tyr Ser Val Ile Ser Asn
 35 40 45

Thr Gly Leu Phe
 50

<210> 1270

<211> 51

<212> PRT

<213> Homo sapiens

<400> 1270

Ser His Ala Tyr Leu Tyr Gly Glu Val Leu Phe Pro Gly Lys Asp Leu
 5 10 15

Thr Lys His Lys Thr Lys Ile Gln Ser Arg Asp Lys Gly Arg Met Gln
 20 25 30

Val Phe Leu Val Glu Ile Ser Ala Ser Gly Asn Leu Ser Leu Lys His
 35 40 45

Trp Asn Trp
 50

<210> 1271

<211> 112

<212> PRT

<213> Homo sapiens

<400> 1271

Leu Pro Glu Gln Arg Asp Leu His Thr Glu Thr Pro Ser Trp Ala Pro
 5 10 15

Gly Thr Met Ala Pro Leu Lys Met Leu Ala Leu Val Thr Leu Leu Leu
 20 25 30

Gly Ala Ser Leu Gln His Ile His Ala Ala Arg Gly Thr Asn Val Gly
 35 40 45

Arg Glu Cys Cys Leu Glu Tyr Phe Lys Gly Ala Ile Pro Leu Arg Lys
 50 55 60

Leu Lys Thr Trp Tyr Gln Thr Ser Glu Asp Cys Ser Arg Asp Ala Ile
 65 70 75 80

Val Phe Val Thr Val Gln Gly Arg Ala Ile Cys Ser Asp Pro Asn Asn
 85 90 95

Lys Arg Val Lys Asn Ala Val Lys Tyr Leu Gln Ser Leu Glu Arg Ser
 100 105 110

<210> 1272
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 1272
 Ala Glu Gly Pro Ala His Arg Asp Ser Leu Leu Gly Ser Trp His His
 5 10 15
 Gly Pro Thr Glu Asp Ala Gly Pro Gly His Pro Pro Pro Gly Gly Phe
 20 25 30
 Ser Ala Ala His Pro Arg Ser Ser Arg Asp Gln Cys Gly Pro Gly Val
 35 40 45
 Leu Pro Gly Val Leu Gln Gly Ser His Ser Pro
 50 55

<210> 1273
 <211> 146
 <212> PRT
 <213> Homo sapiens

<400> 1273
 Pro Pro Leu Asp Pro Gly Ala Gln Gly Gly Gly Gly Glu His Gln Arg
 5 10 15
 Trp Arg Ser Gln Val Val Pro Gly Asp Ser Gln Glu Ser Gly Val Arg
 20 25 30
 Arg Leu Gln Asp Leu Ser Arg Leu Cys Arg Tyr Leu Thr Ala Phe Phe
 35 40 45
 Thr Leu Leu Leu Leu Gly Ser Glu Gln Met Ala Leu Pro Cys Thr Val
 50 55 60
 Thr Lys Thr Met Ala Ser Leu Glu Gln Ser Ser Asp Val Trp Tyr His
 65 70 75 80
 Val Phe Ser Phe Leu Arg Gly Met Ala Pro Leu Lys Tyr Ser Arg Gln
 85 90 95
 His Ser Arg Pro Thr Leu Val Pro Arg Ala Ala Trp Met Cys Cys Arg
 100 105 110
 Glu Ala Pro Arg Arg Arg Val Thr Arg Ala Ser Ile Phe Ser Gly Ala
 115 120 125
 Met Val Pro Gly Ala Gln Glu Gly Val Ser Val Cys Arg Ser Leu Cys
 130 135 140
 Ser Gly
 145

<210> 1274
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 1274

425

Thr Pro Thr Val Glu Val Pro Gly Ser Pro Gly Arg Gln Ser Gly Val
 5 10 15
 Trp Gly Glu Glu Ala Ser Arg Pro Leu Lys Ala Leu Gln Val Phe Asn
 20 25 30
 Cys Ile Leu His Ser Leu Val Val Gly Val Arg Thr Asp Gly Pro Ala
 35 40 45
 Leu His Ser Tyr Lys Asn Asp Gly Ile Pro Gly Ala Val Leu Arg Cys
 50 55 60
 Leu Val Pro Arg Leu Gln Leu Ser Lys Gly Asn Gly Ser Leu Glu Val
 65 70 75 80
 Leu Gln Ala Ala Leu Pro Ala His Ile Gly Pro Ser Ser Cys Val Asp
 85 90 95
 Val Leu Gln Arg Ser Pro Gln Glu Glu Gly Asp Gln Gly Gln His Leu
 100 105 110
 Gln Trp Gly His Gly Ala Arg Ser Pro Gly Gly Ser Leu Cys Val Gln
 115 120 125
 Val Pro Leu Leu Arg Glu
 130

<210> 1275
 <211> 115
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(115)
 <223> Xaa = Any amino acid

<400> 1275
 Pro Pro Leu Asp Pro Gly Ala Gln Gly Gly Gly Glu His Gln Arg
 5 10 15
 Trp Arg Ser Gln Val Val Pro Gly Asp Ser Gln Glu Ser Gly Val Arg
 20 25 30
 Arg Leu Gln Asp Leu Ser Arg Leu Cys Arg Tyr Leu Thr Ala Phe Phe
 35 40 45
 Thr Leu Leu Xaa Leu Gly Ser Glu Gln Met Ala Leu Pro Cys Thr Val
 50 55 60
 Thr Lys Thr Met Ala Ser Leu Glu Gln Ser Ser Asp Val Trp Tyr His
 65 70 75 80
 Val Phe Ser Phe Leu Arg Gly Met Ala Pro Leu Lys Tyr Ser Arg Gln
 85 90 95
 His Ser Arg Pro Thr Leu Val Pro Arg Ala Ala Trp Met Cys Cys Xaa
 100 105 110
 Xaa Xaa Pro
 115

<210> 1276
 <211> 102
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(102)
 <223> Xaa = Any amino acid

<400> 1276
 Thr Pro Thr Val Glu Val Pro Gly Ser Pro Gly Arg Gln Ser Gly Val
 5 10 15
 Trp Gly Glu Glu Ala Ser Arg Pro Leu Lys Ala Leu Gln Val Phe Asn
 20 25 30
 Cys Ile Leu His Ser Leu Xaa Val Gly Val Arg Thr Asp Gly Pro Ala
 35 40 45
 Leu His Ser Tyr Lys Asn Asp Gly Ile Pro Gly Ala Val Leu Arg Cys
 50 55 60
 Leu Val Pro Arg Leu Gln Leu Ser Lys Gly Asn Gly Ser Leu Glu Val
 65 70 75 80
 Leu Gln Ala Ala Leu Pro Ala His Ile Gly Pro Ser Ser Cys Val Asp
 85 90 95
 Val Leu Xaa Xaa Xaa Pro
 100

<210> 1277
 <211> 80
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(80)
 <223> Xaa = Any amino acid

<400> 1277
 Gly Xaa Xaa Xaa Gln His Ile His Ala Ala Arg Gly Thr Asn Val Gly
 5 10 15
 Arg Glu Cys Cys Leu Glu Tyr Phe Lys Gly Ala Ile Pro Leu Arg Lys
 20 25 30
 Leu Lys Thr Trp Tyr Gln Thr Ser Glu Asp Cys Ser Arg Asp Ala Ile
 35 40 45
 Val Phe Val Thr Val Gln Gly Arg Ala Ile Cys Ser Asp Pro Asn Xaa
 50 55 60
 Lys Arg Val Lys Asn Ala Val Lys Tyr Leu Gln Ser Leu Glu Arg Ser
 65 70 75 80

<210> 1278
 <211> 64

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<220>  
<221> variant  
<222> (1)...(64)  
<223> Xaa = Any amino acid
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<400> 1278
Met Ile Ile Thr Cys Val Ser Xaa Thr Xaa Cys Xaa Leu Trp Leu Leu
          5                      10                      15

Val Ile Tyr Xaa Leu Pro Val Xaa Xaa Lys Val Xaa Gly Xaa Xaa Thr
          20                      25                      30

Xaa Lys Phe Xaa Lys His Leu Xaa Phe Ser Xaa Lys Leu Xaa Glu Gly
          35                      40                      45

Thr Arg Glu Phe His Xaa Xaa Ile Lys Xaa Ser Xaa Gly Ile Ser Thr
          50                      55                      60

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<210> 1279
<211> 79
<212> PRT
<213> Homo sapiens
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<220>  
<221> variant  
<222> (1)...(79)  
<223> Xaa = Any amino acid
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<400> 1279
Gln Xaa Lys Xaa Phe Lys Leu Gln Gly Xaa Gln Xaa Asn Thr Xaa Leu
      5              10              15

Xaa Xaa Lys Xaa Ile Cys Phe Glu Ser Xaa Cys Met Tyr Ile Tyr Met
      20              25              30

Ile Asn Asp Tyr Asn Val Cys Val Xaa Asp Xaa Met Xaa Ser Leu Val
      35              40              45

Val Ser Tyr Ile Leu Xaa Thr Cys Xaa Xaa Gln Gly Lys Xaa Xaa Thr
      50              55              60

Xaa Xaa Xaa Ile Tyr Xaa Thr Leu Xaa Phe Phe Xaa Glu Val Xaa
      65              70              75

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<210> 1280
<211> 78
<212> PRT
<213> Homo sapiens
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<220>
<221> variant
<222> (1)...(78)
<223> Xaa = Any amino acid
```

<400> 1280
Asn Ser Leu Val Pro Ser Xaa Asn Phe Xaa Glu Lys Xaa Lys Cys Xaa
 5 10 15

Ile Asn Xaa Xaa Xaa Cys Xaa Xaa Leu Thr Leu Xaa Xaa Thr Gly Xaa
 20 25 30
 Gln Tyr Ile Thr Asn Asn Gln Arg Xaa His Xaa Val Xaa Asp Thr His
 35 40 45
 Val Ile Ile Ile Tyr His Ile Tyr Ile His Ala Xaa Thr Phe Lys Ala
 50 55 60
 Asn Xaa Phe Xaa Xaa Gln Xaa Ser Ile Xaa Leu Xaa Thr Leu
 65 70 75

<210> 1281
 <211> 191
 <212> PRT
 <213> Homo sapiens

<400> 1281
 Pro Lys Glu Val Arg Gln Leu Ala Glu Asp Phe Leu Lys Asp Tyr Ile
 5 10 15
 His Ile Asn Ile Gly Ala Leu Glu Leu Ser Ala Asn His Asn Ile Leu
 20 25 30
 Gln Ile Val Asp Val Cys His Asp Val Glu Lys Asp Glu Lys Leu Ile
 35 40 45
 Arg Leu Met Glu Glu Ile Met Ser Glu Lys Glu Asn Lys Thr Ile Val
 50 55 60
 Phe Val Glu Thr Lys Arg Arg Cys Asp Glu Leu Thr Arg Lys Met Arg
 65 70 75 80
 Arg Asp Gly Trp Pro Ala Met Gly Ile His Gly Asp Lys Ser Gln Gln
 85 90 95
 Glu Arg Asp Trp Val Leu Asn Glu Phe Lys His Gly Lys Ala Pro Ile
 100 105 110
 Leu Ile Ala Thr Asp Val Ala Ser Arg Gly Leu Asp Val Glu Asp Val
 115 120 125
 Lys Phe Val Ile Asn Tyr Asp Tyr Pro Asn Ser Ser Glu Asp Tyr Ile
 130 135 140
 His Arg Ile Gly Arg Thr Ala Arg Ser Thr Lys Thr Gly Thr Ala Tyr
 145 150 155 160
 Thr Phe Phe Thr Pro Asn Asn Ile Lys Gln Val Ser Asp Leu Ile Ser
 165 170 175
 Val Leu Arg Glu Ala Asn Gln Ala Ile Asn Pro Lys Leu Leu Gln
 180 185 190

<210> 1282
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 1282
 Leu Lys Gln Leu Gly Ile Asn Cys Leu Ile Ser Phe Thr Lys His Arg

5 10 15
Asp Lys Val Ala His Leu Leu Tyr Val Ile Arg Cys Lys Glu Ser Val
20 25 30
Cys Cys Ala Cys Phe Gly Thr Ala Ser Ser Ser Ser Asn Ser Met Asn
35 40 45
Ile Ile Leu
50

<210> 1283
<211> 51
<212> PRT
<213> Homo sapiens

<400> 1283
Asn Pro Val Thr Leu Leu Leu Thr Leu Val Thr Met Asp Thr His Gly
5 10 15
Arg Pro Pro Ile Ser Pro His Phe Ser Gly Lys Leu Ile Thr Ser Ser
20 25 30
Phe Gly Phe His Lys Asn Asn Gly Phe Ile Leu Leu Leu Thr His Asp
35 40 45
Leu Phe His
50

<210> 1284
<211> 55
<212> PRT
<213> Homo sapiens

<400> 1284
Leu Leu Ser Pro Trp Ile Pro Met Ala Gly His Pro Ser Leu Leu Ile
5 10 15
Phe Leu Val Ser Ser Ser His Leu Leu Leu Val Ser Thr Lys Thr Met
20 25 30
Val Leu Phe Ser Phe Ser Leu Met Ile Ser Ser Ile Arg Arg Ile Ser
35 40 45
Phe Ser Ser Phe Ser Thr Ser
50 55

<210> 1285
<211> 107
<212> PRT
<213> Homo sapiens

<400> 1285
Asp Leu His Thr Glu Thr Pro Ser Trp Ala Pro Gly Thr Met Ala Leu
5 10 15
Leu Lys Met Leu Ala Leu Val Thr Leu Leu Leu Gly Ala Ser Leu Gln
20 25 30
His Ile His Ala Ala Arg Gly Thr Asn Val Gly Arg Glu Cys Cys Leu

35 40 45
 Glu Tyr Phe Lys Gly Ala Ile Pro Leu Arg Lys Leu Lys Thr Trp Tyr
 50 55 60
 Gln Thr Ser Glu Asp Cys Ser Arg Asp Ala Ile Val Phe Val Thr Val
 65 70 75 80
 Gln Gly Arg Ala Ile Cys Ser Asp Pro Asn Asn Lys Arg Val Lys Asn
 85 90 95
 Ala Val Lys Tyr Leu Gln Ser Leu Glu Arg Ser
 100 105

<210> 1286
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 1286
 Pro Ala His Arg Asp Ser Leu Leu Gly Ser Trp His His Gly Pro Thr
 5 10 15
 Glu Asp Ala Gly Pro Gly His Pro Pro Pro Gly Gly Phe Ser Ala Ala
 20 25 30
 His Pro Arg Ser Ser Arg Asp Gln Cys Gly Pro Gly Val Leu Pro Gly
 35 40 45
 Val Leu Gln Gly Ser His Ser Pro
 50 55

<210> 1287
 <211> 141
 <212> PRT
 <213> Homo sapiens

<400> 1287
 Pro Pro Leu Asp Pro Gly Ala Gln Gly Gly Gly Glu His Gln Arg
 5 10 15
 Trp Arg Ser Gln Val Val Pro Gly Asp Ser Gln Glu Ser Gly Val Arg
 20 25 30
 Arg Leu Gln Asp Leu Ser Arg Leu Cys Arg Tyr Leu Thr Ala Phe Phe
 35 40 45
 Thr Leu Leu Leu Leu Gly Ser Glu Gln Met Ala Leu Pro Cys Thr Val
 50 55 60
 Thr Lys Thr Met Ala Ser Leu Glu Gln Ser Ser Asp Val Trp Tyr His
 65 70 75 80
 Val Phe Ser Phe Leu Arg Gly Met Ala Pro Leu Lys Tyr Ser Arg Gln
 85 90 95
 His Ser Arg Pro Thr Leu Val Pro Arg Ala Ala Trp Met Cys Cys Arg
 100 105 110
 Glu Ala Pro Arg Arg Arg Val Thr Arg Ala Ser Ile Phe Ser Arg Ala
 115 120 125

Met Val Pro Gly Ala Gln Glu Gly Val Ser Val Cys Arg
 130 135 140

<210> 1288
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 1288
 Thr Pro Thr Val Glu Val Pro Gly Ser Pro Gly Arg Gln Ser Gly Val
 5 10 15
 Trp Gly Glu Glu Ala Ser Arg Pro Leu Lys Ala Leu Gln Val Phe Asn
 20 25 30
 Cys Ile Leu His Ser Leu Val Val Gly Val Arg Thr Asp Gly Pro Ala
 35 40 45
 Leu His Ser Tyr Lys Asn Asp Gly Ile Pro Gly Ala Val Leu Arg Cys
 50 55 60
 Leu Val Pro Arg Leu Gln Leu Ser Lys Gly Asn Gly Ser Leu Glu Val
 65 70 75 80
 Leu Gln Ala Ala Leu Pro Ala His Ile Gly Pro Ser Ser Cys Val Asp
 85 90 95
 Val Leu Gln Arg Ser Pro Gln Glu Glu Gly Asp Gln Gly Gln His Leu
 100 105 110
 Gln

<210> 1289
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 1289
 Ile Ser Thr Ser Leu Leu Met Leu Leu Val Ser Ser Leu Ser Pro
 5 10 15
 Val Gln Gly Val Leu Glu Val Tyr Tyr Thr Ser Leu Arg Cys Arg Cys
 20 25 30
 Val Gln Glu Ser Ser Val Phe Ile Pro Arg Arg Phe Ile Asp Arg Ile
 35 40 45
 Gln Ile Leu Pro Arg Gly Asn Gly Cys Pro Arg Lys Glu Ile Ile Val
 50 55 60
 Trp Lys Lys Asn Lys Ser Ile Val Cys Val Asp Pro Gln Ala Glu Trp
 65 70 75 80
 Ile Gln Arg Met Met Glu Val Leu Arg Lys Arg Ser Ser Ser Thr Leu
 85 90 95
 Pro Val Pro Val Phe Lys Arg Lys Ile Pro
 100 105

<210> 1290
<211> 53
<212> PRT
<213> Homo sapiens

<400> 1290
Ile Phe Ser Arg Lys Lys Asn Phe Pro Ile Gln Ile Ser Met Arg Leu
 5 10 15

Cys Lys Asn Asn Leu Ala Glu Ala Asp Gly Ala Asn Ser Ser Phe Phe
 20 25 30

Thr His Ser Thr Leu Tyr Thr Leu Gly Val Cys Ile Leu Ile His Arg
 35 40 45

Gly Gly Lys Phe Leu
 50

<210> 1291
<211> 55
<212> PRT
<213> Homo sapiens

<400> 1291
Glu Lys Glu Val Leu Gln Leu Tyr Gln Phe Gln Cys Leu Arg Glu Arg
 5 10 15

Phe Pro Asp Ala Asp Ile Ser Thr Lys Asn Thr Cys Ile Leu Pro Leu
 20 25 30

Ser Leu Leu Trp Ile Leu Val Leu Cys Leu Val Lys Ser Phe Pro Gly
 35 40 45

Lys Arg Thr Ser Pro Tyr Lys
 50 55

<210> 1292
<211> 51
<212> PRT
<213> Homo sapiens

<400> 1292
Asp Tyr Val Lys Ile Thr Leu Gln Lys Leu Met Gly Gln Thr Gln Ala
 5 10 15

Ser Ser Leu Thr Ala Pro Tyr Ile His Leu Glu Phe Ala Phe Leu Phe
 20 25 30

Ile Gly Glu Glu Ser Phe Phe Glu Asn Ser Tyr Ser Val Ile Ser Asn
 35 40 45

Thr Gly Leu
 50

<210> 1293
<211> 51
<212> PRT
<213> Homo sapiens

<400> 1296
Leu Ile Val Leu Glu Ser Lys Lys His Arg Val Gly Gln Tyr Thr Ser
5 10 15

Ser Tyr Pro Ser His Pro Asn Leu Thr Leu Leu Ile Ser Phe Ser Leu
 20 25 30
 Ile Leu Gly Asn His Gln Lys Met Cys Ser Leu Ser Lys Arg Leu Lys
 35 40 45
 Glu Ile Ser Phe Leu Thr Pro Ala Asn Thr Pro Cys Pro Gly Trp Ser
 50 55 60
 Pro Ser Asn Thr Ile Arg Cys Gln Glu Glu
 65 70

<210> 1297
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 1297
 Thr Leu Pro Pro Asp Arg Met Lys Phe Ile Ser Thr Ser Leu Leu Leu
 5 10 15
 Met Leu Leu Val Ser Ser Leu Ser Pro Val Gln Gly Val Leu Glu Val
 20 25 30
 Tyr Tyr Thr Ser Leu Arg Cys Arg Cys Val Gln Glu Ser Ser Val Phe
 35 40 45
 Ile Pro Arg Arg Phe Ile Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn
 50 55 60
 Gly Cys Pro Arg Lys Glu Ile Ile Val Trp Lys Lys Asn Lys Ser Ile
 65 70 75 80
 Ala Cys Val Asp Pro Gln Ala Glu Trp Ile Gln Arg Met Met Glu Val
 85 90 95
 Leu Arg Lys Arg Ser Ser Ser Thr Pro Pro Val Pro Val Phe Lys Arg
 100 105 110
 Lys Ile Pro
 115

<210> 1298
 <211> 53
 <212> PRT
 <213> Homo sapiens

<400> 1298
 Ile Phe Ser Arg Lys Lys Asn Phe Pro Ile Gln Ile Ser Met Arg Leu
 5 10 15
 Cys Lys Asn Asn Leu Ala Glu Ala Asp Gly Ala Asn Ser Ser Phe Phe
 20 25 30
 Thr His Ser Thr Leu Tyr Thr Leu Gly Val Cys Ile Leu Ile His Gln
 35 40 45
 Gly Gly Lys Phe Leu
 50

<210> 1299
<211> 55
<212> PRT
<213> Homo sapiens

<400> 1299
Glu Lys Glu Val Leu Gln Leu His Gln Phe Gln Cys Leu Arg Glu Arg
 5 10 15

Phe Pro Asp Ala Asp Ile Ser Thr Lys Asn Thr Cys Ile Leu Pro Leu
 20 25 30

Ser Leu Leu Trp Ile Leu Val Leu Cys Leu Val Lys Ser Phe Pro Gly
 35 40 45

Lys Arg Thr Ser Pro Tyr Lys
 50 55

<210> 1300
<211> 53
<212> PRT
<213> Homo sapiens

<400> 1300
Ser His Ala Tyr Leu Tyr Gly Glu Val Leu Phe Pro Gly Lys Asp Leu
 5 10 15

Thr Lys His Lys Thr Lys Ile Gln Ser Arg Asp Lys Gly Arg Met Gln
 20 25 30

Val Phe Leu Val Glu Ile Ser Ala Ser Gly Asn Leu Ser Leu Lys His
 35 40 45

Trp Asn Trp Trp Ser
 50

<210> 1301
<211> 125
<212> PRT
<213> Homo sapiens

<400> 1301
Arg Tyr Gln Trp Val Arg Cys Asn Pro Asp Ser Asn Ser Ala Asn Cys
 5 10 15

Leu Glu Glu Lys Gly Pro Met Phe Glu Leu Leu Pro Gly Glu Ser Asn
 20 25 30

Lys Ile Pro Arg Leu Arg Thr Asp Leu Phe Pro Lys Thr Arg Ile Gln
 35 40 45

Asp Leu Asn Arg Ile Phe Pro Leu Ser Glu Asp Tyr Ser Gly Ser Gly
 50 55 60

Phe Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Phe Leu
 65 70 75 80

Thr Glu Met Glu Gln Asp Tyr Gln Leu Val Asp Glu Ser Asp Ala Phe
 85 90 95

His Asp Asn Leu Arg Ser Leu Asp Arg Asn Leu Pro Ser Asp Ser Gln
 100 105 110

Asp Leu Gly Gln His Gly Leu Glu Glu Asp Phe Met Leu
 115 120 125

<210> 1302
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 1302
 Ser Ser Glu Ser Gly Lys Ile Arg Phe Lys Ser Trp Ile Leu Val Phe
 5 10 15

Gly Lys Arg Ser Val Leu Arg Arg Gly Ile Leu Leu Asp Ser Pro Gly
 20 25 30

Ser Ser Ser Asn Ile Gly Pro Phe Ser Ser Arg Gln Phe Ala Glu Leu
 35 40 45

Leu Ser Gly Leu Gln Arg Thr His Trp Tyr Leu
 50 55

<210> 1303
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 1303
 Gly Cys His Gly Lys His His Phe Arg Leu Leu Val Gly Asn Pro Val
 5 10 15

Pro Phe Pro Leu Gly Ser His Ser Gln Ile Leu Ile Gln Ser Arg Ser
 20 25 30

Arg Ser Arg Ser Leu Ile Gln Ser Ser Pro Gln Lys Val Gly Arg Tyr
 35 40 45

Asp Ser Ser Pro Gly Phe Ser Ser Leu Glu Lys Gly Gln Ser Ser Asp
 50 55 60

Gly Gly Ser Cys Trp Ile His Leu Glu Val Val Arg Thr Leu Val Leu
 65 70 75 80

Phe Leu Gln Gly Ser Leu Gln Asn Tyr Cys Leu Asp Cys Ser Ala Pro
 85 90 95

Ile Gly Thr Trp
 100

<210> 1304
 <211> 50
 <212> PRT
 <213> Homo sapiens

<400> 1304
 Ser Trp Glu Pro Gly Gln Val Ser Val Gly Thr Ser Leu Ser Arg Trp
 5 10 15

<210> 1307
<211> 78
<212> PRT
<213> Homo sapiens

<400> 1307
Cys Pro Arg Trp Gly Thr Pro Arg Tyr Trp Leu Gly Ala Leu Tyr Arg
5 10 15
Asn Gln Gln Ser Ser Pro Thr Ala Pro Pro Gly Leu Leu Pro Leu Glu
20 25 30
Tyr Phe Pro Ala Ala Pro His Cys Ser His Ser Arg Gln Trp Arg Cys
35 40 45
Ser Gln Thr His Arg Ile His His His Pro Gln Met Leu Gly Pro Cys
50 55 60
Arg Gln Glu Ile Cys Gly Glu Ile Gln Gly Cys Gly Trp Phe
65 70 75

<210> 1308
<211> 134
<212> PRT
<213> Homo sapiens

<400> 1308
Asn Leu Leu Ile Glu Pro Gln Gln Gly Ala Asp Asn Cys Asp Val Asn
5 10 15
Gln Cys His Ser Phe Ala His Gln Lys Ser Pro Arg Leu Gln Val Ser
20 25 30
Ile Gln Gln Pro Gln Asn Ser Pro His Phe Leu Leu Cys Ile Leu Ser
35 40 45
Gly Leu Phe Val Val Val His Asp Ala Gln Gly Gly Glu His Pro Gly
50 55 60
Thr Gly Trp Gly His Tyr Ile Gly Ile Ser Lys Ala His Pro Leu His
65 70 75 80
His Leu Gly Cys Cys Leu Trp Ser Thr Ser Pro Gln Leu Leu Ile Ala
85 90 95
His Ile Val Gly Asn Gly Val Ala Leu Lys His Thr Glu Ser Ile Ile
100 105 110
Thr Leu Lys Cys Trp Asp Leu Ala Gly Arg Lys Phe Ala Glu Lys Phe
115 120 125
Arg Gly Ala Val Gly Leu
130

<210> 1309
<211> 66
<212> PRT
<213> Homo sapiens

<400> 1309
Ala Ser Ser Ser Pro Arg Ile Arg Leu Thr Ser Ser Phe Ala Phe Ser

5 10 15
 Val Ala Cys Leu Leu Trp Cys Met Met Pro Lys Val Gly Asn Thr Gln
 20 25 30
 Val Leu Ala Gly Gly Thr Ile Ser Glu Ser Ala Lys Leu Thr His Cys
 35 40 45
 Thr Thr Trp Ala Ala Ala Ser Gly Val Leu Pro Arg Ser Ser Ser Leu
 50 55 60
 Leu Thr
 65

<210> 1310
 <211> 141
 <212> PRT
 <213> Homo sapiens

<400> 1310
 Gln Thr Asn Arg Thr Pro Glu Phe Leu Arg Lys Phe Pro Ala Gly Lys
 5 10 15
 Val Pro Ala Phe Glu Gly Asp Asp Gly Phe Cys Val Phe Glu Ser Asn
 20 25 30
 Ala Ile Ala Tyr Tyr Val Ser Asn Glu Glu Leu Arg Gly Ser Thr Pro
 35 40 45
 Glu Ala Ala Ala Gln Val Val Gln Trp Val Ser Phe Ala Asp Ser Asp
 50 55 60
 Ile Val Pro Pro Ala Ser Thr Trp Val Phe Pro Thr Leu Gly Ile Met
 65 70 75 80
 His His Asn Lys Gln Ala Thr Glu Asn Ala Lys Glu Glu Val Arg Arg
 85 90 95
 Ile Leu Gly Leu Leu Asp Ala Tyr Leu Lys Thr Arg Thr Phe Leu Val
 100 105 110
 Gly Glu Arg Val Thr Leu Val Asp Ile Thr Val Val Cys Thr Leu Leu
 115 120 125
 Trp Leu Tyr Lys Gln Val Leu Glu Pro Ser Phe His Gln
 130 135 140

<210> 1311
 <211> 61
 <212> PRT
 <213> Homo sapiens

<400> 1311
 Cys His Lys Arg Ser Leu Pro Ile Cys Thr Tyr Ser Gln Glu Glu His
 5 10 15
 Leu Tyr Gly Lys Asp Gly Ser Pro Val Ser Leu Pro Tyr Thr Leu Gln
 20 25 30
 Gly Leu Ser Glu Ala Ser Leu Met Arg Cys Leu Lys Pro Gly His Gly
 35 40 45

Tyr Lys Gln Leu His Gly Ser Lys Lys Phe Cys Pro Phe
 50 55 60

<210> 1312
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 1312
 Ser Ile Phe Trp Gly Tyr Asp Gly Leu Thr Phe Ile Arg Lys Tyr Gly
 5 10 15
 Phe Ile Leu Ile Val Ala Ser Ser Ser Gly Gly Val Asn His Phe Ile
 20 25 30
 Phe Thr Leu Thr Trp Phe Glu Phe Leu Ser His Tyr Cys Ile Tyr Phe
 35 40 45
 Ala Phe Pro
 50

<210> 1313
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 1313
 Ser Trp Gly Gly Ser Gly Lys Phe Val Ser Val Ser Ser Ser Ser
 5 10 15
 Ser Trp Ile Gly Ile Ile Ser Met Ser Ser Ser Phe Phe Gly Trp Glu
 20 25 30
 Asp Val Ser Val Ser Pro Thr Thr Ser Ser Phe Ile Ser Ile Val Cys
 35 40 45
 Ser Phe Phe Ser Ser Ala Asp Arg Arg Thr Met Leu Asp Leu Gly Leu
 50 55 60
 Glu His Val Leu Phe His Ser Phe Ser Thr Met Pro Ala Ile Thr Ser
 65 70 75 80
 Ser Trp Lys Lys Ala Lys Ile Ser Ile Thr Asp Lys Met Pro Lys Asn
 85 90 95
 Arg Asp Cys Met Leu
 100

<210> 1314
 <211> 150
 <212> PRT
 <213> Homo sapiens

<400> 1314
 Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro Tyr Ile Asn
 5 10 15
 Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser
 20 25 30

Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly Ile Leu Ser
 35 40 45
 Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile Ala Gly Ile
 50 55 60
 Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys Ser Asn Ile
 65 70 75 80
 Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln Thr Ile Glu Ile Lys
 85 90 95
 Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser Gln Pro Lys Asn Glu
 100 105 110
 Glu Asp Ile Glu Ile Ile Pro Ile Gln Glu Glu Glu Glu Glu Thr
 115 120 125
 Glu Thr Asn Phe Pro Glu Pro Pro Gln Asp Gln Glu Ser Ser Pro Ile
 130 135 140
 Glu Asn Asp Ser Ser Pro
 145 150

<210> 1315
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 1315
 Thr Leu Pro Pro Asp Arg Met Lys Phe Ile Ser Thr Ser Leu Leu Leu
 5 10 15
 Met Leu Leu Val Ser Ser Leu Ser Pro Val Gln Gly Val Leu Glu Val
 20 25 30
 Tyr Tyr Thr Ser Leu Arg Cys Arg Cys Val Gln Glu Ser Ser Val Phe
 35 40 45
 Ile Pro Arg Arg Phe Ile Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn
 50 55 60
 Gly Cys Pro Arg Lys Glu Ile Ile Val Trp Lys Lys Asn Lys Ser Ile
 65 70 75 80
 Val Cys Val Asp Pro Gln Ala Glu Trp Ile Gln Arg Met Met Glu Val
 85 90 95
 Leu Arg Lys Arg Ser Ser Ser Thr Leu Pro Val Pro Val Phe Lys Arg
 100 105 110
 Lys Ile Pro
 115

<210> 1316
 <211> 55
 <212> PRT
 <213> Homo sapiens

<400> 1316

Glu Lys Glu Val Leu Gln Leu Tyr Gln Phe Gln Cys Leu Arg Glu Arg
 5 10 15

Phe Pro Asp Ala Asp Ile Ser Thr Lys Asn Thr Cys Ile Leu Pro Leu
 20 25 30

Ser Leu Leu Trp Ile Leu Val Leu Cys Leu Val Lys Ser Phe Pro Gly
 35 40 45

Lys Arg Thr Ser Pro Tyr Lys
 50 55

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<210> 1317
<211> 51
<212> PRT
<213> Homo sapiens
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<400> 1317
Ser His Ala Tyr Leu Tyr Gly Glu Val Leu Phe Pro Gly Lys Asp Leu
          5                      10                      15

Thr Lys His Lys Thr Lys Ile Gln Ser Arg Asp Lys Gly Arg Met Gln
          20                      25                      30

Val Phe Leu Val Glu Ile Ser Ala Ser Gly Asn Leu Ser Leu Lys His
          35                      40                      45

Trp Asn Trp
          50

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<210> 1318
<211> 68
<212> PRT
<213> Homo sapiens
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<400> 1318
Pro Pro Ala Tyr Ala Ala Cys His Thr Gly Asp Arg Phe Ser Arg Arg
          5                      10                      15

Ala Arg Arg Cys Trp Cys Gly Trp Lys Lys Gly Asn Arg Lys Gln Lys
          20                      25                      30

Lys Ser Leu Lys Glu Ser Cys His Phe Leu Leu Val Arg Ile Pro Asp
          35                      40                      45

Leu Gly Glu Val Leu Glu Ser Ser Ser Leu Phe Leu Leu Leu Pro Leu
          50                      55                      60

Leu Gly Leu Glu
          65

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<210> 1319
<211> 101
<212> PRT
<213> Homo sapiens
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<400> 1319
Ser Trp Gly Gly Ser Gly Lys Phe Val Ser Val Ser Ser Ser Ser Ser

5 10 15

Ser Trp Ile Gly Ile Ile Ser Met Ser Ser Ser Phe Phe Gly Trp Glu
 20 25 30
 Asp Val Ser Val Ser Pro Thr Thr Ser Ser Phe Ile Ser Ile Val Cys
 35 40 45
 Ser Phe Phe Ser Ser Ala Asp Arg Arg Thr Met Leu Asp Leu Gly Leu
 50 55 60
 Glu His Val Leu Phe His Ser Phe Ser Thr Met Pro Ala Ile Thr Ser
 65 70 75 80
 Ser Trp Lys Lys Ala Lys Ile Ser Ile Thr Asp Lys Met Pro Lys Asn
 85 90 95
 Arg Asp Cys Met Leu
 100

<210> 1320
 <211> 137
 <212> PRT
 <213> Homo sapiens

<400> 1320
 Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn
 5 10 15
 Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly
 20 25 30
 Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile
 35 40 45
 Ala Gly Ile Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys
 50 55 60
 Ser Asn Ile Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln Thr Ile
 65 70 75 80
 Glu Ile Lys Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser Gln Pro
 85 90 95
 Lys Asn Glu Glu Asp Ile Glu Ile Ile Pro Ile Gln Glu Glu Glu Glu
 100 105 110
 Glu Glu Thr Glu Thr Asn Phe Pro Glu Pro Pro Gln Asp Gln Glu Ser
 115 120 125
 Ser Pro Ile Glu Asn Asp Ser Ser Pro
 130 135

<210> 1321
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 1321
 Asn Lys Lys Ala Met Leu Val Glu Cys Thr Val His Ile Gly Gly Ala
 5 10 15
 Arg Leu Ile Thr Ile Arg Leu Leu Ala Ser Pro Val Gln Ser Phe Leu

20 25 30
 Trp Lys Ala Val Asp Phe Ser Leu Ala Ser Leu Ser Ser Ser Val Ser
 35 40 45

Thr Tyr Arg Ile Ser Arg Ser Gln Pro Tyr Arg
 50 55

<210> 1322
 <211> 64
 <212> PRT
 <213> Homo sapiens

<400> 1322
 Thr Ala Lys Arg Ser Lys Ile Arg Arg Gln Cys Leu Trp Asn Val Gln
 5 10 15

Cys Ile Leu Ala Ala His Ala Ser Leu Arg Phe Ala Cys Leu Leu Leu
 20 25 30

Leu Phe Asn Arg Phe Phe Gly Arg Gln Trp Ile Phe Leu Leu Arg Leu
 35 40 45

Cys Leu Leu Gln Phe Arg Leu Ile Glu Phe Leu Asp Leu Ser His Ile
 50 55 60

<210> 1323
 <211> 57
 <212> PRT
 <213> Homo sapiens

<400> 1323
 Glu Gly Asn Ala Cys Gly Met Tyr Ser Ala Tyr Trp Arg Arg Thr Pro
 5 10 15

His Tyr Asp Ser Pro Ala Cys Phe Ser Cys Ser Ile Val Ser Leu Glu
 20 25 30

Gly Ser Gly Phe Phe Ser Cys Val Ser Val Phe Phe Ser Phe Asp Leu
 35 40 45

Ser Asn Phe Ser Ile Ser Ala Ile Ser
 50 55

<210> 1324
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 1324
 Arg Arg Gln Arg Arg Lys Arg Lys Ile His Cys Leu Pro Lys Lys Arg
 5 10 15

Leu Asn Arg Arg Ser Lys Gln Ala Asn Arg Asn Glu Ala Cys Ala Ala
 20 25 30

Asn Met His Cys Thr Phe His Lys His Cys Leu Leu Ile Leu Leu Leu
 35 40 45

Leu Ala Val

50

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<210> 1325 .
<211> 64
<212> PRT
<213> Homo sapiens
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<220>  
<221> variant  
<222> (1)...(64)  
<223> Xaa = Any amino acid
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<400> 1325
Leu Asn Ile Leu Asn Xaa Ala Leu Leu Ser Val Glu Leu Leu Tyr Phe
      5                      10                      15

Thr Phe Ser Ala Phe Gly Asp His Tyr Leu Ile Glu Phe Val Glu Ile
      20                      25                      30

Asp Phe Pro Asp Arg Ser Leu Phe Phe Asn Glu Gln Met Ile Arg Asn
      35                      40                      45

Asn Leu Thr Pro Tyr Met Thr Met Glu Leu Asn Lys Leu Thr Leu Ile
      50                      55                      60

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<210> 1326
<211> 100
<212> PRT
<213> Homo sapiens
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<400> 1326
Leu Asn Lys Arg Gly Thr Asn Phe Gln Phe Val Lys Leu Gln Ser Arg
      5                                10                        15

Lys Tyr Trp Cys Leu Leu Pro Cys Glu Phe Phe Leu Arg His Ala Glu
      20                                25                        30

Lys Met Tyr Ala Arg Asp Gln Lys Asp Gly Ser Lys Leu Cys His Val
      35                                40                        45

Thr Cys Asn Lys Ile Phe Ser Ser Arg Phe Phe Leu Cys Trp Gln Ile
      50                                55                        60

Ile Ser Pro Cys Ser Phe His Ser Leu Ile Leu Ala Phe Arg Val Thr
      65                                70                        75                        80

Met Ile Ile Leu Pro Met Trp Phe Leu Arg Lys Lys Asp Gln Phe Phe
      85                                90                        95

Val Cys Ser Arg
      100
```

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<210> 1327
<211> 52
<212> PRT
<213> Homo sapiens
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<400> 1327
Asn Ser Lys Ala Glu Ser Ile Gly Ala Cys Tyr Leu Val Asn Ser Ser
          5                      10                    15
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Leu Asp Met Gln Arg Lys Cys Met Gln Glu Thr Lys Lys Met Ala Pro
 20 25 30

Ser Tyr Val Met Leu Pro Val Ile Lys Ser Phe Leu Leu Asp Ser Phe
 35 40 45

Tyr Val Gly Arg
 50

<210> 1328
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 1328
 Asn Lys Lys Ala Met Leu Val Glu Cys Thr Val His Ile Gly Gly Ala
 5 10 15

Arg Leu Ile Thr Ile Arg Leu Leu Ala Ser Pro Val Gln Ser Phe Leu
 20 25 30

Trp Lys Ala Val Asp Phe Ser Leu Ala Ser Leu Ser Ser Ser Val Ser
 35 40 45

Thr Tyr Arg Ile Ser Arg Ser Gln Pro Tyr Arg
 50 55

<210> 1329
 <211> 64
 <212> PRT
 <213> Homo sapiens

<400> 1329
 Thr Ala Lys Arg Ser Lys Ile Arg Arg Gln Cys Leu Trp Asn Val Gln
 5 10 15

Cys Ile Leu Ala Ala His Ala Ser Leu Arg Phe Ala Cys Leu Leu Leu
 20 25 30

Leu Phe Asn Arg Phe Phe Gly Arg Gln Trp Ile Phe Leu Leu Arg Leu
 35 40 45

Cys Leu Leu Gln Phe Arg Leu Ile Glu Phe Leu Asp Leu Ser His Ile
 50 55 60

<210> 1330
 <211> 57
 <212> PRT
 <213> Homo sapiens

<400> 1330
 Glu Gly Asn Ala Cys Gly Met Tyr Ser Ala Tyr Trp Arg Arg Thr Pro
 5 10 15

His Tyr Asp Ser Pro Ala Cys Phe Ser Cys Ser Ile Val Ser Leu Glu
 20 25 30

Gly Ser Gly Phe Phe Ser Cys Val Ser Val Phe Phe Ser Phe Asp Leu
 35 40 45

Ser Asn Phe Ser Ile Ser Ala Ile Ser
50 55

<210> 1331
<211> 51
<212> PRT
<213> Homo sapiens

<400> 1331
Arg Arg Gln Arg Arg Lys Arg Lys Ile His Cys Leu Pro Lys Lys Arg
5 10 15

Leu Asn Arg Arg Ser Lys Gln Ala Asn Arg Asn Glu Ala Cys Ala Ala
20 25 30

Asn Met His Cys Thr Phe His Lys His Cys Leu Leu Ile Leu Leu Leu
35 40 45

Leu Ala Val
50

<210> 1332
<211> 50
<212> PRT
<213> Homo sapiens

<400> 1332
Asp Arg Tyr Trp Tyr Ser Phe Ile Ile Glu Thr Lys Arg Ser Ala Leu
5 10 15

Leu Asp Phe Pro Leu Phe Val Leu Lys Gly Ile Lys Asp Cys Arg Phe
20 25 30

Pro Ala Leu Ser Ser Arg Gly His Tyr Glu Gln Ile Lys Trp Lys Asp
35 40 45

Lys Phe
50

<210> 1333
<211> 51
<212> PRT
<213> Homo sapiens

<400> 1333
Trp Pro Arg Glu Asp Arg Ala Gly Asn Leu Gln Ser Leu Ile Pro Phe
5 10 15

Arg Thr Lys Ser Gly Lys Ser Ser Lys Ala Asp Leu Leu Val Ser Ile
20 25 30

Ile Lys Glu Tyr Gln Tyr Arg Ser Gln Lys Arg Ser Val Ser Leu Gln
35 40 45

Gly Tyr Phe
50

<210> 1334

<211> 90

<212> PRT

<213> Homo sapiens

<400> 1334

Pro Lys Glu Val Arg Gln Leu Ala Glu Asp Phe Leu Lys Asp Tyr Ile
5 10 15

His Ile Asn Ile Gly Ala Leu Glu Leu Ser Ala Asn His Asn Ile Leu
20 25 30

Gln Ile Val Asp Val Cys His Asp Val Glu Lys Asp Glu Lys Leu Ile
35 40 45

Arg Leu Met Glu Glu Ile Met Ser Glu Lys Glu Asn Lys Thr Ile Val
50 55 60

Phe Val Glu Thr Lys Arg Arg Cys Asp Glu Leu Thr Arg Lys Met Arg
65 70 75 80

Arg Asp Gly Trp Pro Ala Met Gly Ile His
85 90

<210> 1335

<211> 52

<212> PRT

<213> Homo sapiens

<400> 1335

Pro Trp Ile Pro Met Ala Gly His Pro Ser Leu Leu Ile Phe Leu Val
5 10 15

Ser Ser Ser His Leu Leu Leu Val Ser Thr Lys Thr Met Val Leu Phe
20 25 30

Ser Phe Ser Leu Met Ile Ser Ser Ile Arg Arg Ile Ser Phe Ser Ser
35 40 45

Phe Ser Thr Ser
50

<210> 1336

<211> 166

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1) ... (166)

<223> Xaa = Any amino acid

<400> 1336

Arg Gln Phe Val Thr Ala Thr Asp Val Val Arg Gly Asn Pro Lys Leu
5 10 15

Asn Leu Ala Phe Ile Ala Asn Leu Phe Asn Arg Tyr Pro Ala Leu His
20 25 30

Lys Pro Glu Asn Gln Asp Ile Asp Trp Gly Ala Leu Glu Gly Glu Thr
35 40 45

Arg Glu Glu Arg Thr Phe Arg Asn Trp Met Asn Ser Leu Gly Val Asn
 50 55 60
 Pro Arg Val Asn His Leu Tyr Ser Asp Leu Ser Asp Ala Leu Val Ile
 65 70 75 80
 Phe Gln Leu Tyr Glu Lys Ile Lys Val Pro Val Asp Trp Asn Arg Val
 85 90 95
 Asn Lys Pro Pro Tyr Pro Lys Leu Gly Gly Asn Met Lys Lys Leu Glu
 100 105 110
 Asn Cys Asn Tyr Ala Val Glu Leu Gly Lys Asn Gln Ala Lys Phe Ser
 115 120 125
 Leu Val Gly Ile Gly Gly Gln Asp Leu Asn Glu Gly Asn Arg Thr Leu
 130 135 140
 Thr Leu Ala Leu Ile Trp Gln Leu Met Arg Arg Tyr Thr Leu Asn Ile
 145 150 155 160
 Leu Xaa Glu Ile Gly Gly
 165

<210> 1337
 <211> 76
 <212> PRT
 <213> Homo sapiens

<400> 1337
 Leu Pro Asn Gln Gly Gln Cys Glu Ser Ala Val Ser Phe Ile Glu Ile
 5 10 15
 Leu Ser Thr Asp Ala Asn Gln Gly Glu Leu Arg Leu Ile Leu Pro Gln
 20 25 30
 Phe Tyr Arg Val Val Thr Ile Leu Lys Leu Leu His Ile Ala Ser Gln
 35 40 45
 Phe Gly Val Trp Arg Phe Val Tyr Ser Val Pro Val Asn Arg Asn Phe
 50 55 60
 Asp Leu Phe Ile Glu Leu Glu Asp Asp Gln Gly Ile
 65 70 75

<210> 1338
 <211> 73
 <212> PRT
 <213> Homo sapiens

<400> 1338
 Val Thr Val Gln Met Ile Asp Ser Arg Val Asn Thr Gln Gly Val His
 5 10 15
 Pro Val Pro Lys Cys Pro Leu Phe Ser Arg Leu Thr Phe Lys Ser Pro
 20 25 30
 Pro Val Asn Val Leu Val Leu Trp Phe Val Gln Gly Arg Val Ser Val
 35 40 45
 Lys Glu Val Gly Asn Lys Ser Gln Val Gln Leu Gly Val Pro Ser Asp

450

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50
Asn Ile Cys Gly Cys Asp Lys Leu Pro
65
70
<210> 1339
<211> 68
<212> PRT
<213> Homo sapiens
<400> 1339
Leu Thr Arg Gly Leu Thr Pro Arg Glu Phe Ile Gln Phe Leu Asn Val
5 10 15
Arg Ser Ser Leu Val Ser Pro Ser Arg Ala Pro Gln Ser Met Ser Trp
20 25 30
Phe Ser Gly Leu Cys Arg Ala Gly Tyr Leu Leu Lys Arg Leu Ala Ile
35 40 45
Lys Ala Lys Phe Asn Leu Gly Phe Pro Arg Thr Thr Ser Val Ala Val
50 55 60
Thr Asn Cys Arg
65

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<210> 1340
<211> 60
<212> PRT
<213> Homo sapiens

<400> 1340
Trp Arg Gly Ser Gly Leu Leu Pro Gln Val Gln Pro Lys Glu Asp Ser
          5                      10                      15
Arg Gln Gly Cys Pro Gln Leu Pro Glu Ala Gly Thr Lys Leu Arg Leu
          20                      25                      30
Leu His Pro Ser Tyr Pro Val Leu Ala Pro Gln Ala Leu Ser Gly Arg
          35                      40                      45
Ala Met Cys Arg Pro Lys Gly Ala Leu Gly Ala Ala
          50                      55                      60

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<210> 1341
<211> 95
<212> PRT
<213> Homo sapiens

<400> 1341
Leu Ala Ser Tyr Ser Pro Ser Thr Thr Asp Met Ala Gln Ser Leu Ala
                    5                      10                      15

Leu Ser Leu Leu Thr Leu Val Leu Ala Phe Gly Ile Pro Arg Thr Gln
                20                      25                      30

Gly Ser Asp Gly Gly Ala Gln Asp Cys Cys Leu Lys Tyr Ser Gln Arg
    35                      40                      45

Lys Ile Pro Ala Lys Val Val Arg Ser Tyr Arg Lys Gln Glu Pro Ser

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50 55 60
 Leu Gly Cys Ser Ile Pro Ala Ile Leu Phe Leu Pro Arg Lys Arg Ser
 65 70 75 80

Gln Ala Glu Leu Cys Ala Asp Pro Lys Glu Leu Trp Val Gln Gln
 85 90 95

<210> 1342
 <211> 50
 <212> PRT
 <213> Homo sapiens

<400> 1342
 Ala Trp Phe Leu Leu Pro Val Ala Ala Asp Asn Leu Gly Gly Asn Leu
 5 10 15

Pro Leu Ala Val Leu Glu Ala Thr Val Leu Ser Pro Ser Ile Thr Ala
 20 25 30

Leu Gly Pro Gly Asp Ala Lys Gly Gln Asn Gln Gly Lys Glu Ala Gln
 35 40 45

Ser Gln
 50

<210> 1343
 <211> 102
 <212> PRT
 <213> Homo sapiens

<400> 1343
 Leu Pro Thr Ser Pro Ser Ala Leu Ala Ser Asp Ser Pro Ser Thr Thr
 5 10 15

Asp Met Ala Gln Ser Leu Ala Leu Ser Leu Leu Ile Leu Val Leu Ala
 20 25 30

Phe Gly Ile Pro Arg Thr Gln Gly Ser Asp Gly Gly Ala Gln Asp Cys
 35 40 45

Cys Leu Lys Tyr Ser Gln Arg Lys Ile Pro Ala Lys Val Val Arg Ser
 50 55 60

Tyr Arg Lys Gln Glu Pro Ser Leu Gly Cys Ser Ile Pro Ala Ile Leu
 65 70 75 80

Phe Leu Pro Arg Lys Arg Ser Gln Ala Glu Leu Cys Ala Asp Pro Lys
 85 90 95

Glu Leu Trp Val Gln Gln
 100

<210> 1344
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 1344
 Trp Arg Gly Ser Gly Leu Leu Pro Gln Val Gln Pro Lys Glu Asp Ser

5 10 15
 Arg Gln Gly Cys Pro Gln Leu Pro Glu Ala Gly Thr Lys Leu Arg Leu
 20 25 30
 Leu His Pro Ser Tyr Pro Val Leu Ala Pro Gln Ala Leu Ser Gly Arg
 35 40 45
 Ala Met Cys Arg Pro Lys Gly Ala Leu Gly Ala Ala
 50 55 60

<210> 1345
 <211> 50
 <212> PRT
 <213> Homo sapiens

<400> 1345
 Ala Trp Phe Leu Leu Pro Val Ala Ala Asp Asn Leu Gly Gly Asn Leu
 5 10 15
 Pro Leu Ala Val Leu Glu Ala Thr Val Leu Ser Pro Ser Ile Thr Ala
 20 25 30
 Leu Gly Pro Gly Asp Ala Lys Gly Gln Asn Gln Asp Lys Glu Ala Gln
 35 40 45
 Ser Gln
 50

<210> 1346
 <211> 76
 <212> PRT
 <213> Homo sapiens

<400> 1346
 Thr Lys Leu Val Met Met Gln Lys Leu Leu Lys Cys Ser Arg Leu Val
 5 10 15
 Leu Ala Leu Ala Leu Ile Leu Val Leu Glu Ser Ser Val Gln Gly Tyr
 20 25 30
 Pro Thr Gln Arg Ala Arg Tyr Gln Trp Val Arg Cys Asn Pro Asp Ser
 35 40 45
 Asn Ser Ala Asn Cys Leu Glu Glu Lys Gly Pro Met Phe Glu Leu Leu
 50 55 60
 Pro Gly Glu Ser Asn Lys Ile Pro Arg Leu Arg Thr
 65 70 75

<210> 1347
 <211> 68
 <212> PRT
 <213> Homo sapiens

<400> 1347
 Cys Arg Ser Tyr Ser Asn Ala Val Gly Leu Ser Trp Leu Leu Pro Ser
 5 10 15
 Ser Trp Phe Trp Asn Pro Gln Phe Lys Val Ile Leu Arg Arg Glu Pro

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<210> 1348
<211> 87
<212> PRT
<213> Homo sapiens
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<210> 1349
<211> 55
<212> PRT
<213> Homo sapiens
```

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<210> 1350
<211> 120
<212> PRT
<213> Homo sapiens
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<400> 1350
Leu Lys Lys Pro Gln Ser Pro His Val Glu Glu Asp Asp Asp Asp Glu

454

[illegible]

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<210> 1351
<211> 124
<212> PRT
<213> Homo sapiens
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<400> 1351
Ile Met His Leu Ser Phe Val Asp Asn Leu Asn Val Glu Val Leu Ser
      5              10              15

Val Ser Leu Val His Leu Ile Leu Glu Lys Ala Leu Asp Gln Ser Gly
      20              25              30

Leu Met Ile Leu Tyr Ala Thr Gly Asn Glu Ser Ala Leu Trp Asn Cys
      35              40              45

Lys His Gln Gly Trp Gly Lys His Asn Cys Asp His Ala Glu Asp Ala
      50              55              60

Gly Val Ile Cys Ser Lys Gly Ala Asp Leu Ser Leu Arg Leu Val Asp
      65              70              75              80

Gly Val Thr Glu Cys Ser Gly Arg Leu Glu Val Arg Phe Gln Gly Glu
      85              90              95

Trp Gly Thr Ile Cys Asp Asp Gly Trp Asp Ser Tyr Asp Ala Ala Val
      100             105             110

Ala Cys Lys Gln Leu Gly Cys Pro Thr Ala Val Pro
      115             120

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<210> 1352
<211> 69
<212> PRT
<213> Homo1 sapiens
```

<400> 1352
Arg Gly Gly Asn Met Cys Ser Gly Arg Ile Glu Ile Lys Phe Gln Gly
 5 10 15

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<210> 1353
<211> 80
<212> PRT
<213> Homo sapiens
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<400> 1353
Leu His Leu Pro Val Ser Gly Ser Asp Leu Leu Pro Leu Ser Lys Ser
      5                      10                      15

Leu Gln His Pro Gln His Asp His Ser Tyr Ala Phe Pro Ile Leu Asp
      20                      25                      30

Val Cys Ser Ser Arg Glu Leu Thr His Phe Arg Leu His Ile Arg Ser
      35                      40                      45

Ser Asn Gln Ile Gly Pro Glu Pro Ser Pro Lys Leu Asp Glu Pro Glu
      50                      55                      60

Lys Leu Thr Ala Leu Pro His Ser Ser Cys Leu Gln Met Thr Asp Ala
      65                      70                      75                      80

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<210> 1354
<211> 59
<212> PRT
<213> Homo sapiens
```

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<400> 1354
Glu Ser Asn Lys Ile Pro Arg Leu Arg Thr Asp Leu Phe Pro Lys Thr
      5              10              15

Arg Ile Gln Asp Leu Asn Arg Ile Phe Pro Leu Ser Glu Asp Tyr Ser
      20              25              30

Gly Ser Gly Phe Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
      35              40              45

Gly Phe Leu Thr Glu Met Asp Lys Asp Ser Asn
      50              55

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<210> 1355
<211> 68
<212> PRT
<213> Homo sapiens
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<400> 1355
Ser Trp Lys Ala Ser Leu Ser Ser Thr Ser Trp Asn Pro Cys Pro Phe
 5 10 15

Pro Leu Gly Ser His Ser Gln Ile Leu Ile Gln Ser Arg Ser Arg Ser
 20 25 30
 Arg Ser Leu Ile Gln Ser Ser Pro Gln Lys Val Gly Arg Tyr Asp Ser
 35 40 45
 Ser Pro Gly Phe Ser Ser Leu Glu Lys Gly Gln Ser Ser Asp Gly Gly
 50 55 60
 Ser Cys Trp Ile
 65

<210> 1356
 <211> 158
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(158)
 <223> Xaa = Any amino acid

<400> 1356
 Met Met Gln Lys Leu Leu Lys Cys Ser Arg Val Val Leu Ala Leu Ala
 5 10 15
 Leu Ile Leu Val Leu Glu Ser Ser Val Gln Gly Tyr Pro Thr Gln Arg
 20 25 30
 Ala Arg Tyr Gln Trp Val Arg Cys Asn Pro Asp Ser Asn Ser Ala Asn
 35 40 45
 Cys Leu Glu Glu Lys Gly Pro Met Phe Xaa Leu Leu Pro Gly Glu Ser
 50 55 60
 Asn Lys Ile Pro Arg Leu Arg Thr Asp Leu Phe Pro Lys Thr Arg Ile
 65 70 75 80
 Gln Asp Leu Asn Arg Ile Phe Xaa Leu Ser Glu Asp Tyr Ser Gly Ser
 85 90 95
 Gly Phe Gly Ser Gly Ser Xaa Ser Gly Ser Gly Ser Gly Ser Gly Phe
 100 105 110
 Leu Thr Glu Met Glu Gln Asp Tyr Gln Leu Val Asp Gln Ser Asp Ala
 115 120 125
 Phe His Asp Asn Leu Arg Ser Leu Asp Arg Asn Leu Pro Ser Xaa Ser
 130 135 140
 Xaa Asp Leu Gly Gln His Gly Leu Glu Glu Asp Phe Met Leu
 145 150 155

<210> 1357
 <211> 68
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant

<222> (1) ... (68)

<223> Xaa = Any amino acid

<400> 1357

Cys Arg Ser Tyr Ser Asn Ala Val Gly Leu Ser Trp Leu Leu Pro Ser
5 10 15

Ser Trp Phe Trp Asn Pro Gln Phe Lys Val Ile Leu Arg Arg Glu Pro
20 25 30

Gly Thr Asn Gly Cys Ala Ala Ile Gln Thr Val Ile Leu Gln Thr Ala
35 40 45

Leu Lys Lys Lys Asp Gln Cys Xaa Asn Tyr Phe Gln Val Asn Pro Thr
50 55 60

Arg Ser Pro Val
65

<210> 1358

<211> 64

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1) ... (64)

<223> Xaa = Any amino acid

<400> 1358

Ser Ser Glu Xaa Gly Lys Ile Arg Phe Lys Ser Trp Ile Leu Val Phe
5 10 15

Gly Lys Arg Ser Val Leu Arg Arg Gly Ile Leu Leu Asp Ser Pro Gly
20 25 30

Ser Ser Xaa Asn Ile Gly Pro Phe Ser Ser Arg Gln Phe Ala Glu Leu
35 40 45

Leu Ser Gly Leu Gln Arg Thr His Trp Tyr Leu Ala Leu Cys Val Gly
50 55 60

<210> 1359

<211> 103

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1) ... (103)

<223> Xaa = Any amino acid

<400> 1359

Gly Cys His Gly Lys His His Phe Gly Leu Leu Val Gly Asn Pro Val
5 10 15

Pro Phe Pro Leu Gly Ser His Ser Gln Ile Leu Ile Gln Xaa Arg Ser
20 25 30

Arg Ser Arg Ser Leu Ile Gln Ser Ser Pro Gln Lys Xaa Gly Arg Tyr
35 40 45

Asp Ser Ser Pro Gly Phe Trp Ser Leu Glu Lys Gly Gln Ser Ser Asp
 50 55 60

Gly Gly Ser Cys Trp Ile His Leu Glu Val Val Xaa Thr Leu Val Leu
 65 70 75 80

Phe Leu Gln Gly Ser Leu Gln Asn Tyr Cys Leu Asp Cys Ser Ala Pro
 85 90 95

Ile Gly Thr Trp Leu Ser Ala
 100

<210> 1360

<211> 123

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(123)

<223> Xaa = Any amino acid

<400> 1360

Val Met Met Gln Lys Leu Leu Lys Cys Ser Arg Leu Val Leu Ala Leu
 5 10 15

Ala Leu Ile Leu Val Leu Glu Ser Ser Val Gln Gly Tyr Pro Thr Gln
 20 25 30

Arg Ala Arg Tyr Gln Trp Val Arg Cys Asn Pro Asp Ser Asn Ser Ala
 35 40 45

Asn Cys Leu Glu Glu Lys Gly Pro Met Phe Glu Leu Leu Pro Gly Glu
 50 55 60

Ser Asn Lys Ile Pro Arg Leu Arg Thr Asp Leu Phe Pro Lys Thr Arg
 65 70 75 80

Ile Gln Asp Leu Asn Arg Ile Phe Xaa Leu Ser Glu Asp Tyr Ser Gly
 85 90 95

Ser Gly Phe Gly Ser Arg Ser Gly Ser Gly Ser Gly Ser Gly
 100 105 110

Phe Leu Thr Glu Met Glu Xaa Gly Leu Pro Asn
 115 120

<210> 1361

<211> 68

<212> PRT

<213> Homo sapiens

<400> 1361

Cys Arg Ser Tyr Ser Asn Ala Val Gly Leu Ser Trp Leu Leu Pro Ser
 5 10 15

Ser Trp Phe Trp Asn Pro Gln Phe Lys Val Ile Leu Arg Arg Glu Pro
 20 25 30

Gly Thr Asn Gly Cys Ala Ala Ile Gln Thr Val Ile Leu Gln Thr Ala

35 40 45
 Leu Lys Lys Lys Asp Gln Cys Ser Asn Tyr Phe Gln Val Asn Pro Thr
 50 55 60

Arg Ser Pro Val
 65

<210> 1362
 <211> 64
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(64)
 <223> Xaa = Any amino acid

<400> 1362
 Ser Ser Glu Xaa Gly Lys Ile Arg Phe Lys Ser Trp Ile Leu Val Phe
 5 10 15

Gly Lys Arg Ser Val Leu Arg Arg Gly Ile Leu Leu Asp Ser Pro Gly
 20 25 30

Ser Ser Ser Asn Ile Gly Pro Phe Ser Ser Arg Gln Phe Ala Glu Leu
 35 40 45

Leu Ser Gly Leu Gln Arg Thr His Trp Tyr Leu Ala Leu Cys Val Gly
 50 55 60

<210> 1363
 <211> 104
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(104)
 <223> Xaa = Any amino acid

<400> 1363
 Gly Leu Ser Trp Lys Ala Ser Leu Ser Ser Thr Ser Trp Val Ile Xaa
 5 10 15

Val Pro Phe Pro Leu Gly Ser His Ser Gln Ile Leu Ile Gln Ser Arg
 20 25 30

Ser Gly Ser Arg Ser Leu Ile Gln Ser Ser Pro Gln Lys Xaa Gly Arg
 35 40 45

Tyr Asp Ser Ser Pro Gly Phe Ser Ser Leu Glu Lys Gly Gln Ser Ser
 50 55 60

Asp Gly Gly Ser Cys Trp Ile His Leu Glu Val Val Arg Thr Leu Val
 65 70 75 80

Leu Phe Leu Gln Gly Ser Leu Gln Asn Tyr Cys Leu Asp Cys Ser Ala
 85 90 95

Pro Ile Gly Thr Trp Leu Ser Ala

100

<210> 1364
 <211> 148
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(148)
 <223> Xaa = Any amino acid

<400> 1364
 Thr Xaa Xaa Val Met Met Gln Lys Leu Leu Lys Cys Ser Arg Leu Val
 5 10 15
 Leu Ala Leu Ala Leu Ile Leu Val Leu Glu Ser Ser Val Gln Gly Tyr
 20 25 30
 Pro Thr Gln Arg Ala Arg Tyr Gln Trp Val Arg Cys Asn Pro Asp Ser
 35 40 45
 Asn Ser Ala Asn Cys Leu Glu Glu Lys Gly Pro Met Xaa Glu Leu Leu
 50 55 60
 Xaa Gly Glu Xaa Asn Xaa Ile Pro Arg Leu Arg Thr Asp Leu Phe Pro
 65 70 75 80
 Lys Thr Arg Ile Gln Asp Leu Asn Arg Ile Phe Pro Leu Ser Glu Asp
 85 90 95
 Tyr Ser Gly Ser Gly Phe Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
 100 105 110
 Gly Ser Gly Phe Leu Thr Glu Met Glu Gln Asp Tyr Gln Leu Xaa Asp
 115 120 125
 Glu Ser Asp Ala Phe His Asp Asn Leu Xaa Ser Leu Asp Arg Asn Leu
 130 135 140
 Pro Xaa Asp Ser
 145

<210> 1365
 <211> 68
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(68)
 <223> Xaa = Any amino acid

<400> 1365
 Cys Arg Ser Tyr Ser Asn Ala Val Gly Leu Ser Trp Leu Leu Pro Ser
 5 10 15
 Ser Trp Phe Trp Asn Pro Gln Phe Lys Val Ile Leu Arg Arg Glu Pro
 20 25 30
 Gly Thr Asn Gly Cys Ala Ala Ile Gln Thr Val Ile Leu Gln Thr Ala

35 40 45
 Leu Lys Lys Lys Asp Gln Cys Xaa Asn Tyr Xaa Gln Val Asn Xaa Thr
 50 55 60
 Xaa Ser Pro Val
 65

<210> 1366
 <211> 103
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(103)
 <223> Xaa = Any amino acid

<400> 1366
 Gly Cys His Gly Lys His His Phe Arg Leu Xaa Val Gly Asn Pro Val
 5 10 15
 Pro Phe Pro Leu Gly Ser His Ser Gln Ile Leu Ile Gln Ser Arg Ser
 20 25 30
 Arg Ser Arg Ser Leu Ile Gln Ser Ser Pro Gln Lys Val Gly Arg Tyr
 35 40 45
 Asp Ser Ser Pro Gly Phe Ser Ser Leu Glu Lys Gly Gln Ser Ser Asp
 50 55 60
 Gly Gly Xaa Cys Xaa Ile His Leu Xaa Val Val Xaa Thr Leu Val Leu
 65 70 75 80
 Phe Leu Gln Gly Ser Leu Gln Asn Tyr Cys Leu Asp Cys Ser Ala Pro
 85 90 95
 Ile Gly Thr Trp Leu Ser Ala
 100

<210> 1367
 <211> 64
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(64)
 <223> Xaa = Any amino acid

<400> 1367
 Ser Ser Glu Ser Gly Lys Ile Arg Phe Lys Ser Trp Ile Leu Val Phe
 5 10 15
 Gly Lys Arg Ser Val Leu Arg Arg Gly Ile Xaa Leu Xaa Ser Pro Xaa
 20 25 30
 Ser Ser Xaa Asn Ile Gly Pro Phe Ser Ser Arg Gln Phe Ala Glu Leu
 35 40 45
 Leu Ser Gly Leu Gln Arg Thr His Trp Tyr Leu Ala Leu Cys Val Gly

50

55

60

<210> 1368
 <211> 50
 <212> PRT
 <213> Homo sapiens

<400> 1368
 Leu Thr Leu Pro Gly Gly Ile Arg Val Arg Arg Arg Gly Arg Gly Trp
 5 10 15
 Arg Ser Gly Gly Asp His Gly Val Ser Arg Pro His Cys Ala Ser His
 20 25 30
 Cys Asp Glu Arg Val Leu Gly Leu Arg Arg Leu Leu Gly Ala Leu Val
 35 40 45
 His Pro
 50

<210> 1369
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 1369
 Gly Asp Gly Val Gly Val Gly Ala Gln Ala Ala Thr Met Ala Tyr His
 5 10 15
 Gly Leu Thr Val Pro Leu Ile Val Met Ser Val Phe Trp Gly Phe Val
 20 25 30
 Gly Phe Leu Val Pro Trp Phe Ile Pro Lys Gly Pro Asn Arg Gly Val
 35 40 45
 Ile Ile Thr Met Leu Val Thr Cys Ser Val Cys Cys Tyr Leu Phe Trp
 50 55 60
 Leu Ile Ala Ile Leu Ala Gln Leu Asn Pro Leu Phe Gly Pro Gln Leu
 65 70 75 80
 Lys Asn Glu Thr Ile Trp Tyr Leu Lys Tyr His Trp Pro
 85 90

<210> 1370
 <211> 65
 <212> PRT
 <213> Homo sapiens

<400> 1370
 Thr Gly His Gln His Gly Asn Asp Asn Ser Pro Val Arg Thr Leu Arg
 5 10 15
 Asp Glu Pro Arg His Gln Glu Ala Asp Glu Ala Pro Glu His Ala His
 20 25 30
 His Asn Glu Arg His Ser Glu Ala Val Ile Arg His Gly Arg Arg Leu
 35 40 45
 Ser Ala Asn Pro Tyr Pro Val Ala Ser Leu Gly Ser His Gln Glu Val

50

55

60

Ser
65

<210> 1371
<211> 68
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(68)
<223> Xaa = Any amino acid

<400> 1371
Cys Xaa Ser Tyr Ser Asn Ala Val Gly Leu Ser Trp Leu Leu Pro Ser
 5 10 15
Ser Trp Phe Trp Asn Pro Gln Phe Lys Val Ile Leu Arg Arg Glu Pro
 20 25 30
Gly Thr Asn Gly Cys Ala Ala Ile Gln Thr Val Ile Leu Gln Thr Ala
 35 40 45
Leu Lys Lys Lys Asp Gln Cys Ser Asn Tyr Phe Xaa Val Asn Pro Thr
 50 55 60
Arg Ser Pro Val
 65

<210> 1372
<211> 143
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(143)
<223> Xaa = Any amino acid

<400> 1372
Xaa Met Met Xaa Lys Leu Leu Lys Cys Ser Arg Leu Val Leu Ala Leu
 5 10 15
Ala Leu Ile Leu Val Leu Glu Ser Ser Val Gln Gly Tyr Pro Thr Gln
 20 25 30
Arg Ala Arg Tyr Gln Trp Val Arg Cys Asn Pro Asp Ser Asn Ser Ala
 35 40 45
Asn Cys Leu Glu Glu Lys Gly Pro Met Phe Glu Leu Leu Pro Xaa Glu
 50 55 60
Ser Asn Lys Ile Pro Arg Leu Arg Thr Asp Leu Phe Xaa Lys Thr Arg
 65 70 75 80
Ile Gln Asp Leu Asn Arg Ile Phe Pro Leu Ser Glu Asp Tyr Ser Gly
 85 90 95
Ser Gly Xaa Xaa Ser Gly Ser Gly Ser Gly Ser Xaa Ser Gly Ser Gly

100	105	110
Phe Leu Thr Glu Met Glu Gln Asp Tyr Gln Leu Xaa Asp Glu Ser Asp		
115	120	125
Ala Phe His Asp Asn Leu Arg Ser Leu Asp Arg Asn Leu Pro Ser		
130	135	140

<210> 1373
 <211> 64
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(64)
 <223> Xaa = Any amino acid

<400> 1373
Ser Ser Glu Ser Gly Lys Ile Arg Phe Lys Ser Trp Ile Leu Val Phe
5 10 15
Xaa Lys Arg Ser Val Leu Arg Arg Gly Ile Leu Leu Asp Ser Xaa Gly
20 25 30
Ser Ser Ser Asn Ile Gly Pro Phe Ser Ser Arg Gln Phe Ala Glu Leu
35 40 45
Leu Ser Gly Leu Gln Arg Thr His Trp Tyr Leu Ala Leu Cys Val Gly
50 55 60

<210> 1374
 <211> 103
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(103)
 <223> Xaa = Any amino acid

<400> 1374
Gly Cys His Gly Lys His His Phe Arg Xaa Leu Val Gly Asn Pro Val
5 10 15
Pro Phe Pro Leu Gly Ser His Ser Gln Ile Xaa Ile Gln Ser Arg Ser
20 25 30
Arg Xaa Xaa Ser Leu Ile Gln Ser Ser Pro Gln Lys Val Gly Arg Tyr
35 40 45
Asp Ser Ser Pro Gly Phe Ser Ser Leu Xaa Lys Gly Gln Ser Ser Asp
50 55 60
Gly Gly Ser Cys Trp Ile His Xaa Glu Val Val Arg Thr Leu Val Leu
65 70 75 80
Phe Leu Gln Gly Ser Leu Gln Asn Tyr Cys Leu Asp Cys Ser Ala Pro
85 90 95
Ile Gly Thr Trp Leu Ser Ala

100

<210> 1375
<211> 73
<212> PRT
<213> Homo sapiens

<400> 1375
Arg Met Leu Ser Tyr Ser Ser Met Leu Pro Pro Ser Gly Leu Met Leu
 5 10 15

His Tyr Thr Leu Leu Gly Ser Asn Leu Pro Leu Arg Leu Lys Ala Leu
 20 25 30

Glu Gly Arg Val Phe Lys Met Leu Asp Leu Val Gln Ala Gln Ile Leu
 35 40 45

Glu Leu Lys Ala Glu Gly Phe Leu Val Ala Glu Lys Lys Gln Asn Leu
 50 55 60

Met Thr Phe Gly Thr Pro Val Leu Arg
 65 70

<210> 1376
<211> 52
<212> PRT
<213> Homo sapiens

<400> 1376
Leu His Ala Ala Ala Glu Trp Leu Asp Ala Pro Leu His Pro Pro Trp
 5 10 15

Ile Gln Pro Ser Ile Lys Ala Glu Gly Ser Arg Gly Gln Ser Ile Gln
 20 25 30

Asp Val Arg Ser Gly Pro Ser Pro Asn Ser Arg Val Lys Ser Arg Gly
 35 40 45

Val Leu Ser Gly
 50

<210> 1377
<211> 64
<212> PRT
<213> Homo sapiens

<400> 1377
Trp Lys Val Gly Ser Lys Glu Gly Val Met Glu His Gln Ala Thr Arg
 5 10 15

Arg Gln His Gly Ala Ile Thr Lys His Pro Leu Gly Phe Cys Leu Ser
 20 25 30

Arg His Leu Ala Leu Thr Leu Asp Leu Val Thr Val Val Trp Leu Ile
 35 40 45

Pro Val Asn Ile Trp Arg Gln Ser Tyr Leu Ala Phe Ala Ser Arg Ala
 50 55 60

<210> 1378
<211> 55
<212> PRT
<213> Homo sapiens

<400> 1378
Leu Lys Thr Gly Val Pro Asn Val Ile Arg Phe Cys Phe Phe Ser Ala
5 10 15
Thr Lys Asn Pro Ser Ala Phe Asn Ser Arg Ile Trp Ala Trp Thr Arg
20 25 30
Ser Asn Ile Leu Asn Thr Leu Pro Ser Arg Ala Phe Ser Leu Asn Gly
35 40 45
Arg Leu Asp Pro Arg Arg Val
50 55

<210> 1379
<211> 69
<212> PRT
<213> Homo sapiens

<400> 1379
Lys Leu Leu Lys Cys Ser Arg Leu Val Leu Ala Leu Ala Leu Ile Leu
5 10 15
Val Leu Glu Ser Ser Val Gln Gly Tyr Pro Thr Gln Arg Ala Arg Tyr
20 25 30
Gln Trp Val Arg Cys Asn Pro Asp Ser Asn Ser Ala Asn Cys Leu Glu
35 40 45
Glu Lys Gly Pro Met Phe Glu Leu Leu Pro Gly Glu Ser Asn Lys Ile
50 55 60
Pro Arg Leu Arg Thr
65

<210> 1380
<211> 66
<212> PRT
<213> Homo sapiens

<400> 1380
Ser Tyr Ser Asn Ala Val Gly Leu Ser Trp Leu Leu Pro Ser Ser Trp
5 10 15
Phe Trp Asn Pro Gln Phe Lys Val Ile Leu Arg Arg Glu Pro Gly Thr
20 25 30
Asn Gly Cys Ala Ala Ile Gln Thr Val Ile Leu Gln Thr Ala Leu Lys
35 40 45
Lys Lys Asp Gln Cys Ser Asn Tyr Phe Gln Val Asn Pro Thr Arg Ser
50 55 60
Pro Val
65

<210> 1381
 <211> 58
 <212> PRT
 <213> Homo sapiens

<400> 1381
 Gln Arg His Cys Gln Trp Leu Arg Gly Leu His Ser His Gly Val Gly
 5 10 15
 Asp Pro Gly Trp Gly Pro Asp Ala Ala Pro Ala Gly Ala Arg Arg His
 20 25 30
 Pro Gly Gly Pro His Gln Ala Cys Gly His Cys Gly Leu Ala His His
 35 40 45
 Ser Pro Glu Arg Ala Ala Gln Cys Arg Leu
 50 55

<210> 1382
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 1382
 His Thr Ala Pro Val Leu Asp Ile Ala Trp Cys Pro His Asn Asp Asn
 5 10 15
 Val Ile Ala Ser Gly Ser Glu Asp Cys Thr Val Met Val Trp Glu Ile
 20 25 30
 Pro Asp Gly Gly Leu Met Leu Pro Leu Arg Glu Pro Val Val Thr Leu
 35 40 45
 Glu Gly His Thr Lys Arg Val Gly Ile Val Ala Trp His Thr Thr Ala
 50 55 60
 Gln Asn Val Leu Leu Ser Ala Gly Cys Asp Asn Val Ile Met Val Trp
 65 70 75 80
 Asp Val Gly Thr Gly Ala Ala Met Leu Thr Leu Gly Pro Glu Val His
 85 90 95
 Pro Asp Thr Ile Tyr Ser Val Asp Trp Ser Arg Asp Gly
 100 105

<210> 1383
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 1383
 Ile Val Ser Gly Cys Thr Ser Gly Pro Ser Val Ser Met Ala Ala Pro
 5 10 15
 Val Pro Thr Ser His Thr Met Ile Thr Leu Ser Gln Pro Ala Leu Ser
 20 25 30
 Ser Thr Phe Trp Ala Val Val Cys Gln Ala Thr Met Pro Thr Arg Leu
 35 40 45

Val Trp Pro Ser Arg Val Thr Thr Gly Ser Arg Arg Gly Ser Ile Arg
 50 55 60
 Pro Pro Ser Gly Ile Ser His Thr Met Thr Val Gln Ser Ser Glu Pro
 65 70 75 80
 Leu Ala Met Thr Leu Ser Leu Cys Gly His Gln Ala Met Ser Ser Thr
 85 90 95
 Gly Ala Val Trp
 100

<210> 1384
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 1384
 Ser Ile Ser Ala Pro Val His Thr Val Asp Arg Val Trp Val His Leu
 5 10 15
 Trp Ala Gln Cys Gln His Gly Arg Pro Ser Ala His Val Pro His His
 20 25 30
 Asp His Val Val Thr Thr Cys Thr Glu Gln His Val Leu Gly Cys Gly
 35 40 45
 Val Pro Gly His Asn Ala His Thr Leu Gly Val Ala Leu Gln Gly Asp
 50 55 60
 Asp Gly Leu Pro Gln Gly Gln His Gln Ala Pro Ile Arg Asp Leu Pro
 65 70 75 80
 His His Asp Cys Ala Val Leu Gly Ala Thr Gly Asn Asp Val Val Ile
 85 90 95
 Val Arg Ala Pro Gly Asp Val
 100

<210> 1385
 <211> 55
 <212> PRT
 <213> Homo sapiens

<400> 1385
 His Met Val Arg Leu Asp Gly Pro Ser Ser Ser Glu Thr Gln Gln Glu
 5 10 15
 Ser Gln Gly Glu Gly Ser Gln Asp His Ser Ser Asp Met Glu His Ser
 20 25 30
 Val Phe Arg Ala His Val Val Gly Ser Ile Ile Asp Asp Cys Glu His
 35 40 45
 Arg Asn Ser Asp Glu Glu Leu
 50 55

<210> 1386
 <211> 97
 <212> PRT

<213> Homo sapiens

<400> 1386

Gln Phe Leu Ile Thr Val Pro Val Leu Thr Val Ile Asn Tyr Arg Pro
 5 10 15

His Asn Met Arg Pro Glu Asp Arg Met Phe His Ile Arg Ala Val Ile
 20 25 30

Leu Arg Ala Leu Ser Leu Ala Phe Leu Leu Ser Leu Arg Gly Ala Gly
 35 40 45

Ala Ile Lys Ala Asp His Val Ser Thr Tyr Ala Ala Phe Val Gln Thr
 50 55 60

His Arg Pro Thr Gly Glu Phe Met Phe Glu Phe Asp Glu Asp Glu Met
 65 70 75 80

Phe Tyr Val Asp Leu Asp Lys Lys Glu Thr Val Trp His Leu Glu Glu
 85 90 95

Phe

<210> 1387

<211> 55

<212> PRT

<213> Homo sapiens

<400> 1387

Val Ser Glu Glu Leu Gly Pro Ser Arg Arg Thr Met Cys Gln Leu Met
 5 10 15

Pro Arg Leu Tyr Arg Arg Ile Asp Gln Gln Gly Ser Leu Cys Leu Asn
 20 25 30

Leu Met Lys Met Arg Cys Ser Met Trp Ile Trp Thr Arg Arg Arg Pro
 35 40 45

Ser Gly Ile Trp Arg Ser Leu
 50 55

<210> 1388

<211> 89

<212> PRT

<213> Homo sapiens

<400> 1388

Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly
 5 10 15

Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu Lys Glu
 20 25 30

Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg
 35 40 45

Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys Gln
 50 55 60

Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg

471

35 40 45
 Trp Glu Gly Arg Ile Ile Tyr Gln Met Pro Val Glu His Val Gln Phe
 50 55 60
 Ile Val Arg His Asp Ile Gln Ser Val Gln Asp Ala Arg Glu Trp Gln
 65 70 75 80
 Val Met Ala Arg Cys Ile Gln Gln Gln Ala Pro Val Arg Lys Ala Gly
 85 90 95
 Lys Val Leu Asn Leu Ser Leu Val Asp Lys Glu Leu Gly Glu Leu Pro
 100 105 110
 Arg Gln Ser Gln Arg Gly Val Asn Thr Gly His His Leu Trp Ser Gly
 115 120 125
 Tyr Asn Ser Pro Leu Thr Pro Lys
 130 135

<210> 1392
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 1392
 Met Met Thr Ser Val Tyr Ser Ser Leu Arg Leu Ser Gly Glu Leu Ser
 5 10 15
 Glu Phe Phe Ile Asn Lys Thr Glu Ile Glu Asp Phe Pro Arg Phe Pro
 20 25 30
 His Arg Gly Leu Leu Leu Asp Thr Ser Arg His Tyr Leu Pro Leu Ser
 35 40 45
 Ser Ile Leu Asp Thr Leu Asp Val Met Ala Tyr Asn Lys Leu Asn Val
 50 55 60
 Phe His Trp His Leu Val Asp Asp Pro Ser Phe Pro Tyr Glu Ser Phe
 65 70 75 80
 Thr Phe Pro Glu Leu Met Arg Lys Gly Ser Tyr Asn Pro Val Thr His
 85 90 95
 Ile Tyr Thr Ala Gln Asp Val Lys Glu Val Ile Glu Tyr Ala Arg Leu
 100 105 110
 Arg Gly Ile Arg Val Leu Thr Glu Phe Asp Thr Pro
 115 120

<210> 1393
 <211> 52
 <212> PRT
 <213> Homo sapiens

<400> 1393
 Asp Cys Leu Gly Ser Ser Pro Ser Ser Leu Ser Thr Arg Leu Arg Leu
 5 10 15
 Arg Thr Phe Pro Ala Phe Leu Thr Gly Ala Cys Cys Trp Ile His Leu
 20 25 30

Ala Ile Thr Cys His Ser Leu Ala Ser Trp Thr Leu Trp Met Ser Trp
 35 40 45

Arg Thr Ile Asn
 50

<210> 1394
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 1394
 Gly Asn Gly His Thr Leu Glu Lys Asn Val Leu Val Val Ser Val Val
 5 10 15

Thr Pro Gly Cys Asn Gln Leu Pro Thr Leu Glu Ser Val Glu Asn Tyr
 20 25 30

Thr Leu Thr Ile Asn Asp Asp Gln Cys Leu Leu Leu Ser Glu Thr Val
 35 40 45

Trp Gly Ala Leu Arg Val Leu Tyr Gln Gln Asp
 50 55

<210> 1395
 <211> 88
 <212> PRT
 <213> Homo sapiens

<400> 1395
 Gly Gln Arg Arg Pro Arg Ser Ile Gly Glu Arg Gly Gly Gly Thr Pro
 5 10 15

Gly Glu Pro Gly Ala Trp Thr Gln Pro Glu Leu Ile Thr Glu Ala Gly
 20 25 30

Val Gln Ser Arg Val Thr Cys Ser Arg Asn Lys Gln Pro Leu Trp Gly
 35 40 45

His Gln Val Glu Arg Gln Asp Asp Lys Glu Gly Ala Arg Val Leu Ala
 50 55 60

Lys Ala Gly Leu Leu Ala Thr Ser Ala Gly Gln Arg Pro Pro Arg Ser
 65 70 75 80

Ala Cys Pro His His Ala Val Pro
 85

<210> 1396
 <211> 157
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(157)
 <223> Xaa = Any amino acid

<400> 1396

Gln Asn Leu Xaa Thr Gly Arg Glu Thr Leu Ser Gly Ser Ala Ala Lys
 115 120 125

Pro Ala Ser Ala Arg Gln Gly Gly Leu Pro Gly Ser Leu Xaa Gly Gly
 130 135 140

Ala Thr Ile Ser Ala Leu Xaa Ser Phe Ser Phe Ser
 145 150 155

<210> 1398
 <211> 75
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(75)
 <223> Xaa = Any amino acid

<400> 1398
 Arg Ala Glu Ala Gly Leu Ala Ala Leu Pro Leu Arg Val Ser Leu Pro
 5 10 15

Xaa Cys Arg Phe Cys Val Thr Val Thr Glu Arg Arg Asp Gly Gly Lys
 20 25 30

Gln Ser Val Gly Ala Ser Val Gln His Ser Trp Pro Ala Ala Pro Leu
 35 40 45

Ser Gln Glu His Gly His Pro Leu Cys Arg Leu Ala Ser Pro Pro Gly
 50 55 60

Ala Pro Arg Val Ala Ala Cys Ser Cys Cys Thr
 65 70 75

<210> 1399
 <211> 111
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(111)
 <223> Xaa = Any amino acid

<400> 1399
 Gln Ser Arg Asn Gly Val Met Gly Ala Ser Arg Ala Trp Gly Pro Leu
 5 10 15

Ser Ser Thr Arg Gly Gln Gln Pro Arg Phe Arg Lys Asn Thr Gly Thr
 20 25 30

Leu Phe Val Val Leu Pro Leu His Leu Val Pro Pro Glu Trp Leu Leu
 35 40 45

Val Pro Ala Ala Arg Asp Pro Gly Leu Asp Ala Ser Leu Cys Asp Glu
 50 55 60

Phe Trp Leu Cys Pro Arg Ser Trp Leu Ser Arg Cys Pro Ser Thr Ser
 65 70 75 80

475

Leu Pro Asp Ala Pro Gly Pro Pro Leu Ser Ser Gly Pro Thr Lys Ala
 85 90 95

Glu Ser Cys Pro Pro Gly Thr Trp Ser Pro Ala Phe Xaa Xaa Arg
 100 105 110

<210> 1400

<211> 104

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(104)

<223> Xaa = Any amino acid

<400> 1400

Trp Gly Gln Ala Glu Arg Gly Gly Leu Cys Pro Ala Leu Val Ala Ser
 5 10 15

Ser Pro Ala Phe Ala Arg Thr Arg Ala Pro Ser Leu Ser Ser Cys Leu
 20 25 30

Ser Thr Trp Cys Pro Gln Ser Gly Cys Leu Phe Leu Leu His Val Thr
 35 40 45

Arg Asp Trp Thr Pro Ala Ser Val Met Ser Ser Gly Cys Val His Ala
 50 55 60

Pro Gly Ser Pro Gly Val Pro Pro Pro Leu Ser Pro Met Leu Leu Gly
 65 70 75 80

Leu Leu Cys Pro Gln Ala Pro Pro Arg Leu Ser Leu Ala Arg Leu Gly
 85 90 95

Pro Gly His Gln Pro Xaa Xaa Xaa
 100

<210> 1401

<211> 53

<212> PRT

<213> Homo sapiens

<400> 1401

Ala Asn Thr Leu Ile Asn Gln Ser Pro Gly Lys Gln Leu Glu Cys Ile
 5 10 15

Ile Leu Trp Ser Ser Ile Leu Cys Ser Cys Ala Asp Ile Ser Leu Ser
 20 25 30

His Cys Val Ser Leu Ser Val Asp Thr Leu Lys Val Ala Leu Trp Lys
 35 40 45

Met Ser Lys Phe Phe
 50

<210> 1402

<211> 67

<212> PRT

<213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(67)
 <223> Xaa = Any amino acid

<400> 1402
 Lys Pro Pro Phe Phe Xaa Leu Leu Lys Arg Lys Gly Pro Gln Asp Thr
 5 10 15
 Ile Phe Glu Trp Leu Met Val Phe Lys Xaa Phe Arg Glu Leu Pro Ala
 20 25 30
 Phe Tyr Leu Glu Thr Glu Lys Ala Arg Lys Ile Leu Ser Phe Leu Ala
 35 40 45
 Cys Ile Ser Arg Val Gly Ala Asn Asp Ser Lys Leu Val Ser Lys Pro
 50 55 60
 Ile Pro Leu
 65

<210> 1403
 <211> 120
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(120)
 <223> Xaa = Any amino acid

<400> 1403
 Pro Ala Ile Cys Thr Asp Lys Tyr Arg Cys Leu Lys His Asn Leu Asn
 5 10 15
 Ser Leu Ile Lys Arg Ser Asn, Ser Thr Ala Ala Thr Asn Glu Xaa Pro
 20 25 30
 Glu Val Thr Val Phe Ser Lys Ser Pro Val Thr Leu Gly Gln Pro Asn
 35 40 45
 Ile Leu Ile Cys Leu Val Asp Asn Ile Phe Pro Pro Val Xaa Asn Ile
 50 55 60
 Thr Trp Leu Ser Asn Gly His Ser Val Thr Glu Xaa Val Ser Glu Thr
 65 70 75 80
 Ser Phe Leu Ser Lys Ser Asp His Ser Phe Phe Lys Ile Ser Thr Ser
 85 90 95
 Pro Ser Ser Leu Leu Xaa Glu Glu Ser Tyr Asp Cys Lys Xaa Xaa His
 100 105 110
 Trp Gly Leu Gly Gln Ala Ser Ser
 115 120

<210> 1404
 <211> 52
 <212> PRT
 <213> Homo sapiens

<220>

<221> variant

<222> (1)...(52)

<223> Xaa = Any amino acid

<400> 1404

Ala Met Gly Thr Gln Ser Gln Xaa Val Phe Leu Arg Pro Ala Ser Ser
 5 10 15

Pro Arg Val Ile Ile Pro Ser Ser Arg Ser Val Pro His Pro Pro Pro
 20 25 30

Phe Trp Xaa Arg Arg Val Met Thr Ala Arg Xaa Xaa Thr Gly Asp Trp
 35 40 45

Asp Lys Pro Leu
 50

<210> 1405

<211> 60

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(60)

<223> Xaa = Any amino acid

<400> 1405

Val Pro Ile Ala Gln Pro Cys Asp Val Xaa His Arg Arg Lys Asp Val
 5 10 15

Val His Lys Thr Asp Glu Asp Val Gly Leu Thr Gln Cys His Gly Arg
 20 25 30

Leu Gly Lys His Cys Asp Leu Arg Xaa Leu Ile Gly Ser Ser Gly Arg
 35 40 45

Val Gly Ala Phe Asn Gln Thr Val Gln Val Met Phe
 50 55 60

<210> 1406

<211> 52

<212> PRT

<213> Homo sapiens

<400> 1406

Ser Asp Cys Ser Ser Tyr Val Leu Gly Ser Asp Ile Cys Gln Cys Lys
 5 10 15

Leu Arg Val Lys Ser Lys Leu Ser Glu Asn Arg Gln Thr Pro Asp Ser
 20 25 30

Leu Leu Pro Pro Gln Val His Val Glu Leu Leu Ile Ser Ile Lys Phe
 35 40 45

Met Gly Val Leu
 50

<210> 1407
 <211> 75
 <212> PRT
 <213> Homo sapiens

<400> 1407
 Ser Ser His Leu Leu Ser Tyr Ile His Leu Gly Ile Pro Ile Ser Asn
 5 10 15
 Val Ser Leu Glu Ile Arg Ala Pro Gly Gly Gln Val Thr Glu Gly Gln
 20 25 30
 Lys Leu Ile Leu Leu Cys Ser Val Ala Gly Gly Thr Gly Asn Val Thr
 35 40 45
 Phe Ser Trp Tyr Arg Glu Ala Thr Gly Thr Ser Met Gly Lys Lys Thr
 50 55 60
 Gln Arg Ser Leu Ser Ala Glu Leu Glu Ile Pro
 65 70 75

<210> 1408
 <211> 63
 <212> PRT
 <213> Homo sapiens

<400> 1408
 Asp Ile Gln Met Ser Leu Ser Thr Phe Leu Lys Asp Asn Cys Tyr Arg
 5 10 15
 Phe Pro Thr Ser Ile Gly Met Leu Ile Met Asp Tyr Leu Tyr Asn Leu
 20 25 30
 His Ile Pro Thr Phe Cys Ile Arg Glu Trp Asn Gln Ser Asn Pro Val
 35 40 45
 Pro Arg Val Ser Leu Arg Val Leu Thr Cys Cys Leu Ile Ser Ile
 50 55 60

<210> 1409
 <211> 68
 <212> PRT
 <213> Homo sapiens

<400> 1409
 Gly Ile Ser Ser Ser Ala Asp Arg Glu Arg Trp Val Phe Phe Pro Ile
 5 10 15
 Leu Val Pro Val Ala Ser Leu Tyr Gln Glu Asn Val Thr Phe Pro Val
 20 25 30
 Pro Pro Ala Thr Glu Gln Ser Arg Ile Ser Phe Cys Pro Ser Val Thr
 35 40 45
 Cys Pro Pro Gly Ala Arg Ile Ser Lys Leu Thr Leu Glu Met Gly Ile
 50 55 60
 Pro Arg Trp Ile
 65

<210> 1410
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 1410
 Gly Val Phe Leu His Thr Phe Thr Ser Ser Ala Leu Ser Ile Tyr Thr
 5 10 15
 His Thr Gln His Pro Gln Tyr Leu Thr Ser Asn Arg Leu Tyr His Leu
 20 25 30
 Tyr Leu Thr Met Thr Pro Gly Arg Arg Ser Lys Phe Phe Phe Thr Ile
 35 40 45
 Ser Asn Ser Ser Leu Ser Leu Phe
 50 55

<210> 1411
 <211> 50
 <212> PRT
 <213> Homo sapiens

<400> 1411
 Ile Ser Gln Ile Thr Lys Ser Ser Leu Arg Gln Gln Phe Lys Thr Val
 5 10 15
 Pro Gly Ile Lys Ile Tyr Ser His Leu Arg Ser Leu Pro Ser His Leu
 20 25 30
 His Leu Leu Ser Leu Lys Tyr Ile His Thr His Pro Thr Pro Ser Ile
 35 40 45
 Leu Asp
 50

<210> 1412
 <211> 70
 <212> PRT
 <213> Homo sapiens

<400> 1412
 Arg Ser Ala Tyr Ala Ala Arg Trp Val Ala Lys Ser Leu Val Lys Gly
 5 10 15
 Gly Leu Cys Arg Arg Val Leu Val Gln Val Ser Tyr Ala Ile Gly Val
 20 25 30
 Ser His Pro Leu Ser Ile Ser Ile Phe His Tyr Gly Thr Ser Gln Lys
 35 40 45
 Ser Glu Arg Glu Leu Leu Glu Ile Val Lys Lys Asn Phe Asp Leu Arg
 50 55 60
 Pro Gly Val Ile Val Arg
 65 70

<210> 1413
 <211> 53
 <212> PRT

<213> Homo sapiens

<400> 1413

Gly Leu Leu Met Leu Leu Val Gly Trp Gln Asn Pro Leu Leu Lys Glu
5 10 15

Val Cys Ala Gly Gly Phe Leu Phe Arg Ser Leu Met Leu Leu Glu Phe
20 25 30

Leu Ile His Tyr Leu Ser Pro Phe Ser Ile Met Val Pro Leu Arg Arg
35 40 45

Val Arg Glu Ser Tyr
50

<210> 1414

<211> 69

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(69)

<223> Xaa = Any amino acid

<400> 1414

Xaa His Lys Ile Cys Ser Ile Asp Val His Glu Ser Ser Cys Cys Xaa
5 10 15

Gly Ala Val Ser Thr Asp Xaa Trp Asn Asn Trp Pro Val Arg Lys Leu
20 25 30

Ile Lys Ala Ala Asn Ser Thr Xaa Glu Cys Asn Arg Xaa Xaa Gln Gly
35 40 45

Leu Ile Ser Leu Ser Asp Gly Gly Leu Xaa Ile Cys Xaa Pro Gly Xaa
50 55 60

Tyr Cys Val Ile Asn
65

<210> 1415

<211> 64

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(64)

<223> Xaa = Any amino acid

<400> 1415

Xaa Pro Xaa Gln Gln Xaa Ser Ser Pro Pro Ser Glu Arg Leu Ile Arg
5 10 15

Pro Cys Xaa Xaa Leu Leu His Ser Xaa Val Leu Phe Ala Ala Leu Met
20 25 30

Ser Phe Leu Thr Gly Gln Leu Phe Xaa Lys Ser Val Asp Thr Ala Pro
35 40 45

Xaa Gln Gln Glu Asp Ser Trp Thr Ser Ile Glu His Ile Leu Trp Xaa
50 55 60

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<220>
<221> variant
<222> (1)...(92)
<223> Xaa = Any amino acid
```

Ser Lys Trp Xaa Val Ser Ser Val Tyr Asp Thr Ile Xaa Ser Trp Xaa
20 25 30

Thr Asn Xaa Lys Ser Ser Ile Arg Lys Ala Asn Lys Ala Leu Xaa Xaa
35 40 45

Ser Ile Ala Phe Xaa Cys Thr Val Cys Ser Phe Asp Glu Leu Pro His
50 55 60

Arg Pro Ile Ile Pro Xaa Val Cys Gly Tyr Arg Ser Xaa Thr Ala Arg
65 70 75 80

Gly Leu Met Asp Val Tyr Arg Thr Tyr Leu Val Xaa
85 90

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<220>
<221> variant
<222> (1)...(77)
<223> Xaa = Any amino acid
```

Ser Ser Ser Arg Xaa Leu Lys Gly Leu Ser Phe Cys Arg Arg Thr Cys
20 25 30

Phe Ser Ser Ser Asn Ser Ala Val Leu Phe Gly Ile His Pro Leu Gln
35 40 45

Val Phe Tyr Val Xaa Asn His His Phe Asn Cys Phe Thr Asn Pro Ala
50 55 60

Phe Leu Ile Asp Gly Ser Gln His Leu Ser Pro Thr Gly
65 70 75

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<210> 1418
<211> 75
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<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(75)
<223> Xaa = Any amino acid

<400> 1418
Pro Phe Leu Glu Leu His Val Asn Leu Cys Gly Gln Ala Ala Phe Ala
 5 10 15

Gly Val Phe Thr Gly Arg Gln Arg Leu Gln Ala Cys Leu Pro Ala Gly
 20 25 30

Ser Val Cys Arg Arg Val Tyr Met Gln Ala Xaa His His Val Arg Pro
 35 40 45

Leu Val Gln Gly Phe Arg Gly Pro Ala Gln Val Asn Arg Leu Cys Ser
 50 55 60

His Lys Phe Thr Glu Leu Xaa Gly Cys Ala Thr
 65 70 75

<210> 1419
<211> 74
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(74)
<223> Xaa = Any amino acid

<400> 1419
Ala Ala Arg Glu Pro Val Trp Ala Gly Ser Val Cys Arg Arg Val Tyr
 5 10 15

Gly Gln Ala Ala Phe Ala Gly Val Phe Thr Gly Arg Gln Arg Leu Gln
 20 25 30

Ala Cys Leu His Ala Gly Val Xaa Pro Cys Glu Thr Thr Gly Pro Gly
 35 40 45

Phe Gln Arg Ser Cys Ser Gly Glu Ser Ala Val Phe Ser Gln Val His
 50 55 60

Gly Ala Xaa Trp Val Cys Asn Met Lys Tyr
 65 70

<210> 1420
<211> 66
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(66)
<223> Xaa = Any amino acid

<400> 1420

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<400> 1422
Val Gln Asp Leu Leu Asn Pro Lys Arg Leu His Thr Thr Leu Met Tyr
           5                      10                      15

Ala Pro Gln Arg Leu Met Gly Arg Gly Arg Ala Gly Lys Pro Gly Lys
           20                      25                      30

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Leu Gly Val Phe Ser Gly Tyr Thr Pro Ser Ser Val Ser Phe Trp Ile
 35 40 45

Gln Leu Leu Met Arg Leu
 50

<210> 1423
 <211> 76
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(76)
 <223> Xaa = Any amino acid

<400> 1423
 Thr Gln Thr Asp Gln Arg Glu Met Gly Pro His Arg Ala Xaa Cys Val
 5 10 15

Asn Ala Met Glu Gly Lys Xaa Leu Ala Gln Asp Val Arg Ala Lys Gly
 20 25 30

Tyr Leu Glu Cys Ser Ala Leu Ser Asn Arg Gly Val Gln Gln Val Phe
 35 40 45

Glu Cys Val Val Arg Thr Ala Val Asn Gln Ala Arg Arg Arg Asn Arg
 50 55 60

Arg Arg Leu Phe Ser Ile Asn Glu Cys Lys Ile Phe
 65 70 75

<210> 1424
 <211> 138
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(138)
 <223> Xaa = Any amino acid

<400> 1424
 Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Gln Phe Tyr Val Asp Leu
 5 10 15

Gly Arg Lys Glu Thr Ala Trp Cys Leu Pro Val Leu Arg Gln Phe Arg
 20 25 30

Phe Asp Pro Gln Phe Ala Leu Thr Asn Ile Ala Val Leu Lys His Asn
 35 40 45

Leu Asn Ser Leu Ile Lys Arg Ser Asn Ser Thr Ala Ala Thr Asn Glu
 50 55 60

Val Pro Glu Val Thr Val Phe Ser Lys Ser Pro Val Thr Leu Gly Gln
 65 70 75 80

Pro Asn Ile Leu Ile Cys Leu Val Asp Asn Ile Phe Pro Pro Val Xaa
 85 90 95

Asn Ile Thr Trp Leu Ser Asn Gly His Ser Val Thr Xaa Xaa Val Ser
 100 105 110

Glu Thr Ser Phe Leu Ser Lys Ser Asp His Xaa Phe Phe Xaa Ile Xaa
 115 120 125

Tyr Pro Thr Leu Leu Pro Ser Ser Glu Glu
 130 135

<210> 1425
 <211> 60
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(60)
 <223> Xaa = Any amino acid

<400> 1425
 Val Pro Ile Ala Gln Pro Cys Asp Val Xaa His Arg Arg Lys Asp Val
 5 10 15

Val His Lys Thr Asp Glu Asp Val Gly Leu Thr Gln Cys His Gly Arg
 20 25 30

Leu Gly Lys His Cys Asp Leu Arg Asn Leu Ile Gly Ser Ser Gly Arg
 35 40 45

Val Gly Ala Phe Asn Gln Thr Val Gln Val Met Phe
 50 55 60

<210> 1426
 <211> 66
 <212> PRT
 <213> Homo sapiens

<400> 1426
 Pro Ser Val Thr Gly Asp Leu Glu Asn Thr Val Thr Ser Gly Thr Ser
 5 10 15

Leu Val Ala Ala Val Glu Leu Glu Arg Leu Ile Arg Leu Phe Lys Leu
 20 25 30

Cys Phe Arg Thr Ala Met Phe Val Ser Ala Asn Cys Gly Ser Asn Leu
 35 40 45

Asn Cys Leu Arg Thr Gly Lys His Gln Ala Val Ser Phe Leu Pro Arg
 50 55 60

Ser Thr
 65

<210> 1427
 <211> 55
 <212> PRT
 <213> Homo sapiens

<400> 1427

486

Lys Leu Tyr Asn Ala Cys Ile Met Lys Lys Asp Leu Pro Phe Pro Tyr
 5 10 15
 Ile Leu Ile Glu Leu His Arg Leu Ala Val His Phe Val Ile His Val
 20 25 30
 Ile Arg Ile Leu Asp Ser Ile Ala Phe Glu Ile Cys Phe Phe Leu Gly
 35 40 45
 Thr Lys Ser Gln Leu Ile Val
 50 55

<210> 1428
 <211> 52
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(52)
 <223> Xaa = Any amino acid

<400> 1428
 Pro Lys Glu Val Arg Gln Leu Ala Glu Asp Phe Leu Lys Asp Tyr Ile
 5 10 15
 His Ile Asn Ile Gly Ala Leu Glu Leu Xaa Ala Asn His Asn Ile Leu
 20 25 30
 Xaa Xaa Val Asp Val Cys His Asp Xaa Xaa Lys Asp Glu Lys Leu Ile
 35 40 45
 Arg Leu Met Glu
 50

<210> 1429
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 1429
 Leu Ala Cys Cys Ser Gly Pro Trp Ser Cys Pro Val Leu Gln His Gly
 5 10 15
 Val Ser Glu Ala Pro Trp Arg Leu Leu His Gly Ser Ser Asp Ser Asp
 20 25 30
 Thr Asp Gly Ala Glu Leu Pro Thr Gly Phe Gly Trp Gly His Gln Thr
 35 40 45
 Thr Phe Leu Gly Val Leu Tyr Val
 50 55

<210> 1430
 <211> 177
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant

<222> (1)...(177)

<223> Xaa = Any amino acid

<400> 1430

Leu Pro Ala Ala Leu Ala Pro Gly Pro Val Leu Phe Ser Ser Met Val
 5 10 15

Cys Leu Arg Leu Pro Gly Gly Ser Cys Met Ala Val Leu Thr Val Thr
 20 25 30

Leu Met Val Leu Ser Ser Pro Leu Ala Leu Ala Gly Asp Thr Arg Pro
 35 40 45

Arg Phe Leu Glu Tyr Ser Thr Ser Glu Cys His Phe Phe Asn Gly Thr
 50 55 60

Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu Tyr
 65 70 75 80

Val Arg Phe Asp Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu Leu
 85 90 95

Gly Arg Pro Asp Glu Glu Tyr Trp Asn Ser Gln Lys Asp Phe Leu Glu
 100 105 110

Asp Arg Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly Val
 115 120 125

Gly Glu Ser Phe Thr Val Gln Arg Arg Val His Pro Lys Val Thr Val
 130 135 140

Tyr Pro Ser Lys Thr His Pro Cys Ser Thr Thr Thr Ser Trp Ser Val
 145 150 155 160

Leu Xaa Val Val Ser Ile Gln Ala Ala Leu Asn Xaa Val Val Pro Glu
 165 170 175

Trp

<210> 1431

<211> 56

<212> PRT

<213> Homo sapiens

<400> 1431

Ala Pro His Trp Leu Trp Leu Gly Thr Pro Asp His Val Ser Trp Ser
 5 10 15

Thr Leu Arg Leu Ser Val Ile Ser Ser Met Gly Arg Ser Gly Cys Gly
 20 25 30

Ser Trp Thr Asp Thr Ser Ile Thr Lys Arg Ser Thr Cys Ala Ser Thr
 35 40 45

Ala Thr Trp Gly Ser Ser Gly Arg
 50 55

<210> 1432

<211> 70

<212> PRT

<213> Homo sapiens

<400> 1432

Ser Ser His Gln Pro Arg Ser Cys Val Cys Ser Arg Cys Pro Pro Arg
 5 10 15

Pro Ala Cys Leu Pro Gly Ser Pro Ser Gly Cys Ser Ser Thr Pro His
 20 25 30

Gln Ala Ala Pro Ala Pro Ser Pro Pro Gly Thr Pro Pro Arg Arg Cys
 35 40 45

Arg Ser Ala Arg Thr Pro Leu Gly Tyr Arg Ser Ile Cys Pro Gly Thr
 50 55 60

Ala Pro Ala Pro Ser His
 65 70

<210> 1433

<211> 53

<212> PRT

<213> Homo sapiens

<400> 1433

Ser Thr Pro Arg Asn Val Val Trp Cys Pro Gln Pro Lys Pro Val Gly
 5 10 15

Ser Ser Ala Pro Ser Val Ser Leu Ser Glu Leu Pro Cys Arg Ser Leu
 20 25 30

Gln Gly Ala Ser Asp Thr Pro Cys Trp Arg Thr Gly Gln Asp Gln Gly
 35 40 45

Pro Glu Gln Gln Ala
 50

<210> 1434

<211> 146

<212> PRT

<213> Homo sapiens

<400> 1434

Arg Ile His Ser His Leu Arg Met Asp Ser Pro Leu His Cys Glu Ala
 5 10 15

Leu Thr Asn Pro Val Val Val Ser Ala Val Gly Val His Arg Gly Pro
 20 25 30

Pro Val Phe Gln Glu Val Leu Leu Ala Val Pro Val Leu Leu Ile Arg
 35 40 45

Pro Pro Gln Leu Arg His Arg Pro Glu Leu Pro His Val Ala Val Glu
 50 55 60

Ala His Val Leu Leu Leu Val Ile Glu Val Ser Val Gln Glu Pro His
 65 70 75 80

Pro Leu Arg Pro Ile Glu Glu Met Thr Leu Arg Arg Arg Val Leu Gln
 85 90 95

Glu Thr Trp Ser Gly Val Pro Ser Gln Ser Gln Trp Gly Ala Gln His

100 105 110
 His Gln Cys His Cys Gln Asn Cys His Ala Gly Ala Ser Arg Glu Pro
 115 120 125
 Gln Thr His His Ala Gly Glu Gln Asp Arg Thr Arg Gly Gln Ser Ser
 130 135 140
 Arg Gln
 145

<210> 1435
 <211> 58
 <212> PRT
 <213> Homo sapiens

<400> 1435
 His Ser Asp Val Glu Tyr Ser Lys Lys Arg Gly Leu Val Ser Pro Ala
 5 10 15
 Lys Ala Ser Gly Glu Leu Ser Thr Ile Ser Val Thr Val Arg Thr Ala
 20 25 30
 Met Gln Glu Pro Pro Gly Ser Leu Arg His Thr Met Leu Glu Asn Arg
 35 40 45
 Thr Gly Pro Gly Ala Arg Ala Ala Gly Lys
 50 55

<210> 1436
 <211> 69
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(69)
 <223> Xaa = Any amino acid

<400> 1436
 Glu Gly Lys Leu Ser Asp Asn Arg Ser Ser Ile Arg Trp Val Cys Pro
 5 10 15
 Cys Ile Ala Cys Gln Arg Leu Ala His His Gln Gly Ser Gly Val Ala
 20 25 30
 Val Leu Pro Cys Val Val Cys Ile Ala Ser Leu Ser Ser Ala Cys Leu
 35 40 45
 Ser Pro Ser Xaa Pro Pro Ser Pro Leu Xaa Leu Tyr Gln Val Cys His
 50 55 60
 Gly Glu Gln Glu Tyr
 65

<210> 1437
 <211> 50
 <212> PRT
 <213> Homo sapiens

490

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<400> 1437
Leu Trp Lys Arg Ala Pro Pro Gly Ala Xaa Gly Lys Asp Cys Phe Ser
      5                      10                      15

Leu Ser Ser Pro Ile Pro Gly Tyr Ser Arg Ala Asp Gln Gln Gly His
      20                      25                      30

Phe His Leu Thr Ser Cys Cys Ser Leu Met Phe Pro Trp Asp Lys Arg
      35                      40                      45

Gly Asn
      50

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<220>
<221> variant
<222> (1)...(59)
<223> Xaa = Any amino acid
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<400> 1438
Val Leu Leu Xaa His Pro Leu Pro Xaa Gly Ser Thr Arg Tyr Ala Thr
      5                      10                      15

Gly Ser Arg Asn Ile Asn Pro Arg Ile Leu Thr Leu Ser Gly Asn Thr
      20                      25                      30

Glu Cys Thr Pro Gly Met Leu Gly Glu Thr Arg Gly Ile Leu Leu Thr
      35                      40                      45

Ile Asn Leu Gly Ser Lys Arg Pro Tyr Leu Ile
      50                      55

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<220>  
<221> variant  
<222> (1)...(68)  
<223> Xaa = Any amino acid
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<400> 1439
Gln Pro Gln Gln His  Pro Leu Gly  Leu Ser  Leu Tyr Arg  Met  Pro Glu
                    5              10              15

Ala Cys Ala  Ser  Pro Arg  Val Gly  Arg  Ser Cys  Ala Ala  Leu Arg Cys
                20              25              30

Val His  Ser  Leu Ser  Leu Leu Cys  Leu Leu Lys  Ser  Phe  Leu Xaa Thr
                35              40              45

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491

Leu Ser Leu Xaa Ala Leu Pro Gly Met Pro Arg Gly Ala Gly Ile Leu
 50 55 60

Ile Leu Glu Ser
 65

<210> 1440
 <211> 54
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(54)
 <223> Xaa = Any amino acid

<400> 1440
 Leu Ser Val Ala Ile Gln Ser Val Leu Gln Gly Cys Trp Val Lys Pro
 5 10 15

Gly Glu Phe Tyr Ser Pro Leu Thr Leu Gly Val Arg Gly His Thr Ser
 20 25 30

Ser Glu Thr Leu Pro Ala Arg Ala Gly Arg Ser Lys Gly Xaa Phe Pro
 35 40 45

Xaa Pro Leu Arg Xaa Tyr
 50

<210> 1441
 <211> 100
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(100)
 <223> Xaa = Any amino acid

<400> 1441
 Asn Ser Pro Gly Phe Thr Gln His Pro Trp Ser Thr Leu Cys Ile Ala
 5 10 15

Thr Glu Ser Gln Asp Ser Arg Ile Asn Ile Pro Ala Pro Arg Gly Ile
 20 25 30

Pro Gly Arg Ala Xaa Arg Glu Arg Val Xaa Lys Lys Asp Leu Ser Lys
 35 40 45

Gln Arg Arg Glu Arg Leu Cys Thr Gln Arg Arg Ala Ala Gln Leu Arg
 50 55 60

Pro Thr Leu Gly Asp Ala Gln Ala Ser Gly Met Arg Tyr Arg Asp Arg
 65 70 75 80

Pro Ser Gly Cys Cys Cys Gly Cys His Leu Ile Ser Pro Leu Ile Pro
 85 90 95

Arg Glu His Gln
 100

<210> 1442
 <211> 72
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(72)
 <223> Xaa = Any amino acid

<400> 1442
 Tyr Xaa Gly Ala Lys Xaa Gly Gly Xaa Gly Leu Leu Asn Gly Pro Pro
 5 10 15
 Gly Gln Val Lys Phe Gln Met Arg Tyr Gly Leu Leu Leu Pro Arg Leu
 20 25 30
 Met Val Ser Arg Ile Pro Arg Val Ser Pro Ser Ile Pro Gly Val His
 35 40 45
 Ser Val Leu Pro Leu Arg Val Arg Ile Leu Gly Leu Ile Phe Leu Leu
 50 55 60
 Pro Val Ala Tyr Leu Val Glu Xaa
 65 70

<210> 1443
 <211> 115
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(115)
 <223> Xaa = Any amino acid

<400> 1443
 Pro Met Trp Leu Val Phe Xaa Leu Xaa Leu Ala Arg Phe His Thr Leu
 5 10 15
 Thr Ser Leu Ser Gln Pro Gln Glu Thr Met Ile Gly Leu Leu Leu Leu
 20 25 30
 Gly Glu Lys Arg Thr Gln Asp Thr His Ser Glu Trp Leu Ser Ser Trp
 35 40 45
 Thr Val Tyr Leu His Thr Pro Arg Val Phe His Ser Leu Met Val Leu
 50 55 60
 Ser Arg Asp Pro Glu Thr Ile Cys Arg Leu Ser Glu Glu Lys Ala Thr
 65 70 75 80
 Leu Ser Thr Ser Leu Val Trp Pro Thr Asn Arg Leu Val Val Val Pro
 85 90 95
 Val Val Arg Ser Gln Arg Arg Arg Val Pro Ser Gln Glu Pro Glu Arg
 100 105 110
 Ala Asn Trp
 115

<210> 1444
 <211> 50
 <212> PRT
 <213> Homo sapiens

<400> 1444
 Leu Asp Gly Phe Ile Ser Arg Ser Arg Asp Asn Leu Pro Val Val Arg
 5 10 15
 Gly Glu Gly His Thr Gln His Ile Leu Gly Met Ala His Lys Ser Pro
 20 25 30
 Arg Gly Gly Ala Arg Cys Glu Ile Pro Glu Ala Gln Gly Ser Ile Pro
 35 40 45
 Gly Ala
 50

<210> 1445
 <211> 114
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(114)
 <223> Xaa = Any amino acid

<400> 1445
 Gln Phe Ala Leu Ser Gly Ser Trp Asp Gly Thr Leu Arg Leu Trp Asp
 5 10 15
 Leu Thr Thr Gly Thr Thr Thr Arg Arg Phe Val Gly His Thr Lys Asp
 20 25 30
 Val Leu Ser Val Ala Phe Ser Ser Asp Asn Arg Gln Ile Val Ser Gly
 35 40 45
 Ser Arg Asp Lys Thr Ile Lys Leu Trp Asn Thr Leu Gly Val Cys Lys
 50 55 60
 Tyr Thr Val Gln Asp Glu Ser His Ser Glu Trp Val Ser Cys Val Arg
 65 70 75 80
 Phe Ser Pro Asn Ser Ser Asn Pro Ile Ile Val Ser Cys Gly Trp Asp
 85 90 95
 Lys Leu Val Lys Val Trp Asn Leu Ala Xaa Cys Lys Xaa Lys Thr Asn
 100 105 110
 His Ile

<210> 1446
 <211> 74
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant

<400> 1446

<210> 1447

<211> 60

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1) ... (60)

<223> Xaa = Any amino acid

<400> 1447

Leu Ala Phe Xaa Met Glu Asp Leu Arg Phe Val Ala
50 55 60

<210> 1448

<211> 60

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1) . . . (60)

<223> Xaa = Any amino acid

<400> 1448

Thr Gly Gln Leu Phe Gln Lys Ser Val Asp Xaa Ala Pro Thr Gln Gln
35 40 45

495

Glu Asp Ser Trp Thr Ser Leu Glu His Ile Leu Trp
 50 55 60

<210> 1449
 <211> 58
 <212> PRT
 <213> Homo sapiens

<400> 1449
 Ser Asn Ile Lys Ala Ile Arg Arg His Pro Cys His His Leu Thr Gln
 5 10 15

Gly Gly Arg Cys Trp Ser Trp Val Gln Leu Gly Arg Arg Ser Arg Ser
 20 25 30

Arg Lys Gln Gly Asp Tyr Gly Ser Gln Ser Val Ser Lys Trp Ala Gly
 35 40 45

Leu Pro Gly Arg Asp Tyr Ser Glu Gly Gln
 50 55

<210> 1450
 <211> 146
 <212> PRT
 <213> Homo sapiens

<400> 1450
 Ala Asn Gly Ser Ala Glu Thr Ser Ala Leu Asp Thr Gly Phe Ser Leu
 5 10 15

Asn Leu Ser Glu Leu Arg Glu Tyr Thr Glu Gly Leu Thr Glu Ala Lys
 20 25 30

Glu Asp Asp Asp Gly Asp His Ser Ser Leu Gln Ser Gly Gln Ser Val
 35 40 45

Ile Ser Leu Leu Ser Ser Glu Glu Leu Lys Lys Leu Ile Glu Glu Val
 50 55 60

Lys Val Leu Asp Glu Ala Thr Leu Lys Gln Leu Asp Gly Ile His Val
 65 70 75 80

Thr Ile Leu His Lys Glu Glu Gly Ala Gly Leu Gly Phe Ser Leu Ala
 85 90 95

Gly Gly Ala Asp Leu Glu Asn Lys Val Ile Thr Val His Arg Val Phe
 100 105 110

Pro Asn Gly Leu Ala Ser Gln Glu Gly Thr Ile Gln Lys Gly Asn Glu
 115 120 125

Val Leu Ser Ser Thr Ala Ser Leu Ser Arg Gly Pro Arg Thr Met Met
 130 135 140

Pro Trp
 145

<210> 1451
 <211> 62

<212> PRT

<213> Homo sapiens

<400> 1451

Thr Val Ile Thr Leu Phe Ser Arg Ser Ala Pro Pro Ala Lys Leu Asn
 5 10 15

Pro Arg Pro Ala Pro Ser Ser Leu Cys Lys Met Val Thr Trp Met Pro
 20 25 30

Ser Asn Cys Phe Asn Val Ala Ser Ser Arg Thr Phe Thr Ser Ser Met
 35 40 45

Ser Phe Phe Asn Ser Ser Glu Leu Ser Arg Glu Ile Thr Asp
 50 55 60

<210> 1452

<211> 109

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(109)

<223> Xaa = Any amino acid

<400> 1452

Ser Pro Ala Arg Pro Leu Ile Arg Ser Asp Lys Met Lys Glu Thr Ile
 5 10 15

Met Asn Gln Glu Lys Leu Ala Lys Leu Gln Ala Gln Val Arg Ile Gly
 20 25 30

Gly Lys Gly Thr Ala Arg Arg Lys Lys Lys Val Val His Arg Thr Ala
 35 40 45

Thr Ala Asp Asp Lys Lys Leu Gln Phe Ser Leu Lys Lys Leu Xaa Val
 50 55 60

Asn Asn Ile Ser Gly Ile Glu Glu Val Asn Met Phe Thr Asn Gln Gly
 65 70 75 80

Thr Val Ile His Phe Asn Asn Pro Lys Val Gln Ala Ser Leu Ala Ala
 85 90 95

Asn Thr Phe Thr Ile Thr Gly His Ala Glu Thr Lys Gln
 100 105

<210> 1453

<211> 81

<212> PRT

<213> Homo sapiens

<400> 1453

Gly Glu Leu Lys Phe Phe Val Ile Cys Cys Gly Cys Ser Met Asn His
 5 10 15

Leu Leu Leu Ser Ala Ser Ser Ser Phe Pro Thr Asn Ala His Leu Cys
 20 25 30

Leu Gln Phe Gly Glu Phe Phe Leu Val His Asp Cys Phe Phe His Leu

35 40 45
 Val Gly Ala Asn Lys Gly Pro Arg Gly Gly Leu Gly Leu Val Leu Lys
 50 55 60
 Gly Ser Arg Val Asp His Leu Arg Leu Gly Ala His Thr Arg Gly Arg
 65 70 75 80
 Lys

<210> 1454
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(59)
 <223> Xaa = Any amino acid

<400> 1454
 Thr Tyr Ser Pro Leu Gln Tyr Gln Arg Tyr Cys Leu Pro Xaa Thr Ser
 5 10 15
 Leu Arg Arg Thr Glu Val Phe Cys His Leu Leu Trp Leu Phe Tyr Glu
 20 25 30
 Pro Pro Ser Ser Phe Cys Glu Gln Phe Leu Ser His Gln Cys Ala Leu
 35 40 45
 Val Pro Ala Val Trp Arg Val Phe Pro Gly Ser
 50 55

<210> 1455
 <211> 153
 <212> PRT
 <213> Homo sapiens

<400> 1455
 Leu Arg Asp Ser Arg Asp Cys Val Thr Ser Phe Val Ser Phe Asp Leu
 5 10 15
 Glu Ser Leu Ser Arg Thr Met Arg His Ser Lys Arg Thr Tyr Cys Pro
 20 25 30
 Asp Trp Asp Asp Lys Asp Trp Asp Tyr Gly Lys Trp Arg Ser Ser Ser
 35 40 45
 Ser His Lys Arg Arg Lys Arg Ser His Ser Ser Ala Gln Glu Asn Lys
 50 55 60
 Arg Cys Lys Tyr Asn His Ser Lys Met Cys Asp Ser His Tyr Leu Glu
 65 70 75 80
 Ser Arg Ser Ile Asn Glu Lys Asp Tyr His Ser Arg Arg Tyr Ile Asp
 85 90 95
 Glu Tyr Arg Asn Asp Tyr Thr Gln Gly Cys Glu Pro Gly His Arg Gln
 100 105 110

Arg Asp His Glu Ser Arg Tyr Gln Asn His Ser Ser Lys Ser Ser Gly
 115 120 125

Arg Ser Gly Arg Ser Ser Tyr Lys Ser Lys His Arg Ile His His Ser
 130 135 140

Thr Ser His Arg Arg Ser His Gly Val
 145 150

<210> 1456
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 1456
 Asp Thr Gln Arg Glu Leu Ile Val Leu Ile Gly Met Thr Arg Ile Gly
 5 10 15

Ile Met Glu Asn Gly Gly Ala Ala Val Ile Lys Glu Gly Arg Asp
 20 25 30

His Ile Ala Val Pro Arg Arg Thr Ser Ala Ala Asn Thr Ile Thr Leu
 35 40 45

Lys Cys Val Ile Ala Ile Ile Trp Lys Ala Gly Leu
 50 55 60

<210> 1457
 <211> 98
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(98)
 <223> Xaa = Any amino acid

<400> 1457
 Met Arg Lys Ile Ile Ile Val Asp Ala Thr Leu Met Ser Thr Glu Met
 5 10 15

Thr Thr Leu Lys Asp Val Asn Leu Asp Ile Ala Lys Glu Thr Met Lys
 20 25 30

Ala Gly Ile Arg Thr Ile Val Ala Ser Leu Leu Val Glu Val Glu Glu
 35 40 45

Val Val Ile Lys Ala Asn Thr Gly Phe Thr Thr Val Leu His Ile Val
 50 55 60

Val His Met Gly Tyr Glu Pro Phe Leu Pro Ala Arg Ala Gly Ala Xaa
 65 70 75 80

Gly Glu Phe Gln His Thr Xaa Arg Arg Ser Arg Gly Ser Glu Leu Gly
 85 90 95

Pro Xaa

<210> 1458

499

<211> 73
 <212> PRT
 <213> Homo sapiens

<400> 1458
 Lys Arg Phe Ile Pro His Val Asn Asp Asp Val Lys Tyr Cys Gly Glu
 5 10 15
 Ser Cys Val Cys Phe Tyr Asn Tyr Phe Phe His Phe Tyr Gln Lys Thr
 20 25 30
 Cys Tyr Tyr Gly Ser Asp Thr Gly Phe His Gly Leu Phe Gly Asp Val
 35 40 45
 Gln Val His Ile Leu Glu Cys Ser His Phe Cys Thr His Gln Cys Ser
 50 55 60
 Val Asp Tyr Asp Asn Leu Ser His Leu
 65 70

<210> 1459
 <211> 62
 <212> PRT
 <213> Homo sapiens

<400> 1459
 Ser Asp Cys Ile Cys Ser Ala Cys Ser Pro Gly His Cys Tyr Val Ile
 5 10 15
 Ser Ser Phe Phe Tyr Asp Cys Cys Cys Ser Ser Ile Phe His Asn Pro
 20 25 30
 Asn Pro Cys His Pro Asn Gln Asp Asn Lys Phe Ser Leu Ser Val Ser
 35 40 45
 Leu Ser Trp Thr Lys Thr Pro Ser Arg Arg Arg Gln Ser Leu
 50 55 60

<210> 1460
 <211> 89
 <212> PRT
 <213> Homo sapiens

<400> 1460
 Ser Thr Val Val Asn Pro Val Phe Ala Phe Ile Thr Thr Ser Ser Thr
 5 10 15
 Ser Thr Arg Arg Leu Ala Thr Met Val Leu Ile Pro Ala Phe Met Val
 20 25 30
 Ser Leu Ala Met Ser Arg Phe Thr Ser Leu Ser Val Val Ile Ser Val
 35 40 45
 Leu Ile Asn Val Ala Ser Thr Met Ile Ile Phe Leu Ile Tyr Arg Pro
 50 55 60
 Ala Phe Gln Ile Met Ala Ile Thr His Phe Arg Val Ile Val Phe Ala
 65 70 75 80
 Ala Leu Val Leu Leu Gly Thr Ala Met
 85

Gln His Glu Arg Arg His Phe Pro Phe Leu Arg
 65 70 75

<210> 1464
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 1464
 Thr Lys Lys Arg Lys Met Pro Pro Leu Met Leu Leu Asp Ala Glu Gly
 5 10 15
 Leu Leu Val Trp Leu Val Ser Phe Cys Pro Glu Ser Pro Val Cys Ile
 20 25 30
 Cys Thr Ile Thr Arg Arg Leu Met Val Ser Arg Arg Lys Arg Lys Arg
 35 40 45
 Phe Ile Leu Val Gly Ser Ser Trp Leu Ser Trp
 50 55

<210> 1465
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(59)
 <223> Xaa = Any amino acid

<400> 1465
 Pro Cys Leu Arg Ser Xaa Xaa Thr Xaa Lys Arg Pro Cys Leu Pro Xaa
 5 10 15
 Met Thr Leu Met Glu Glu Met Leu Arg Glu Ala Phe Xaa Cys Met Thr
 20 25 30
 Gln Gly Lys Thr Ala Lys Asn Leu Val Leu Ala Leu Leu Ile Leu Leu
 35 40 45
 Phe Val Leu Phe Leu Gly Val Leu Arg Ala Lys
 50 55

<210> 1466
 <211> 63
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(63)
 <223> Xaa = Any amino acid

<400> 1466
 Ser Gly Cys Cys His Phe Ala Leu Lys Thr Pro Lys Asn Lys Thr Asn
 5 10 15
 Asn Lys Met Arg Arg Ala Arg Thr Arg Phe Leu Ala Val Leu Pro Cys

502

20 25 30

Val Met His Xaa Asn Ala Ser Leu Ser Ile Ser Ser Met Ser Val Ile
 35 40 45

Xaa Gly Arg His Gly Leu Xaa Arg Val Xaa Leu Asp Leu Arg Gln
 50 55 60

<210> 1467
 <211> 65
 <212> PRT
 <213> Homo sapiens

<400> 1467

Lys Ser Gly Val Gly Ile Pro Phe His Met His Ile Asp Tyr Phe Leu
 5 10 15

Ser Phe Phe Lys Thr Cys Phe Ser Gly Phe Leu Asn Val Pro Asp Asp
 20 25 30

Ser Leu Ser Cys Arg Thr Val Asn Val Asn Leu Ser Arg Gly Leu Trp
 35 40 45

Leu Asp Val Asn Leu Ile Lys Leu Leu Cys Pro Arg Asn Ser Ala Pro
 50 55 60

Pro
 65

<210> 1468
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 1468

Lys Met Glu His Ser Asp Glu Asn Ile Gln Phe Trp Met Ala Cys Glu
 5 10 15

Thr Tyr Lys Lys Ile Ala Ser Arg Trp Ser Arg Ile Ser Arg Ala Lys
 20 25 30

Lys Leu Tyr Lys Ile Tyr Ile Gln Pro Gln Ser Pro Arg Glu Ile Asn
 35 40 45

Ile Asp Ser Ser Thr Arg Glu Thr Ile Ile Arg Asn Ile Gln Glu Pro
 50 55 60

Thr Glu Thr Cys Phe Glu Glu Ala Gln Lys Ile Val Tyr Met His Met
 65 70 75 80

Glu Arg Asp Ser Tyr Pro Arg Phe Leu Lys Ser Glu Met Tyr Gln Lys
 85 90 95

Leu Leu Lys Thr Met Gln Ser Asn Asn Ser Phe
 100 105

<210> 1469
 <211> 74
 <212> PRT
 <213> Homo sapiens

<400> 1469

Lys Trp Ser Thr Val Thr Arg Ile Phe Asn Ser Gly Trp His Val Lys
 5 10 15

Pro Ile Arg Lys Leu Pro His Gly Gly Ala Glu Phe Leu Gly Gln Arg
 20 25 30

Ser Phe Ile Arg Phe Thr Ser Ser His Ser Pro Leu Glu Arg Leu Thr
 35 40 45

Leu Thr Val Arg Gln Glu Arg Leu Ser Ser Gly Thr Phe Arg Asn Pro
 50 55 60

Leu Lys His Val Leu Lys Lys Leu Arg Lys
 65 70

<210> 1470

<211> 63

<212> PRT

<213> Homo sapiens

<400> 1470

Leu Leu Pro Leu Tyr Pro Glu Ile Leu Glu Met Gln Glu Trp Trp Leu
 5 10 15

Gly Trp Lys Ile Met Ile Asp Ser Val Glu Gly Gln Ala Val Gly Val
 20 25 30

Phe Trp Gly Gln Ser Arg Val Asn Thr Val Pro His Tyr Leu Asp Leu
 35 40 45

Leu Ala Pro Ile Pro Gly Gln Met Leu Lys Lys Lys Asn Val Asn
 50 55 60

<210> 1471

<211> 181

<212> PRT

<213> Homo sapiens

<400> 1471

Ser Arg Ala Glu Met Leu Gly Ala Ile Asn Gln Glu Ser Arg Val Ser
 5 10 15

Lys Ala Val Glu Val Met Ile Gln His Val Glu Asn Leu Lys Arg Met
 20 25 30

Tyr Ala Lys Glu His Ala Glu Leu Glu Glu Leu Lys Gln Val Leu Leu
 35 40 45

Gln Asn Glu Arg Ser Phe Asn Pro Leu Glu Asp Asp Asp Asp Cys Gln
 50 55 60

Ile Lys Lys Arg Ser Ala Ser Leu Asn Ser Lys Pro Ser Ser Leu Arg
 65 70 75 80

Arg Val Thr Ile Ala Ser Leu Pro Arg Asn Ile Gly Asn Ala Gly Met
 85 90 95

Val Ala Gly Met Glu Asn Asn Asp Arg Phe Ser Arg Arg Ser Ser Ser
 100 105 110

Trp Arg Ile Leu Gly Ser Lys Gln Ser Glu His Arg Pro Ser Leu Pro
 115 120 125
 Arg Phe Ile Ser Thr Tyr Ser Trp Ala Asp Ala Glu Glu Lys Cys
 130 135 140
 Glu Leu Lys Thr Lys Asp Asp Ser Glu Pro Ser Gly Glu Glu Thr Val
 145 150 155 160
 Glu Arg Thr Arg Lys Pro Ser Leu Ser Glu Lys Lys Asn Asn Pro Ser
 165 170 175
 Lys Trp Asp Val Ser
 180

<210> 1472
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 1472
 Val Leu Ile Asn Arg Gly Asn Glu Gly Arg Cys Ser Leu Cys Phe Asp
 5 10 15
 Pro Lys Ile Arg Gln Leu Leu Asp Leu Leu Leu Asn Arg Ser Leu Phe
 20 25 30
 Ser Ile Pro Ala Thr Ile Pro Ala Phe Pro Ile Phe Leu Gly Lys Glu
 35 40 45
 Ala Ile Val Thr Leu Arg Arg Glu Asp Gly Leu Glu Phe Arg Glu Ala
 50 55 60
 Glu Arg Phe Leu Ile Trp Gln Ser Ser Ser Ser Arg Gly Leu Lys
 65 70 75 80
 Asp Leu Ser Phe Cys Arg Arg Thr Cys Phe Ser Ser Ser Asn Ser Ala
 85 90 95
 Cys Ser Leu Ala Tyr Ile Leu Phe Lys Phe Ser Thr Cys
 100 105

<210> 1473
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 1473
 Ile Val Ser Gly Cys Thr Ser Gly Pro Ser Val Ser Met Ala Ala Pro
 5 10 15
 Val Pro Thr Ser His Thr Met Ile Thr Leu Ser Gln Pro Ala Leu Ser
 20 25 30
 Ser Thr Phe Trp Ala Val Val Cys Gln Ala Thr Met Pro Thr Arg Leu
 35 40 45
 Val Trp Pro Ser Arg Val Thr Thr Gly Ser Arg Arg Gly Ser Ile Arg
 50 55 60

505

Pro Pro Ser Gly Ile Ser His Thr Met Thr Val Gln Ser Ser Glu Pro
 65 70 75 80
 Leu Ala Met Thr Leu Ser Leu Cys Gly His Gln Ala Met Ser Ser Ala
 85 90 95
 Gly Ala Val Trp
 100

<210> 1474
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 1474
 Ser Ile Ser Ala Pro Val His Thr Val Asp Arg Val Trp Val His Leu
 5 10 15
 Trp Ala Gln Cys Gln His Gly Arg Pro Ser Ala His Val Pro His His
 20 25 30
 Asp His Val Val Thr Thr Cys Thr Glu Gln His Val Leu Gly Cys Gly
 35 40 45
 Val Pro Gly His Asn Ala His Thr Leu Gly Val Ala Leu Gln Gly Asp
 50 55 60
 Asp Gly Leu Pro Gln Gly Gln His Gln Ala Pro Ile Arg Asp Leu Pro
 65 70 75 80
 His His Asp Cys Ala Val Leu Gly Ala Thr Gly Asn Asp Val Val Ile
 85 90 95
 Val Arg Ala Pro Gly Asp Val
 100

<210> 1475
 <211> 58
 <212> PRT
 <213> Homo sapiens

<400> 1475
 Gln Arg His Cys Gln Trp Leu Arg Gly Leu His Ser His Gly Val Gly
 5 10 15
 Asp Pro Gly Trp Gly Pro Asp Ala Ala Pro Ala Gly Ala Arg Arg His
 20 25 30
 Pro Gly Gly Pro His Gln Ala Cys Gly His Cys Gly Leu Ala His His
 35 40 45
 Ser Pro Glu Arg Ala Ala Gln Cys Arg Leu
 50 55

<210> 1476
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 1476

His Thr Ala Pro Ala Leu Asp Ile Ala Trp Cys Pro His Asn Asp Asn
 5 10 15
 Val Ile Ala Ser Gly Ser Glu Asp Cys Thr Val Met Val Trp Glu Ile
 20 25 30
 Pro Asp Gly Gly Leu Met Leu Pro Leu Arg Glu Pro Val Val Thr Leu
 35 40 45
 Glu Gly His Thr Lys Arg Val Gly Ile Val Ala Trp His Thr Thr Ala
 50 55 60
 Gln Asn Val Leu Leu Ser Ala Gly Cys Asp Asn Val Ile Met Val Trp
 65 70 75 80
 Asp Val Gly Thr Gly Ala Ala Met Leu Thr Leu Gly Pro Glu Val His
 85 90 95
 Pro Asp Thr Ile Tyr Ser Val Asp Trp Ser Arg Asp Gly
 100 105

<210> 1477
 <211> 94
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(94)
 <223> Xaa = Any amino acid

<400> 1477
 Xaa Leu Ala Cys Cys Ser Gly Pro Trp Ser Cys Pro Val Leu Gln His
 5 10 15
 Gly Val Ser Glu Ala Pro Trp Arg Leu Leu His Gly Ser Ser Asp Ser
 20 25 30
 Asp Thr Asp Gly Ala Glu Leu Pro Thr Cys Phe Gly Leu Gly Thr Pro
 35 40 45
 Asp His Val Ser Trp Ser Thr Leu Arg Leu Ser Val Ile Ser Ser Met
 50 55 60
 Gly Arg Ser Gly Cys Gly Ser Trp Thr Asp Thr Ser Ile Thr Lys Arg
 65 70 75 80
 Ser Thr Cys Ala Ser Thr Ala Thr Trp Gly Ser Ser Gly Arg
 85 90

<210> 1478
 <211> 57
 <212> PRT
 <213> Homo sapiens

<400> 1478
 Val Leu Pro Ala Ala Leu Ala Pro Gly Pro Val Leu Phe Ser Ser Met
 5 10 15
 Val Cys Leu Arg Leu Pro Gly Gly Ser Cys Met Ala Val Leu Thr Val
 20 25 30

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<210> 1479
<211> 93
<212> PRT
<213> Homo sapiens
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<220>  
<221> variant  
<222> (1)...(93)  
<223> Xaa = Any amino acid
```

<400> 1479
Ala Pro His Leu Leu Trp Ala Gly Asp Thr Arg Pro Arg Phe Leu Glu
 5 10 15

Tyr Ser Thr Ser Glu Cys His Phe Phe Asn Gly Thr Glu Arg Val Arg
20 25 30

Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu Tyr Val Arg Phe Asp
35 40 45

Ser Asp Val Gly Glu Phe Arg Ala Val Xaa Glu Leu Gly Arg Ala Asp
50 55 60

Glu Glu Tyr Trp Asn Ser Xaa Xaa Gly Leu Pro Gly Xaa Gln Ala Xaa
65 70 75 80

Arg Gly Gly His Leu Leu Xaa Thr Gln Leu Arg Gly Trp
85 90

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<210> 1480
<211> 121
<212> PRT
<213> Homo sapiens
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<220>
<221> variant
<222> (1)...(121)
<223> Xaa = Any amino acid
```

<400> 1480
Val Ser Thr Ala Xaa Arg Leu Xaa Ser Arg Lys Ser Xaa Xaa Ala Val
 5 10 15

Pro Val Leu Leu Ile Ser Pro Pro Gln Leu Xaa His Arg Pro Glu Leu
20 25 30

Pro His Val Ala Val Glu Ala His Val Leu Leu Leu Val Ile Glu Val
35 40 45

Ser Val Gln Glu Pro His Pro Leu Arg Pro Ile Glu Glu Met Thr Leu
50 55 60

Arg Arg Arg Val Leu Gln Glu Thr Trp Ser Gly Val Pro Ser Pro Lys
65 70 75 80

Gln Val Gly Ser Ser Ala Pro Ser Val Ser Leu Ser Glu Leu Pro Cys
 85 90 95

Arg Ser Leu Gln Gly Ala Ser Asp Thr Pro Cys Trp Arg Thr Gly Gln
 100 105 110

Asp Gln Gly Pro Glu Gln Gln Ala Arg
 115 120

<210> 1481
 <211> 54
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(54)
 <223> Xaa = Any amino acid

<400> 1481
 Gln Pro Arg Ser Cys Xaa Cys Ser Arg Cys Pro Pro Xaa Pro Ala Cys
 5 10 15

Xaa Pro Gly Ser Pro Xaa Trp Leu Phe Gln Tyr Ser Ser Ser Ala Arg
 20 25 30

Pro Ser Xaa Val Thr Ala Arg Asn Ser Pro Thr Ser Leu Ser Lys Arg
 35 40 45

Thr Tyr Ser Ser Trp Leu
 50

<210> 1482
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 1482
 His Ser Asp Val Glu Tyr Ser Lys Lys Arg Gly Leu Val Ser Pro Ala
 5 10 15

Gln Ser Lys Trp Gly Ala Gln His His Gln Cys His Cys Gln Asn Cys
 20 25 30

His Ala Gly Ala Ser Arg Glu Pro Gln Thr His His Ala Gly Glu Gln
 35 40 45

Asp Arg Thr Arg Gly Gln Ser Ser Arg Gln Asp
 50 55

<210> 1483
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(67)
 <223> Xaa = Any amino acid

<400> 1483

Asn Pro Val Val Val Xaa Ala Val Gly Val His Arg Xaa Pro Pro Xaa
 5 10 15

Phe Gln Glu Val Leu Xaa Gly Cys Ser Ser Thr Pro His Gln Pro Ala
 20 25 30

Pro Ala Xaa Ser Pro Pro Gly Thr Pro Pro Arg Arg Cys Arg Ser Ala
 35 40 45

Arg Thr Pro Leu Gly Tyr Arg Ser Ile Cys Pro Gly Thr Ala Pro Ala
 50 55 60

Pro Ser His
 65

<210> 1484

<211> 55

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(55)

<223> Xaa = Any amino acid

<400> 1484

Ser Thr Pro Arg Asn Val Val Trp Cys Pro Gln Pro Lys Ala Ser Gly
 5 10 15

Glu Leu Ser Thr Ile Ser Val Thr Val Arg Thr Ala Met Gln Glu Pro
 20 25 30

Pro Gly Ser Leu Arg His Thr Met Leu Glu Asn Arg Thr Gly Pro Gly
 35 40 45

Ala Arg Ala Ala Gly Lys Xaa
 50 55

<210> 1485

<211> 80

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(80)

<223> Xaa = Any amino acid

<400> 1485

Gln Thr Ile Tyr Asn Ile Ser Ser Leu Lys Ser Ser Phe Lys Asp His
 5 10 15

Arg Gln Thr Ser Ser Pro Leu Tyr Phe Ser Trp Gly Asp Lys Gly Lys
 20 25 30

Lys Arg Lys Cys Lys Leu Ser Tyr Ser His Ser Glu Asn Leu Trp Phe
 35 40 45

His Ala Ile Leu Ser Gln Leu Lys Val Thr Asn Leu Arg Ser Ser Asp

50 55 60
 Leu Lys Leu Lys Asn Gln Xaa Pro Tyr Ile Arg Met Ser Cys Cys His
 65 70 75 80

<210> 1486
 <211> 76
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(76)
 <223> Xaa = Any amino acid

<400> 1486
 Val Leu Pro Gly Thr Leu Ile Pro Leu Cys Gln Val Met His Ser Gln
 5 10 15
 Ile Leu Gly Thr Arg Val Trp Thr Ser Leu Gly Gly Ile Ile Leu Pro
 20 25 30
 Ala Ile Ile Glu Leu Xaa Gly Arg Leu Asn Asn Ile Ile Tyr Met Thr
 35 40 45
 Tyr Val Xaa Ala Arg Leu Ala Pro Gly Lys Tyr Ser Gly Cys Thr Asn
 50 55 60
 His Cys Ser Tyr Thr Xaa Gln Xaa Leu Lys Glu Ser
 65 70 75

<210> 1487
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(67)
 <223> Xaa = Any amino acid

<400> 1487
 Glu Gln Trp Leu Val His Pro Glu Tyr Phe Pro Gly Ala Lys Arg Xaa
 5 10 15
 Ser Thr Tyr Val Met Tyr Ile Met Leu Phe Asn Leu Xaa Asn Asn Ser
 20 25 30
 Ile Met Ala Gly Arg Ile Met Pro Pro Lys Asp Val His Thr Leu Val
 35 40 45
 Pro Arg Ile Cys Glu Cys Ile Thr Trp Gln Arg Gly Ile Lys Val Pro
 50 55 60
 Gly Arg Thr
 65

<210> 1488
 <211> 67
 <212> PRT

<213> Homo sapiens

<400> 1488

Lys Ile Ser Asn Leu Lys Met Gly His Asn Tyr Thr Phe Thr Val Gln
5 10 15
Ala Arg Cys Leu Phe Gly Asn Gln Ile Cys Gly Glu Pro Ala Ile Leu
20 25 30
Leu Tyr Asp Glu Leu Gly Ser Gly Ala Asp Ala Ser Ala Thr Gln Ala
35 40 45
Ala Arg Ser Thr Asp Val Ala Val Val Val Pro Ile Leu Phe Leu
50 55 60
Ile Leu Leu
65

<210> 1489

<211> 58

<212> PRT

<213> Homo sapiens

<400> 1489

Arg Trp Val Ile Ile Thr Arg Ser Pro Ser Lys Gln Asp Ala Phe Leu
5 10 15
Ala Thr Arg Ser Val Gly Ser Leu Pro Ser Cys Cys Thr Met Ser Trp
20 25 30
Gly Leu Val Gln Met His Leu Gln Arg Arg Leu Pro Asp Leu Arg Met
35 40 45
Leu Leu Leu Trp Trp Cys Pro Ser Tyr Ser
50 55

<210> 1490

<211> 61

<212> PRT

<213> Homo sapiens

<400> 1490

Asp Gly His His His Ser Ser Asn Ile Arg Arg Ser Gly Ser Leu Arg
5 10 15
Cys Arg Cys Ile Cys Thr Arg Pro Gln Leu Ile Val Gln Gln Asp Gly
20 25 30
Arg Leu Pro Thr Asp Leu Val Ala Lys Lys Ala Ser Cys Leu Asp Gly
35 40 45
Glu Arg Val Ile Met Thr His Leu Gln Val Gly Asn Phe
50 55 60

<210> 1491

<211> 56

<212> PRT

<213> Homo sapiens

<400> 1491

Ser	Ser	Ile	Arg	Asn	Lys	Met	Gly	Thr	Thr	Thr	Ala	Ala	Thr	Ser	Val
				5					10					15	
Asp	Leu	Ala	Ala	Cys	Val	Ala	Asp	Ala	Ser	Ala	Pro	Asp	Pro	Ser	Ser
			20					25					30		
Ser	Tyr	Ser	Arg	Met	Ala	Gly	Ser	Pro	Gln	Ile	Trp	Leu	Pro	Lys	Arg
			35				40					45			
His	Leu	Ala	Trp	Thr	Val	Asn	Val								
	50					55									

```
<210> 1492
<211> 67
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> variant
<222> (1)...(67)
<223> Xaa = Any amino acid
```

```

<400> 1492
Pro Arg Met Met Lys Thr Val Pro Thr Thr Met Pro Thr Arg Pro Thr
          5                      10                      15

Asp Asn Pro Arg Ala Gln Thr Thr Val Ser Val Ser Ser Asp Ile Gly
          20                      25                      30

Ala Gly Ile Ser Gly Ser Gln Cys Phe Arg Arg Gly Leu Ser Ser Pro
          35                      40                      45

Gln Cys Ser Thr Leu Gln Ser Xaa Leu Ser Ser Xaa Glu Gly Arg Arg
          50                      55                      60

Val Arg Xaa
          65

```

```
<210> 1493
<211> 66
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> variant  
<222> (1)...(66)  
<223> Xaa = Any amino acid
```

```

<400> 1493
Xaa Leu Thr. Leu Leu Pro Ser Xaa Glu Glu Xaa Tyr Asp Cys Lys Val
          5                      10                      15

Glu His Trp Gly Leu Asp Lys Pro Leu Leu Lys His Trp Glu Pro Glu
          20                      25                      30

Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr Val Val Cys Ala Leu
          35                      40                      45

Gly Leu Ser Val Gly Leu Val Gly Ile Val Val Gly Thr Val Phe Ile
          50                      55                      60

```

Ile Arg
65

<210> 1494
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(60)
<223> Xaa = Any amino acid

<400> 1494
Thr Ser Ser Pro Ala Ala Pro Thr Ser Ala Cys Ala Ser Arg Pro Pro
 5 10 15

Gly Pro Ser Trp Thr Trp Gly Arg Ala Pro Arg Thr Glu Ser Ser Gln
 20 25 30

Pro Arg Gly Ser Ser Ser Cys Ser Ala Arg Trp Cys Leu Gly Arg Cys
 35 40 45

Cys Cys Xaa Gly Asn Asp Gly Lys Asn Xaa Asn Xaa
 50 55 60

<210> 1495
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(60)
<223> Xaa = Any amino acid

<400> 1495
Pro Ala Val Leu Arg His Leu Pro Pro Arg Ala Pro Ala Ala Pro Gln
 5 10 15

Ala Leu Pro Gly His Gly Gly Gly His Gln Glu Pro Asn His His Ser
 20 25 30

Arg Gly Asp His Pro Pro Val Leu Arg Gly Gly Ala Trp Asp Ala Ala
 35 40 45

Ala Val Xaa Glu Thr Met Ala Arg Thr Xaa Thr Xaa
 50 55 60

<210> 1496
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(60)
<223> Xaa = Any amino acid

<400> 1496

Gln Gln Ser Cys Gly Thr Tyr Leu Arg Val Arg Gln Pro Pro Pro Arg
 5 10 15
 Pro Phe Leu Asp Met Gly Glu Gly Thr Lys Asn Arg Ile Ile Thr Ala
 20 25 30
 Glu Gly Ile Ile Leu Leu Phe Cys Ala Val Val Pro Gly Thr Leu Leu
 35 40 45
 Leu Xaa Arg Lys Arg Trp Gln Glu Arg Xaa Leu Xaa
 50 55 60

<210> 1497
 <211> 60
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(60)
 <223> Xaa = Any amino acid

<400> 1497
 Xaa Glu Xaa Ser Phe Leu Pro Ser Phe Pro Xaa Gln Gln Gln Arg Pro
 5 10 15
 Arg His His Arg Ala Glu Gln Glu Asp Asp Pro Leu Gly Cys Asp Asp
 20 25 30
 Ser Val Leu Gly Ala Leu Pro His Val Gln Glu Gly Pro Gly Gly Arg
 35 40 45
 Leu Ala His Ala Glu Val Gly Ala Ala Gly Leu Leu
 50 55 60

<210> 1498
 <211> 53
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(53)
 <223> Xaa = Any amino acid

<400> 1498
 Xaa Ser Xaa Arg Ser Cys His Arg Phe Xaa Asn Ser Ser Ser Val Pro
 5 10 15
 Gly Thr Thr Ala Gln Asn Arg Arg Met Ile Pro Ser Ala Val Met Ile
 20 25 30
 Arg Phe Leu Val Pro Ser Pro Met Ser Arg Lys Gly Leu Gly Gly Gly
 35 40 45
 Trp Arg Thr Arg Arg
 50

<210> 1499
 <211> 51

<212> PRT

<213> Homo sapiens

<400> 1499

Pro Ala Tyr Asn Gly Asp Val Val Phe Leu Phe Thr Phe Val Tyr Tyr
 5 10 15

Ala Cys Val Phe Ser Thr Thr Leu Gly Ser Gly Arg Asn Gly Gln Thr
 20 25 30

Glu Asp Glu Leu Tyr Pro Gly Pro Ala Gly Pro Ala Cys Ser Pro Leu
 35 40 45

Cys Ser Pro
 50

<210> 1500

<211> 79

<212> PRT

<213> Homo sapiens

<400> 1500

Gln Pro Thr Met Gly Met Leu Cys Phe Cys Ser Pro Ser Phe Thr Met
 5 10 15

Pro Val Ser Ser Pro Pro Arg Trp Gly Leu Gly Gly Met Asp Arg Gln
 20 25 30

Arg Met Ser Ser Thr Gln Gly Leu Gln Asp Leu Pro Val Ala His Ser
 35 40 45

Ala Arg Leu Ser Thr Thr Thr Pro Ala Lys Glu Asp Ser Ile Trp Gln
 50 55 60

Ser Phe Phe Gln Val Pro Ser Tyr Thr Cys Ala Ser Ala Phe Ser
 65 70 75

<210> 1501

<211> 71

<212> PRT

<213> Homo sapiens

<400> 1501

Leu Gly Thr Trp Lys Lys Leu Cys Gln Met Glu Ser Ser Leu Ala Gly
 5 10 15

Val Val Val Leu Arg Arg Ala Glu Trp Ala Thr Gly Arg Ser Cys Arg
 20 25 30

Pro Trp Val Glu Leu Ile Leu Cys Leu Ser Ile Pro Pro Arg Pro Gln
 35 40 45

Arg Gly Gly Glu Asp Thr Gly Ile Val Asn Glu Gly Glu Gln Lys His
 50 55 60

Asn Ile Pro Ile Val Gly Trp
 65 70

<210> 1502

<211> 67

<212> PRT

<213> Homo sapiens

<400> 1502

Lys Ser Arg Gly Thr Gly Ile Ala Gly His Leu Glu Glu Ala Leu Pro
 5 10 15
 Asn Gly Ile Leu Leu Gly Arg Ser Gly Ser Ala Lys Ala Ser Arg Val
 20 25 30
 Gly Tyr Arg Gln Val Leu Gln Ala Leu Gly Arg Ala His Pro Leu Ser
 35 40 45
 Val His Ser Ser Gln Thr Pro Ala Trp Trp Arg Arg His Arg His Ser
 50 55 60
 Lys Arg Arg
 65

<210> 1503

<211> 71

<212> PRT

<213> Homo sapiens

<400> 1503

Arg Gly Glu Lys Ala Glu Arg Val Pro Val Ile Phe Lys Arg Gln Asn
 5 10 15
 Ile Ser Pro Leu Pro Arg Lys Leu Phe Ser Pro Arg Glu Lys Met Glu
 20 25 30
 Val Ile Leu Thr Val His Cys Arg Gly Ile Ser Ser Cys Pro Ile Phe
 35 40 45
 Cys Met Thr Cys His Gly Thr Ala Leu Phe Gln Thr Val His Cys Asp
 50 55 60
 Leu Trp Val Phe Glu Phe Gln
 65 70

<210> 1504

<211> 73

<212> PRT

<213> Homo sapiens

<400> 1504

Thr Lys Ile Ser Leu Asn Ile Glu Val Trp Asn Tyr Phe Phe Asp Ile
 5 10 15
 Ser Ala Asn Ser Leu Lys Leu Lys Asp Pro Gln Ile Thr Val Asn Ser
 20 25 30
 Leu Lys Gln Gly Cys Thr Met Ala Ser His Ala Lys Asp Gly Thr Arg
 35 40 45
 Arg Asn Thr Thr Ala Val Asn Cys Glu Asp Asn Phe His Phe Phe Pro
 50 55 60
 Arg Arg Glu Gln Phe Thr Gly Gln Arg
 65 70

<210> 1505
<211> 74
<212> PRT
<213> Homo sapiens

<400> 1505
Ala Ala Arg Glu Pro Val Trp Ala Gly Ser Val Cys Arg Arg Val Tyr
 5 10 15

Gly Gln Ala Ala Phe Ala Gly Val Phe Thr Gly Arg Gln Arg Leu Gln
 20 25 30

Ala Cys Leu His Ala Gly Val Ala Pro Cys Glu Thr Thr Gly Pro Gly
 35 40 45

Phe Gln Arg Ser Cys Ser Gly Glu Ser Ala Val Phe Ser Gln Val His
 50 55 60

Gly Ala Glu Trp Val Cys Asn Met Lys Tyr
 65 70

<210> 1506
<211> 66
<212> PRT
<213> Homo sapiens

<400> 1506
Leu Asp Asp Gly Leu Gln Pro Leu Ser Val Pro Ser Val Pro His Ser
 5 10 15

Thr Ser Ile Ser Cys Cys Thr Pro Thr Gln Leu Arg Glu Leu Val Arg
 20 25 30

Thr Gln Pro Ile His Leu Ser Arg Thr Ser Glu Thr Leu Asp Gln Trp
 35 40 45

Ser His Met Val Leu Arg Leu His Val Asn Thr Pro Ala Asn Ala Ala
 50 55 60

Cys Arg
 65

<210> 1507
<211> 98
<212> PRT
<213> Homo sapiens

<400> 1507
Ile Ala Gly Thr Leu Lys Phe Asn Pro Glu Thr Asp Tyr Leu Thr Gly
 5 10 15

Thr Asp Gly Lys Lys Phe Arg Leu Glu Ala Pro Asp Ala Asp Glu Leu
 20 25 30

Pro Lys Gly Glu Phe Asp Pro Gly Gln Asp Thr Tyr Gln His Pro Pro
 35 40 45

Lys Asp Ser Ser Gly Gln His Val Asp Val Ser Pro Thr Ser Gln Arg
 50 55 60

518

Leu Gln Leu Leu Glu Pro Phe Asp Lys Trp Asp Gly Lys Asp Leu Glu
 65 70 75 80

Asp Leu Gln Ile Leu Ile Lys Val Lys Gly Lys Cys Thr Thr Asp His
 85 90 95

Ile Ser

<210> 1508

<211> 62

<212> PRT

<213> Homo sapiens

<400> 1508

Gly Ser Ala Gly Pro Pro Gly Pro Cys His Pro Thr Cys Gln Lys Ala
 5 10 15

Pro Gly Ala Ala Gly Ala Gly Trp Trp Gly Ser Arg Pro His Ala Ala
 20 25 30

Arg Cys Cys Pro Trp Val Gly Ala Gly Arg Cys Pro Ala Leu Gly Gln
 35 40 45

Thr Pro Leu Trp Glu Ala His Leu His Pro Glu Pro Pro Ala
 50 55 60

<210> 1509

<211> 97

<212> PRT

<213> Homo sapiens

<400> 1509

Asp Val Val Ser Gly Thr Leu Pro Phe Asp Leu Asp Glu Asp Leu Gln
 5 10 15

Val Leu Gln Val Leu Ala Ile Pro Leu Val Lys Arg Leu Gln Glu Leu
 20 25 30

Gln Ala Leu Ala Gly Gly Ala His Val His Met Leu Pro Ala Ala Val
 35 40 45

Leu Gly Trp Val Leu Val Gly Val Leu Pro Trp Val Lys Leu Pro Phe
 50 55 60

Gly Lys Leu Ile Cys Ile Arg Ser Leu Gln Pro Glu Leu Leu Ala Ile
 65 70 75 80

Arg Ala Arg Gln Val Val Gly Leu Trp Val Glu Leu Glu Gly Ser Arg
 85 90 95

Asn

<210> 1510

<211> 54

<212> PRT

<213> Homo sapiens

<400> 1510

Glu Met Trp Ser Val Val His Phe Pro Leu Thr Leu Met Arg Ile Cys
 5 10 15
 Arg Ser Ser Arg Ser Leu Pro Ser His Leu Ser Lys Gly Ser Arg Ser
 20 25 30
 Cys Arg Arg Trp Leu Val Gly Leu Thr Ser Thr Cys Cys Pro Leu Leu
 35 40 45
 Ser Leu Gly Gly Cys Trp
 50

<210> 1511
 <211> 137
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(137)
 <223> Xaa = Any amino acid

<400> 1511
 Pro Cys Leu Xaa Ser Xaa Val Thr Arg Lys Arg Pro Cys Leu Pro Ser
 5 10 15
 Met Thr Leu Met Glu Glu Met Leu Arg Glu Ala Phe Arg Cys Met Thr
 20 25 30
 Gln Glu Pro Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro
 35 40 45
 Leu Phe Arg Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe
 50 55 60
 Met Arg Glu Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn Gly Leu
 65 70 75 80
 Phe His Ile Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Arg Asp Leu
 85 90 95
 Cys Thr His Leu Cys Asp Cys Val Val Pro Ser Leu Gly Glu Ala Leu
 100 105 110
 Cys Ile Leu Phe Ser Gly Ser Leu Leu Ala Xaa Thr Glu Lys Lys Leu
 115 120 125
 Xaa Glu Val Val Trp Ser Lys Glu Lys
 130 135

<210> 1512
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(67)
 <223> Xaa = Any amino acid

<400> 1512

520

Leu Pro Xaa Ile Xaa Gly His Ser Glu Glu Ala Met Ser Thr Leu Asn
 5 10 15
 Asp Thr His Gly Gly Asn Ala Glu Arg Ser Ile Gln Met His Asp Thr
 20 25 30
 Arg Ala Asn Glu Arg Pro Tyr Cys Tyr Ala Ile Trp Ser Lys Thr Thr
 35 40 45
 Leu Gln Glu Asp Val Phe Thr Gly Gly Pro His Ala Lys Leu Leu His
 50 55 60
 Glu Gly Ile
 65

<210> 1513
 <211> 137
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(137)
 <223> Xaa = Any amino acid

<400> 1513
 His Phe Ser Phe Asp Gln Thr Thr Xaa Trp Ser Phe Phe Ser Val Xaa
 5 10 15
 Ala Arg Ser Asp Pro Glu Asn Asn Ile His Asn Ala Ser Pro Arg Glu
 20 25 30
 Gly Thr Thr Gln Ser His Arg Trp Val His Arg Ser Leu Ala Gly Ile
 35 40 45
 Ile Arg Arg Pro Pro Arg Ala Met Trp Lys Ser Pro Phe Ile Ile Trp
 50 55 60
 Thr Ala Pro Lys Val Leu Asp Ser Leu Met Lys Lys Leu Cys Val Gly
 65 70 75 80
 Pro Thr Ser Glu Asp Ile Leu Leu Lys Ser Gly Phe Gly Pro Asp Cys
 85 90 95
 Ile Ala Ile Gly Pro Phe Ile Gly Ser Cys Val Met His Leu Asn Ala
 100 105 110
 Ser Leu Ser Ile Ser Ser Met Ser Val Ile Glu Gly Arg His Gly Leu
 115 120 125
 Phe Arg Val Thr Xaa Asp Xaa Arg Gln
 130 135

<210> 1514
 <211> 61
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(61)

<223> Xaa = Any amino acid

<400> 1514

```

Ile Phe Pro Leu Thr Lys Gln Leu Xaa Gly Val Phe Ser Pro Xaa Leu
      5              10              15

Pro Gly Val Ile Arg Lys Ile Ile Tyr Ile Met Pro Pro Pro Glu Arg
      20              25              30

Val Pro His Ser His Thr Asp Gly Cys Ile Asp Pro Leu Leu Gly Ser
      35              40              45

Ser Glu Asp Pro Pro Gly Gln Cys Gly Arg Ala His Ser
      50              55              60

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<210> 1515

<211> 87

<212> PRT

<213> Homo sapiens

<400> 1515

```

Leu Gly Gly Pro Gly Lys Gly Leu Gly His Glu Pro Gly Ser Ser Glu
      5              10              15

Ala Val Thr Glu Ala Arg Glu Pro Ala Pro Arg Ser Trp Gly Asp Leu
      20              25              30

Ala Leu Thr Pro Gly Leu Gly Ala His Leu Gln Thr Thr Ser Leu Pro
      35              40              45

Leu Ser Ala Ala Ser Leu Cys Pro His Arg Trp Leu Ser Gly Gln Cys
      50              55              60

Pro Gly Pro Arg Arg Cys Asp Leu Pro Pro Cys Gln Pro Cys Cys His
      65              70              75              80

Pro Cys Pro Ala Ala Gly Arg
      85

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<210> 1516

<211> 113

<212> PRT

<213> Homo sapiens

<400> 1516

```

Trp Gly Val Arg Glu Arg Gly Trp Ala Met Ser Gln Ala Ala Pro Lys
      5              10              15

Gln Ser Leu Arg Pro Gly Ser Leu His Pro Gly His Gly Ala Thr Trp
      20              25              30

Leu Ser Leu Leu Ala Trp Val Leu Thr Tyr Arg Pro Leu His Phe Pro
      35              40              45

Cys Pro Gln Arg His Tyr Val Leu Ile Gly Gly Cys Leu Val Asn Val
      50              55              60

Gln Ala Leu Val Gly Val Ile Phe Leu His Ala Ser Leu Ala Val Ile
      65              70              75              80

Leu Val Gln Gln Gln Glu Asp Arg His Asp Asp Glu Glu Asp Asp Gln

```


522

85

90

95

Gln Arg Leu Asp His Asp Asp Thr Ile Leu Gln Arg Val Pro Leu Leu
 100 105 110

Gln

<210> 1517

<211> 79

<212> PRT

<213> Homo sapiens

<400> 1517

Leu Lys Gln Arg Asn Thr Leu Lys Asp Gly Ile Ile Met Ile Gln Thr
 5 10 15

Leu Leu Ile Ile Leu Phe Ile Ile Val Pro Ile Phe Leu Leu Asp
 20 25 30

Lys Asp Asp Ser Lys Ala Gly Met Glu Glu Asp His Thr Tyr Glu Gly
 35 40 45

Leu Asp Ile Asp Gln Thr Ala Thr Tyr Glu Asp Ile Val Thr Leu Arg
 50 55 60

Thr Gly Glu Val Lys Trp Ser Val Gly Glu His Pro Gly Gln Glu
 65 70 75

<210> 1518

<211> 51

<212> PRT

<213> Homo sapiens

<400> 1518

Pro Ala Tyr Asn Gly Asp Val Val Phe Leu Phe Thr Phe Val Tyr Tyr
 5 10 15

Ala Cys Val Phe Ser Thr Thr Leu Gly Ser Gly Arg Asn Gly Gln Thr
 20 25 30

Glu Asp Glu Leu Tyr Pro Gly Pro Ala Gly Pro Ala Cys Ser Pro Leu
 35 40 45

Cys Ser Pro
 50

<210> 1519

<211> 79

<212> PRT

<213> Homo sapiens

<400> 1519

Gln Pro Thr Met Gly Met Leu Cys Phe Cys Ser Pro Ser Phe Thr Met
 5 10 15

Pro Val Ser Ser Pro Pro Arg Trp Gly Leu Gly Gly Met Asp Arg Gln
 20 25 30

Arg Met Ser Ser Thr Gln Gly Leu Gln Asp Leu Pro Val Ala His Ser

523

35

40

45

Ala Arg Leu Ser Thr Thr Thr Pro Ala Lys Glu Asp Ser Ile Trp Gln
 50 55 60

Ser Phe Phe Gln Val Pro Ser Tyr Thr Cys Ala Ser Ala Phe Leu
 65 70 75

<210> 1520

<211> 71

<212> PRT

<213> Homo sapiens

<400> 1520

Leu Gly Thr Trp Lys Lys Leu Cys Gln Met Glu Ser Ser Leu Ala Gly
 5 10 15

Val Val Val Leu Arg Arg Ala Glu Trp Ala Thr Gly Arg Ser Cys Arg
 20 25 30

Pro Trp Val Glu Leu Ile Leu Cys Leu Ser Ile Pro Pro Arg Pro Gln
 35 40 45

Arg Gly Gly Glu Asp Thr Gly Ile Val Asn Glu Gly Glu Gln Lys His
 50 55 60

Asn Ile Pro Ile Val Gly Trp
 65 70

<210> 1521

<211> 68

<212> PRT

<213> Homo sapiens

<400> 1521

Glu Lys Ser Arg Gly Thr Gly Ile Ala Gly His Leu Glu Glu Ala Leu
 5 10 15

Pro Asn Gly Ile Leu Leu Gly Arg Ser Gly Ser Ala Lys Ala Ser Arg
 20 25 30

Val Gly Tyr Arg Gln Val Leu Gln Ala Leu Gly Arg Ala His Pro Leu
 35 40 45

Ser Val His Ser Ser Gln Thr Pro Ala Trp Trp Arg Arg His Arg His
 50 55 60

Ser Lys Arg Arg
 65

<210> 1522

<211> 117

<212> PRT

<213> Homo sapiens

<400> 1522

Lys Lys Gln Arg Arg Arg Ser His Lys Ala Ile Glu Met Glu His Pro
 5 10 15

Leu Gly Glu Leu Arg Gln Gly Ala Pro Glu Thr Asp Phe Gln Asp Ser

524

20 25 30
 Phe Phe Glu Val Leu Cys Gly Val Lys Tyr Ser Ser Ala Lys Arg Val
 35 40 45
 Thr Gly Lys Gly Pro Val Lys Gln Gln Phe Leu Ile Ser Ser Leu Ser
 50 55 60
 Ser Leu Arg Ile Ile Tyr Pro Lys Ile Leu Cys Ile Tyr Lys Met Tyr
 65 70 75 80
 Thr Ser Leu Gln Phe Thr Lys His Ser Leu Leu Pro Asn Thr Tyr Pro
 85 90 95
 Cys Cys Met Ala Asn Glu Met Ser Asn Pro Thr Gly Tyr Met Ala Val
 100 105 110
 Glu Leu His Ser Lys
 115

<210> 1523
 <211> 68
 <212> PRT
 <213> Homo sapiens

<400> 1523
 Met Gln Ser Ile Leu Gly Tyr Ile Ile Leu Arg Glu Asp Lys Asp Asp
 5 10 15
 Ile Lys Asn Cys Cys Phe Thr Gly Pro Leu Pro Val Thr Leu Phe Ala
 20 25 30
 Glu Glu Tyr Leu Thr Pro His Ser Thr Ser Lys Lys Leu Ser Trp Lys
 35 40 45
 Ser Val Ser Gly Ala Pro Cys Leu Asn Ser Pro Ser Gly Cys Ser Ile
 50 55 60
 Ser Ile Ala Leu
 65

<210> 1524
 <211> 88
 <212> PRT
 <213> Homo sapiens

<400> 1524
 Thr Val Ile Asn Tyr Arg Pro His Asn Met Arg Pro Glu Asp Arg Met
 5 10 15
 Phe His Ile Arg Ala Val Ile Leu Arg Ala Leu Ser Leu Ala Phe Leu
 20 25 30
 Leu Ser Leu Arg Gly Ala Gly Ala Ile Lys Ala Asp His Val Ser Thr
 35 40 45
 Tyr Ala Ala Phe Val Gln Thr His Arg Pro Thr Gly Glu Phe Met Phe
 50 55 60
 Glu Phe Asp Glu Asp Glu Met Phe Tyr Val Asp Leu Asp Lys Lys Glu
 65 70 75 80

Thr Val Trp His Leu Glu Glu Phe
85

<210> 1525
<211> 55
<212> PRT
<213> Homo sapiens

<400> 1525
Val Ser Glu Glu Leu Gly Pro Ser Arg Arg Thr Met Cys Gln Leu Met
5 10 15

Pro Arg Leu Tyr Arg Arg Ile Asp Gln Gln Gly Ser Leu Cys Leu Asn
20 25 30

Leu Met Lys Met Arg Cys Ser Met Trp Ile Trp Thr Arg Arg Arg Pro
35 40 45

Ser Gly Ile Trp Arg Ser Leu
50 55

<210> 1526
<211> 52
<212> PRT
<213> Homo sapiens

<400> 1526
Gly Gln Pro Gly Val Leu Leu Leu Val Gln Ile His Glu Leu Leu Pro
5 10 15

Gly Pro Gln Ala Val Arg Val Val Gly Asp Cys Leu Pro Glu Cys Arg
20 25 30

Ala Leu Gly His Gly Val Leu Gly Pro Pro Lys Lys Gln Glu Pro Glu
35 40 45

Pro Leu Lys Ala
50

<210> 1527
<211> 75
<212> PRT
<213> Homo sapiens

<400> 1527
Leu Pro Arg Thr Thr Ser Ser Arg Arg Lys Ser Thr Arg Asn Cys Asn
5 10 15

Leu Ser Phe Ile Ser Met Val Lys Gly Ser Gln Ala Cys Cys Phe Ser
20 25 30

Ser Lys Tyr Thr Asn Phe Ser Gln Ala His Arg Arg Ser Gly Trp Ser
35 40 45

Val Thr Ala Ser Pro Ser Val Gly His Ser Ala Met Ala Ser Ser Gly
50 55 60

Arg Leu Arg Ser Lys Ser Gln Ser Leu Ser Arg
65 70 75

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<400> 1530
Leu Lys Asp Glu Arg Asp Trp Gln Gly Ser Arg Asn Glu Ser Ala Leu
          5                      10                      15

Gly Glu Tyr Tyr Leu Val Ala Pro Ile Ile Tyr Cys Leu Gly His Thr
          20                      25                      30

Leu Leu Pro Thr Cys Tyr His Ala Gly Pro Gln His Phe Arg Asp Gln
          35                      40                      45

Lys Arg Trp Gly His Gln Cys Lys Pro Lys Thr Thr Ile Gln Arg Thr
          50                      55                      60

Val Pro Ala His Ala Ala Ser Ser Ser Phe Ala Phe Arg Val Val Ser
          65                      70                      75                      80

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Pro His Leu Leu Thr Gln Glu Cys Ile Thr Arg Leu Pro Glu Gln Val
 85 90 95

<210> 1531
 <211> 54
 <212> PRT
 <213> Homo sapiens

<400> 1531
 Asp Ile Pro Phe Tyr Leu Leu Ala Ile Met Leu Asp Leu Ser Ile Ser
 5 10 15

Gly Thr Arg Lys Asp Gly Asp Thr Asn Ala Ser Pro Arg Leu Pro Ser
 20 25 30

Arg Gly Pro Phe Leu Pro Met Leu Leu Pro Leu Val Leu Leu Ser Glu
 35 40 45

Trp Cys His Pro Thr Cys
 50

<210> 1532
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 1532
 Val Ser Phe Gly Gly Ile Leu Pro Gly Gly Ser His His Leu Leu Leu
 5 10 15

Arg Thr Tyr Pro Phe Thr Tyr Leu Leu Ser Cys Trp Thr Ser Ala Phe
 20 25 30

Gln Gly Pro Glu Lys Met Gly Thr Pro Met Gln Ala Gln Asp Tyr His
 35 40 45

Pro Glu Asp Arg Ser Cys Pro Cys Cys Phe Leu
 50 55

<210> 1533
 <211> 55
 <212> PRT
 <213> Homo sapiens

<400> 1533
 Ala Arg Val Pro Gly Ser Ser Leu Thr Gly Leu Lys Leu Gly Ile Val
 5 10 15

Arg Leu Arg Ala Pro Arg Arg Ala Ala Val Ala Leu Leu Leu Glu
 20 25 30

His Val Ala Asp His Glu Ala Cys Gln Ala His Glu Glu Glu Asp Gln
 35 40 45

His Lys Gln Glu Glu His Ile
 50 55

<210> 1534

<211> 66
<212> PRT
<213> Homo sapiens

<400> 1534
Gln Gly Leu Met Ser Glu Pro Gln Pro Asp Leu Glu Pro Pro Gln His
 5 10 15

Gly Leu Tyr Met Leu Phe Leu Leu Val Leu Val Phe Phe Leu Met Gly
 20 25 30

Leu Ala Gly Phe Met Ile Cys His Val Leu Lys Lys Lys Gly Tyr Arg
 35 40 45

Cys Arg Thr Ser Arg Gly Ser Glu Pro Asp Asp Ala Gln Leu Gln Pro
 50 55 60

Arg Glu
65

<210> 1535
<211> 54
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(54)
<223> Xaa = Any amino acid

<400> 1535
Thr Val Ile Cys Trp Phe Ser Leu Lys Asn Asp Leu Trp Cys Glu Ala
 5 10 15

Gln Ile Ser Gly Asn Ile Arg Lys Thr Trp Ser Gly Gly Gly Ser Ser
 20 25 30

Gly Ala Cys Ile Thr Xaa Pro Ala Pro Gln Leu Phe Pro Ala Ser Ser
 35 40 45

Ala Ser Cys Arg Thr Tyr
50

<210> 1536
<211> 55
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(55)
<223> Xaa = Any amino acid

<400> 1536
Leu Tyr Val Arg Gln Leu Ala Glu Glu Ala Gly Lys Ser Cys Gly Ala
 5 10 15

Xaa Ser Val Met Gln Ala Pro Glu Glu Pro Pro Pro Asp Gln Val Phe
 20 25 30

Arg Met Phe Pro Asp Ile Cys Ala Ser His Gln Arg Ser Phe Phe Arg

529

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          35          40          45
Glu Asn Gln Gln Ile Thr Val
50          55

<210> 1537
<211> 61
<212> PRT
<213> Homo sapiens

<400> 1537
Cys Arg Pro Pro Arg Ser Arg Arg Gln Thr Arg Ser Ser Gly Cys Phe
          5          10          15

Gln Ile Phe Val Pro His Thr Arg Asp His Phe Ser Glu Lys Thr Asn
          20          25          30

Arg Ser Pro Ser Lys Cys Val Ala Trp Ala Pro His Pro Val Cys Val
          35          40          45

Leu His Pro Ser Pro Cys Tyr Ser Gly Pro His His Asp
          50          55          60

<210> 1538
<211> 96
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(96)
<223> Xaa = Any amino acid

<400> 1538
Val Cys Pro Ala Thr Gly Arg Arg Gly Trp Glu Glu Leu Trp Ser Arg
          5          10          15

Xaa Cys Asp Ala Gly Pro Arg Gly Ala Ala Arg Pro Gly Leu Pro
          20          25          30

Asp Val Ser Arg Tyr Leu Cys Leu Thr Pro Glu Ile Ile Phe Gln Arg
          35          40          45

Lys Pro Thr Asp His Arg Leu Ser Ala Ser Leu Gly Arg Pro Thr Pro
          50          55          60

Ser Ala Ser Cys Ile His Leu Pro Val Thr Val Ala Arg Ile Met Ile
          65          70          75          80

Lys Glu Cys Gly Ser Leu Cys Leu Gly Trp Asp Ala Leu Leu Cys Thr
          85          90          95

<210> 1539
<211> 115
<212> PRT
<213> Homo sapiens

<400> 1539
Pro Met Trp Leu Val Phe Ser Leu Gln Leu Ala Arg Phe His Thr Leu
          5          10          15

```


Thr Ser Leu Ser Gln Pro Arg Glu Thr Met Ile Gly Leu Leu Leu
 20 25 30
 Gly Glu Lys Arg Thr Gln Asp Thr His Ser Glu Trp Leu Ser Ser Trp
 35 40 45
 Thr Val Tyr Leu His Thr Pro Arg Val Phe His Ser Leu Met Val Leu
 50 55 60
 Ser Arg Asp Pro Glu Thr Ile Cys Arg Leu Ser Glu Glu Lys Ala Thr
 65 70 75 80
 Leu Ser Thr Ser Leu Val Trp Pro Thr Asn Arg Leu Val Val Val Pro
 85 90 95
 Val Val Arg Ser Gln Arg Arg Arg Val Pro Ser Gln Glu Pro Glu Arg
 100 105 110
 Ala Asn Trp
 115

<210> 1540
 <211> 50
 <212> PRT
 <213> Homo sapiens

<400> 1540
 Leu Asp Gly Phe Ile Ser Arg Ser Arg Asp Asn Leu Pro Val Val Arg
 5 10 15
 Gly Glu Gly His Thr Gln His Ile Leu Gly Met Ala His Lys Ser Pro
 20 25 30
 Arg Gly Gly Ala Arg Cys Glu Ile Pro Glu Ala Gln Gly Ser Ile Pro
 35 40 45
 Gly Ala
 50

<210> 1541
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 1541
 Gln Phe Ala Leu Ser Gly Ser Trp Asp Gly Thr Leu Arg Leu Trp Asp
 5 10 15
 Leu Thr Thr Gly Thr Thr Thr Arg Arg Phe Val Gly His Thr Lys Asp
 20 25 30
 Val Leu Ser Val Ala Phe Ser Ser Asp Asn Arg Gln Ile Val Ser Gly
 35 40 45
 Ser Arg Asp Lys Thr Ile Lys Leu Trp Asn Thr Leu Gly Val Cys Lys
 50 55 60
 Tyr Thr Val Gln Asp Glu Ser His Ser Glu Trp Val Ser Cys Val Arg
 65 70 75 80

531

Phe Ser Pro Asn Ser Ser Asn Pro Ile Ile Val Ser Arg Gly Trp Asp
85 90 95

Lys Leu Val Lys Val Trp Asn Leu Ala Asn Cys Lys Leu Lys Thr Asn
100 105 110

His Ile

<210> 1542

<211> 74

<212> PRT

<213> Homo sapiens

<400> 1542

Val Trp Pro Ser Pro Leu Thr Thr Gly Arg Leu Ser Leu Asp Leu Glu
5 10 15

Ile Lys Pro Ser Ser Tyr Gly Ile Pro Trp Val Cys Ala Asn Thr Leu
20 25 30

Ser Arg Met Arg Ala Thr Gln Ser Gly Cys Leu Val Ser Ala Ser Arg
35 40 45

Pro Thr Ala Ala Thr Leu Ser Ser Ser Pro Val Ala Gly Thr Ser Trp
50 55 60

Ser Arg Tyr Gly Thr Trp Leu Thr Ala Ser
65 70

<210> 1543

<211> 55

<212> PRT

<213> Homo sapiens .

<400> 1543

Leu Tyr Val Arg Gln Leu Ala Glu Glu Ala Gly Lys Ser Cys Gly Ala
5 10 15

Gly Ser Val Met Gln Ala Pro Glu Glu Pro Pro Pro Asp Gln Val Phe
20 25 30

Arg Met Phe Pro Asp Thr Cys Ala Ser His Gln Arg Ser Phe Phe Arg
35 40 45

Glu Asn Gln Gln Ile Thr Val
50 55

<210> 1544

<211> 61

<212> PRT

<213> Homo sapiens

<400> 1544

Cys Arg Pro Pro Arg Ser Arg Arg Gln Thr Arg Ser Ser Gly Cys Phe
5 10 15

Gln Ile Leu Val Pro His Thr Arg Asp His Phe Ser Glu Lys Thr Asn
20 25 30

532

Arg Ser Pro Ser Lys Cys Val Ala Trp Ala Pro His Pro Val Cys Val
35 40 45

Leu His Pro Ser Pro Cys Tyr Ser Gly Pro His His Asp
50 55 60

```
<210> 1545
<211> 96
<212> PRT
<213> Homo sapiens
```

<400> 1545
Val Cys Pro Ala Thr Gly Arg Arg Gly Trp Glu Glu Leu Trp Ser Arg
 5 10 15

Leu Cys Asp Ala Gly Pro Arg Gly Ala Ala Ala Arg Pro Gly Leu Pro
20 25 30

Asp Val Ser Arg Tyr Leu Cys Leu Thr Pro Glu Ile Ile Phe Gln Arg
35 40 45

Lys Pro Thr Asp His Arg Leu Ser Ala Ser Leu Gly Arg Pro Thr Pro
50 55 60

Ser Ala Ser Cys Ile His Leu Pro Val Thr Val Ala Arg Ile Met Ile
65 70 75 80

Lys Glu Cys Gly Ser Leu Cys Leu Gly Trp Asp Ala Leu Leu Cys Thr
85 90 95

```
<210> 1546
<211> 54
<212> PRT
<213> Homo sapiens
```

```

<400> 1546
Thr Val Ile Cys Trp Phe Ser Leu Lys Asn Asp Leu Trp Cys Glu Ala
          5              10              15

```

Gln Val Ser Gly Asn Ile Arg Lys Thr Trp Ser Gly Gly Gly Ser Ser
20 25 30

Gly Ala Cys Ile Thr Glu Pro Ala Pro Gln Leu Phe Pro Ala Ser Ser
35 40 45

Ala Ser Cys Arg Thr Tyr
50

```
<210> 1547
<211> 52
<212> PRT
<213> Homo sapiens
```

<400> 1547
Ser Pro Ala Glu Ser Leu Thr Leu Ser Ser Cys Ala Leu Ser Phe Thr
5 10 15

Val Pro Pro Thr Gln Asp Pro Asn Phe Phe Tyr Ser Ile Leu Phe Pro
20 25 30

Leu Val Asn Arg Arg Ala Gln Tyr Asp Leu Phe Ser Lys Glu Pro Ala
35 40 45

Gly Ile Trp Phe
50

```
<210> 1548
<211> 62
<212> PRT
<213> Homo sapiens
```

<400> 1548
Lys Lys Leu Gly Ser Trp Val Gly Gly Thr Val Lys Leu Arg Ala His
5 10 15

Glu Leu Lys Val Ser Asp Ser Ala Gly Leu His Arg Glu Ser Cys Ala
20 25 30

His His Ser Val Gln Val Leu Ser Leu Pro Arg Gln His Arg Thr Pro
35 40 45

Ala Pro Leu Leu Thr Trp Ile Ile Glu Phe Pro Pro Lys Ile
50 55 60

```
<210> 1549
<211> 62
<212> PRT
<213> Homo sapiens
```

<400> 1549
Ser Glu Val Gly Ala Ala Leu Lys Lys Leu Pro Arg Arg Thr Asn Arg
 5 10 15

His Arg Ser Asp Arg Asp Phe Val Ile Arg Thr Arg Phe Leu Pro Ala
20 25 30

Pro Leu Lys Thr Gly His Ile Val Leu Phe Cys Leu Gln Glu Glu Thr
35 40 45

Arg Trp Asn Lys Arg Asn Trp Asp Leu Gly Leu Glu Gly Gln
50 55 60

```
<210> 1550
<211> 62
<212> PRT
<213> Homo sapiens
```

<400> 1550
Ser Leu Glu His Met Asn Ser Arg Leu Val Thr Leu Gln Asp Phe Thr
 5 10 15

Glu Arg Ala Val Pro Ile Ile Gln Ser Lys Cys Phe Leu Cys Pro Asp
20 25 30

Ser Thr Glu Leu Gln Pro Arg Tyr Leu His Gly Ser Ser Ser Phe His
35 40 45

Leu Lys Tyr Asp Ser Ile Tyr Phe Glu Ser Leu Leu Pro Asn
50 55 60

<210> 1551
<211> 64
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(64)
<223> Xaa = Any amino acid

<400> 1551
Glu Pro Xaa Pro Leu Arg Pro Ile Glu Glu Met Thr Leu Arg Arg Arg
5 10 15
Val Leu Gln Glu Thr Trp Xaa Gly Val Pro Ser Gln Ser Gln Trp Gly
20 25 30
Ala Xaa His His Xaa Cys His Xaa Gln Asn Xaa His Ala Gly Thr Ser
35 40 45
Arg Glu Pro Xaa Thr His His Ala Gly Xaa Gln Asp Arg Thr Arg Gly
50 55 60

<210> 1552
<211> 53
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(53)
<223> Xaa = Any amino acid

<400> 1552
His Ser Asp Val Glu Tyr Ser Lys Lys Arg Xaa Leu Val Ser Pro Ala
5 10 15
Lys Ala Ser Gly Glu Leu Xaa Thr Ile Xaa Val Thr Xaa Arg Thr Xaa
20 25 30
Met Gln Glu Pro Pro Gly Ser Xaa Arg His Thr Met Leu Xaa Asn Arg
35 40 45
Thr Gly Pro Gly Ala
50

<210> 1553
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(51)
<223> Xaa = Any amino acid

<400> 1553
Gly Pro Trp Ser Cys Pro Val Xaa Gln His Gly Val Ser Xaa Ala Pro
5 10 15

535

Trp Arg Phe Leu His Xaa Ser Ser Xaa Ser Asp Xaa Asp Gly Xaa Glu
 20 25 30
 Leu Pro Thr Gly Phe Gly Trp Gly His Gln Xaa Thr Phe Leu Gly Val
 35 40 45
 Leu Tyr Val
 50

<210> 1554
 <211> 64
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(64)
 <223> Xaa = Any amino acid

<400> 1554
 Ala Pro Gly Pro Val Leu Xaa Ser Ser Met Val Cys Xaa Arg Leu Pro
 5 10 15
 Gly Gly Ser Cys Met Xaa Val Leu Xaa Val Thr Xaa Met Val Xaa Ser
 20 25 30
 Ser Pro Leu Ala Leu Ala Gly Asp Thr Xaa Pro Arg Phe Leu Glu Tyr
 35 40 45
 Ser Thr Ser Glu Cys His Phe Phe Asn Gly Thr Glu Arg Xaa Arg Phe
 50 55 60

<210> 1555
 <211> 94
 <212> PRT
 <213> Homo sapiens

<400> 1555
 Pro Ile Ile Glu Ile Ser Ala Pro Ala Cys Lys Ala Ser Met Asn Ala
 5 10 15
 Leu Val Pro Asp Leu Ala Ile Val Pro Arg Leu Leu Ile Lys Ser Ala
 20 25 30
 Leu Val Ile Pro Ile Pro Val Ser Thr Ile Val Arg Val Arg Ser Cys
 35 40 45
 Leu Phe Gly Ile Arg Leu Ile Cys Ser Ser Phe Ser Glu Ser Asn Leu
 50 55 60
 Leu Gly Ser Val Lys Leu Ser Tyr Arg Ile Leu Ser Asn Ala Ser Asp
 65 70 75 80
 Glu Phe Glu Met Ser Ser Leu Arg Lys Ile Ser Leu Phe Glu
 85 90

<210> 1556
 <211> 61
 <212> PRT
 <213> Homo sapiens

<400> 1556

Asn His Arg Asp Ile Cys Thr Ser Leu Gln Ser Phe His Glu Arg Phe
 5 10 15

Gly Pro Arg Leu Gly Asp Ser Thr Lys Val Ile Asp Gln Val Ser Leu
 20 25 30

Gly His Ser Asn Ser Ser Ile His Asn Ser Glu Ser Ser Ile Leu Phe
 35 40 45

Val Arg Tyr Lys Val Asn Met Gln Leu Phe Leu Arg Val
 50 55 60

<210> 1557

<211> 58

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(58)

<223> Xaa = Any amino acid

<400> 1557

Gly Asn Pro Asp Pro Arg Pro Thr Asp Gly Gly Xaa Gly Gly Xaa Xaa
 5 10 15

Val Arg Leu Ser Gly Arg Asn Cys Pro Val Asp Val Ile Asp His Gln
 20 25 30

Tyr Phe Leu Leu Glu Gln Arg Asp Leu Ser Glu Arg Ala His Phe Lys
 35 40 45

Phe Ile Arg Cys Ile Gly Gln Asn Pro Val
 50 55

<210> 1558

<211> 139

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(139)

<223> Xaa = Any amino acid

<400> 1558

Xaa Thr Gly Ala Val Ser Phe Xaa Met Xaa Glu Glu Thr Gln Thr Gln
 5 10 15

Asp Gln Pro Met Glu Glu Xaa Glu Val Xaa Thr Phe Ala Phe Gln Ala
 20 25 30

Glu Ile Ala Gln Leu Met Ser Leu Ile Ile Asn Thr Phe Tyr Ser Asn
 35 40 45

Lys Glu Ile Phe Leu Arg Glu Leu Ile Ser Asn Ser Ser Asp Ala Leu
 50 55 60

Asp Lys Ile Arg Tyr Glu Ser Leu Thr Asp Pro Ser Lys Leu Asp Ser

50

<210> 1561
 <211> 52
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(52)
 <223> Xaa = Any amino acid

<400> 1561
 Asp Phe Gly Gly Cys Pro Asp Tyr Glu Trp Ala Leu Pro His Cys Pro
 5 10 15
 Gly Gly Ser Ser Asp Asp Pro Xaa Arg Asp Leu Cys Xaa His Leu Cys
 20 25 30
 Asp Cys Val Val Pro Ser Leu Gly Arg His Tyr Val Tyr Tyr Phe Arg
 35 40 45
 Ile Thr Pro Gly
 50

<210> 1562
 <211> 125
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(125)
 <223> Xaa = Any amino acid

<400> 1562
 Asp Cys Gln Lys Ser Xaa Ser Cys Ser Pro His Phe Val Ile Xaa Phe
 5 10 15
 Xaa Phe Arg Ser Xaa Glu Ser Lys Xaa Thr Xaa Pro Arg Asn Ser Val
 20 25 30
 Asn Gly Thr Phe Pro Ala Xaa Pro Met Lys Gly Pro Ile Ala Met Gln
 35 40 45
 Ser Gly Pro Lys Pro Leu Phe Arg Arg Met Xaa Ser Leu Val Gly Pro
 50 55 60
 Thr Gln Ser Phe Phe Met Arg Glu Ser Lys Thr Leu Gly Ala Val Gln
 65 70 75 80
 Ile Met Asn Gly Leu Phe His Ile Ala Leu Gly Gly Leu Leu Met Ile
 85 90 95
 Pro Xaa Gly Ile Tyr Xaa Pro Ile Cys Val Thr Val Trp Tyr Pro Leu
 100 105 110
 Trp Gly Gly Ile Met Tyr Ile Ile Ser Gly Ser Leu Leu
 115 120 125

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<210> 1563
<211> 89
<212> PRT
<213> Homo sapiens
```

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<220>  
<221> variant  
<222> (1)...(89)  
<223> Xaa = Any amino acid
```

```

<400> 1563
Ile Pro Xaa Gly Ile Ile Arg Arg Pro Pro Arg Ala Met Trp Lys Ser
                    5                                10                    15

Pro Phe Ile Ile Trp Thr Ala Pro Lys Val Leu Asp Ser Leu Met Lys
                20                                25                    30

Lys Leu Cys Val Gly Pro Thr Ser Glu Xaa Ile Leu Leu Lys Ser Gly
                35                                40                    45

Phe Gly Pro Asp Cys Ile Ala Ile Gly Pro Phe Ile Xaa Ser Ala Gly
                50                                55                    60

Lys Val Pro Phe Thr Glu Phe Leu Gly Xaa Xaa Ile Leu Leu Ser Xaa
                65                                70                    75                    80

Leu Leu Lys Xaa Lys Xaa Ile Thr Lys
                85

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```
<210> 1564
<211> 62
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> variant
<222> (1)...(62)
<223> Xaa = Any amino acid
```

```

<400> 1564
Ser Gly Asn Asn Ile His Asn Ala Ser Pro Glu Arg Val Pro His Ser
          5                      10                      15

His Thr Asp Gly Xaa Ile Asp Pro Xaa Trp Asp His Gln Lys Thr Pro
          20                      25                      30

Gln Gly Asn Val Glu Glu Pro Ile His Asn Leu Asp Ser Pro Gln Ser
          35                      40                      45

Leu Arg Phe Pro His Glu Glu Ala Leu Arg Gly Ala His Gln
          50                      55                      60

```

```
<210> 1565
<211> 64
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> variant
<222> (1)...(64)
<223> Xaa = Any amino acid
```

<400> 1565

Ile Ser Gly Xaa Cys Xaa Phe Ala Leu Xaa Thr Pro Lys Xaa Lys Xaa
 5 10 15

Asn Asn Lys Met Arg Arg Ala Arg Xaa Arg Phe Leu Ala Val Leu Pro
 20 25 30

Cys Val Met His Xaa Asn Ala Ser Xaa Ser Ile Ser Ser Met Ser Val
 35 40 45

Ile Glu Gly Arg His Gly Leu Phe Arg Val Thr Xaa Asp Xaa Arg Gln
 50 55 60

<210> 1566

<211> 131

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(131)

<223> Xaa = Any amino acid

<400> 1566

Leu Glu Lys Xaa Lys Xaa Xaa Leu Lys Asn Val Asp Glu Asn Ile Arg
 5 10 15

Xaa Leu Xaa Gly Arg Asp Pro Asn Asp Xaa Arg Pro Ile Gln Ala Arg
 20 25 30

Leu Leu Ala Leu Ser Gly Pro Xaa Gly Xaa Arg Gly Arg Gly Ser Xaa
 35 40 45

Leu Leu Arg Arg Gly Phe Xaa Xaa Ser Xaa Gly Gly Pro Xaa Ala Xaa
 50 55 60

Gln Arg Asp Leu Glu Gly Ala Val Xaa Xaa Leu Gly Gly Glu Arg Xaa
 65 70 75 80

Thr Arg Arg Glu Ser Arg Gln Glu Ser Asp Pro Xaa Asp Asp Asp Val
 85 90 95

Lys Lys Pro Xaa Leu Gln Xaa Ser Val Val Ala Thr Xaa Lys Glu Arg
 100 105 110

Thr Arg Xaa Asp Xaa Ile Gln Xaa Gln Asn Met Asp Glu Lys Gly Lys
 115 120 125

Gln Arg Asn
 130

<210> 1567

<211> 55

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(55)

<223> Xaa = Any amino acid

<400> 1567

Gly Val Asp Ser Xaa Ile Val Xaa Glu Asp Xaa Gln Xaa Asn Arg Glu
 5 10 15

Thr Leu Lys Gly Gln Ser Xaa Xaa Trp Ala Gly Ser Xaa Gly Pro Glu
 20 25 30

Glu Asn His Ala Arg Lys Ala Thr Arg Xaa Met Met Met Leu Lys Ser
 35 40 45

Xaa His Cys Xaa Leu Gln Leu
 50 55

<210> 1568

<211> 119

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(119)

<223> Xaa = Any amino acid

<400> 1568

Xaa Trp Ile Xaa Ser Xaa Arg Val Arg Ser Leu Xaa Val Ala Thr Thr
 5 10 15

Glu Xaa Cys Asn Xaa Gly Phe Leu Thr Ser Ser Xaa Ser Gly Ser Leu
 20 25 30

Ser Trp Arg Asp Ser Leu Leu Val Xaa Arg Ser Pro Pro Ser Xaa Xaa
 35 40 45

Thr Ala Pro Ser Arg Ser Leu Cys Xaa Ala Xaa Gly Pro Pro Xaa Leu
 50 55 60

Xaa Xaa Asn Pro Arg Leu Ser Asn Xaa Leu Pro Arg Pro Xaa Pro Xaa
 65 70 75 80

Pro Gly Pro Glu Arg Ala Ser Asn Leu Ala Trp Met Gly Leu Xaa Ser
 85 90 95

Phe Gly Ser Arg Xaa Val Ser Xaa Arg Met Phe Ser Ser Thr Phe Leu
 100 105 110

Xaa Leu Xaa Xaa Ala Phe Ser
 115

<210> 1569

<211> 53

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(53)

<223> Xaa = Any amino acid

<400> 1569

Leu Pro Leu Gln Gly Leu Ser Val Xaa Leu Xaa Val Leu Xaa His Tyr

542

5 10 15
 Xaa Arg Ile His Ala Ser Val Ile Xaa Tyr His Val Leu Xaa Leu Xaa
 20 25 30
 Gln Asp Gln Lys Gly Pro Ala Ile Trp Leu Gly Trp Ala Ser Xaa His
 35 40 45
 Ser Asp Pro Ala Xaa
 50

<210> 1570
 <211> 73
 <212> PRT
 <213> Homo sapiens

<400> 1570
 Arg Asp Asn Val Ile Cys Thr Pro Tyr Asp Ile Ser Thr Phe Leu Ala
 5 10 15
 Thr Thr Ser Gly Arg His Ser Pro Lys Leu Glu Lys Lys Glu Ile Glu
 20 25 30
 Asp Phe Cys Leu Cys Lys Val Leu Lys Ile Cys Ser Lys Leu Ile Lys
 35 40 45
 Leu Ser Leu Arg Ser Phe Leu Gln Gln Met Ile Pro Thr Trp Val Phe
 50 55 60
 Val Tyr Ser Ser Leu Leu Leu Lys His
 65 70

<210> 1571
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 1571
 Thr Asn Thr His Val Gly Ile Ile Cys Cys Arg Lys Glu Arg Lys Asp
 5 10 15
 Ser Phe Ile Asn Leu Glu Gln Ile Leu Arg Thr Leu His Arg Gln Lys
 20 25 30
 Ser Ser Ile Ser Phe Phe Ser Asn Phe Gly Glu Cys Leu Pro Leu Val
 35 40 45
 Val Ala Lys Asn Val Glu Ile Ser
 50 55

<210> 1572
 <211> 194
 <212> PRT
 <213> Homo sapiens

<400> 1572
 Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Gln Phe Tyr Val Asp Leu
 5 10 15
 Gly Arg Lys Glu Thr Val Trp Cys Leu Pro Val Leu Arg Gln Phe Arg

20 25 30
 Phe Asp Pro Gln Phe Ala Leu Thr Asn Ile Ala Val Leu Lys His Asn
 35 40 45
 Leu Asn Ser Leu Ile Lys Arg Ser Asn Ser Thr Ala Ala Thr Asn Glu
 50 55 60
 Val Pro Glu Val Thr Val Phe Ser Lys Ser Pro Val Thr Leu Gly Gln
 65 70 75 80
 Pro Asn Ile Leu Ile Cys Leu Val Asp Asn Ile Phe Pro Pro Val Val
 85 90 95
 Asn Ile Thr Trp Leu Ser Asn Gly His Ser Val Thr Glu Gly Val Ser
 100 105 110
 Glu Thr Ser Phe Leu Ser Lys Ser Asp His Ser Phe Phe Lys Ile Ser
 115 120 125
 Tyr Leu Thr Leu Leu Pro Ser Ala Glu Glu Ser Tyr Asp Cys Lys Val
 130 135 140
 Glu His Trp Gly Leu Asp Lys Pro Leu Leu Lys His Trp Glu Pro Glu
 145 150 155 160
 Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr Val Val Cys Ala Leu
 165 170 175
 Gly Leu Ser Val Gly Leu Val Gly Ile Val Val Gly Thr Val Phe Ile
 180 185 190
 Ile Arg

<210> 1573
 <211> 52
 <212> PRT
 <213> Homo sapiens

<400> 1573
 Ala Met Gly Thr Gln Ser Gln Lys Val Phe Leu Arg Pro Ala Ser Ser
 5 10 15
 Pro Arg Val Ile Ile Pro Ser Ser Arg Ser Val Thr Ser Pro Ser Ser
 20 25 30
 Leu Leu Leu Arg Arg Val Met Thr Ala Arg Trp Ser Thr Gly Asp Trp
 35 40 45
 Thr Ser Leu Phe
 50

<210> 1574
 <211> 55
 <212> PRT
 <213> Homo sapiens

<400> 1574
 Pro Arg Met Met Lys Thr Val Pro Thr Thr Met Pro Thr Arg Pro Thr
 5 10 15

Asp Asn Pro Arg Ala Gln Thr Thr Val Ser Val Ser Ser Asp Ile Gly
 20 25 30

Ala Gly Ile Ser Gly Ser Gln Cys Phe Arg Arg Gly Leu Ser Ser Pro
 35 40 45

Gln Cys Ser Thr Leu Gln Ser
 50 55

<210> 1575
 <211> 66
 <212> PRT
 <213> Homo sapiens

<400> 1575
 Pro Ser Val Thr Gly Asp Leu Glu Asn Thr Val Thr Ser Gly Thr Ser
 5 10 15

Leu Val Ala Ala Val Glu Leu Glu Arg Leu Ile Arg Leu Phe Lys Leu
 20 25 30

Cys Phe Arg Thr Ala Met Phe Val Ser Ala Asn Cys Gly Ser Asn Leu
 35 40 45

Asn Cys Leu Arg Thr Gly Lys His Gln Thr Val Ser Phe Leu Pro Arg
 50 55 60

Ser Thr
 65

<210> 1576
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 1576
 His Arg Gly Trp Asn Leu Arg Leu Pro Val Phe Gln Lys Arg Leu Val
 5 10 15

Gln Ser Pro Val Leu His Leu Ala Val Ile Thr Leu Leu Ser Arg Arg
 20 25 30

Glu Glu Gly Glu Val Thr Asp Leu Glu Glu Gly Met Ile Thr Leu Gly
 35 40 45

Glu Glu Ala Gly Leu Arg Asn Thr Phe Cys Asp
 50 55

<210> 1577
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 1577
 Val Pro Ile Ala Gln Pro Cys Asp Val Asp His Arg Arg Lys Asp Val
 5 10 15

Val His Lys Thr Asp Glu Asp Val Gly Leu Thr Gln Cys His Gly Arg
 20 25 30

Ala Ala Gly Pro Leu Ala Asp Ser Val Cys His Pro Cys Pro Val Phe
 35 40 45

Thr Pro Gly Leu Pro Lys
 50

<210> 1581
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 1581
 Gln Ile Gln Cys Val Thr Leu Val Leu Cys Ser Arg Gln Gly Phe Leu
 5 10 15
 Asn Glu Arg His Arg Leu Pro Ala Tyr Gly Lys Val Ser Ser Lys Gly
 20 25 30
 Ile Glu Val Arg Asp Arg Val Glu Leu Trp Val Phe Ile Val Phe His
 35 40 45
 Ala Lys Pro Thr Lys Ser Lys Ile Glu Phe Lys Leu Asn Lys Leu Leu
 50 55 60
 Leu Gln Asn Gly Arg Gly Lys Arg Leu Arg Lys Val Tyr Glu Asn Glu
 65 70 75 80
 Leu Thr Tyr Leu Val Lys Ser
 85

<210> 1582
 <211> 85
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(85)
 <223> Xaa = Any amino acid

<400> 1582
 Ser Gln Glu Ser Val Gln Glu Pro Phe Leu Thr Pro Val Met Asp Asn
 5 10 15
 Lys Ala Xaa Pro Glu Glu Asp Glu Pro Gln His Glu Ala Ser Asn Ala
 20 25 30
 Thr Gln His Leu Ala Leu Gly Arg Phe Arg Leu Ser Pro Pro Leu His
 35 40 45
 Gly Asp Gly Val Leu Glu Ala Gly Val Leu His Val Ala Gly Val Asp
 50 55 60
 Val Ser Met Leu Gly Ser His Phe Gln His His Gln Asp Leu Glu Xaa
 65 70 75 80
 Pro Val Thr Xaa Ser
 85

```
<210> 1583
<211> 56
<212> PRT
<213> Homo sapiens
```

```

<400> 1583
Asp Tyr Phe Asn Trp Asp Trp Leu Ser Leu Phe Cys Asn Ala Cys Leu
      5                                10                                15

Ser Leu Pro Arg Ile Pro Asn Cys Leu Cys Gln Pro Val Pro Leu Arg
      20                                25                                30

Ser Glu Ser Tyr Ser Gly Cys His Ala Ala Thr Arg Ser Ser Pro Phe
      35                                40                                45

Ile Pro Thr Pro Arg Arg Trp Leu
      50                                55

```

```
<210> 1584
<211> 70
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> variant  
<222> (1)...(70)  
<223> Xaa = Any amino acid
```

```

<400> 1584
Ile Cys Pro Glu Gln Asp Ala Glu Trp His Trp Arg Leu Arg Ala Gly
      5                                10                                15

Ala His Leu Pro Arg Xaa Gly Pro Tyr Tyr Pro Ser Gln Glu Ser Glu
      20                                25                                30

Arg Ala Pro Ala Leu Thr Pro Glu Thr Ile Leu Thr Gly Ile Gly Tyr
      35                                40                                45

His Phe Ser Val Thr Pro Ala Cys Pro Cys Pro Glu Phe Pro Thr Ala
      50                                55                                60

Cys Val Ser Leu Ser Pro
      65                                70

```

```
<210> 1585
<211> 82
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> variant
<222> (1)...(82)
<223> Xaa = Any amino acid
```

<400> 1585
Leu Gly Xaa Gly Asp₅ Trp Xaa Phe Gln Ile₁₀ Leu Val Met Leu₁₅ Glu Met
Thr Pro Gln₂₀ His Gly Asp Val Tyr Thr₂₅ Cys His Val Glu₃₀ His Pro Ser

```
<210> 1586
<211> 56
<212> PRT
<213> Homo sapiens
```

```
<210> 1587
<211> 52
<212> PRT
<213> Homo sapiens
```

```
<210> 1588
<211> 99
<212> PRT
<213> Homo sapiens
```

```

<400> 1588
Ser Val Ala Ala Glu Asp Leu Phe Val His Tyr Gly Arg Asp Gly Gln
          5                      10                      15

Ala Val Glu Ala Val Ser Glu Gly Phe Pro Gln Phe Asp Val Val Ala
          20                      25                      30

```

549

Ser Leu Ala Leu Ile Val Glu Thr Ile Asp Ala Val Asp Ala Gly Thr
 35 40 45
 Leu Val Val Pro Thr Glu Gln Glu Glu Val Leu Gly Val Leu Asp Leu
 50 55 60
 Ile Gly Gln Gln Gln Ala Asp Gly Leu Gln Gly Leu Leu Ala Pro Val
 65 70 75 80
 His Ile Val Pro Gln Lys Glu Val Val Ala Leu Gly Arg Glu Thr Ala
 85 90 95
 Ile Leu Lys

<210> 1589
 <211> 145
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(145)
 <223> Xaa = Any amino acid

<400> 1589
 Leu Thr Glu Asn Glu Ile Arg Gly Leu Cys Leu Lys Ser Arg Glu Ile
 5 10 15
 Phe Leu Ser Gln Pro Ile Leu Xaa Glu Leu Glu Ala Pro Leu Lys Ile
 20 25 30
 Cys Gly Asp Ile His Gly Gln Tyr Tyr Asp Leu Leu Arg Leu Phe Glu
 35 40 45
 Tyr Gly Gly Phe Pro Pro Glu Ser Asn Tyr Leu Phe Leu Gly Asp Tyr
 50 55 60
 Val Asp Arg Gly Lys Gln Ser Leu Glu Thr Ile Cys Leu Leu Leu Ala
 65 70 75 80
 Tyr Lys Ile Lys Tyr Pro Glu Asn Phe Phe Leu Leu Arg Gly Asn His
 85 90 95
 Glu Cys Ala Ser Ile Asn Arg Ile Tyr Gly Phe Tyr Asp Glu Cys Lys
 100 105 110
 Arg Arg Tyr Asn Ile Lys Leu Trp Lys Thr Phe Thr Asp Cys Phe Asn
 115 120 125
 Cys Leu Pro Ile Ala Ala Ile Val Asp Glu Lys Ile Phe Cys Cys His
 130 135 140
 Gly
 145

<210> 1590
 <211> 116
 <212> PRT
 <213> Homo sapiens

550

<220>

<221> variant

<222> (1)...(116)

<223> Xaa = Any amino acid

<400> 1590

Ala Ser Pro Phe Xaa Trp Ser Trp Arg His Pro Ser Arg Ser Ala Val
 5 10 15

Thr Tyr Thr Ala Ser Thr Thr Thr Phe Cys Asp Tyr Leu Ser Met Ala
 20 25 30

Val Ser Leu Pro Arg Ala Thr Thr Ser Phe Trp Gly Thr Met Trp Thr
 35 40 45

Gly Ala Ser Ser Pro Trp Arg Pro Ser Ala Cys Cys Trp Pro Ile Arg
 50 55 60

Ser Ser Thr Pro Arg Thr Ser Ser Cys Ser Val Gly Thr Thr Ser Val
 65 70 75 80

Pro Ala Ser Thr Ala Ser Met Val Ser Thr Met Ser Ala Arg Asp Ala
 85 90 95

Thr Thr Ser Asn Cys Gly Lys Pro Ser Leu Thr Ala Ser Thr Ala Cys
 100 105 110

Pro Ser Arg Pro
 115

<210> 1591

<211> 62

<212> PRT

<213> Homo sapiens

<400> 1591

Val Phe Leu Ser Pro Trp Val Lys Ser Glu Ser Gly Ser Leu Cys Leu
 5 10 15

Ser Val Leu Val Tyr Cys Trp Ser Glu Ser Lys Phe Leu Ile Lys Ala
 20 25 30

Val Asp Leu Ala Leu Thr Val Tyr Ala Asp Ile Gly Glu Thr Ile Trp
 35 40 45

Leu Phe Gln Thr Ser Gln Asp Leu Ser Lys Lys Thr Trp Leu
 50 55 60

<210> 1592

<211> 86

<212> PRT

<213> Homo sapiens

<400> 1592

Glu Pro Ser Gln Gln Leu Leu Ser Arg Ile Tyr Ser Leu Thr Ser Asn
 5 10 15

Lys Gln Ala Leu Arg Asp Thr Glu Ser Gln Ile Gln Ile Leu Pro Met
 20 25 30

Gly Ile Lys Arg Leu Arg Leu Ser Pro His Leu Glu Asn Tyr Leu His

35 40 45
 His Lys Tyr Ile Ile Thr Gly Ser Leu Tyr Glu Ala Asp Thr Lys Cys
 50 55 60
 Tyr Arg His Ser Gln Asn Ile Ile Leu Gly Asn Asn Val Ile Lys Met
 65 70 75 80
 Pro Asn Leu Ser Gln Gln
 85

<210> 1593
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 1593
 Thr Lys Pro Leu Tyr Val Ala Leu Ala Gln Arg Lys Glu Glu Arg Gln
 5 10 15
 Ala His Leu Thr Asn Gln Tyr Met Gln Arg Met Ala Ser Val Arg Ala
 20 25 30
 Val Pro Asn Pro Val Ile Asn Pro Tyr Gln Pro Ala Pro Pro Ser Gly
 35 40 45
 Tyr Phe Met Ala Ala Ile Pro Gln Thr Gln Asn Arg Ala Ala Tyr Tyr
 50 55 60
 Pro Pro Ser Gln Ile Ala Gln Leu Arg Pro Ser Pro Arg Trp Thr Ala
 65 70 75 80
 Gln Gly Ala Arg Pro His Pro Phe Gln Asn Met Pro Gly Ala Ile Arg
 85 90 95

Pro

<210> 1594
 <211> 57
 <212> PRT
 <213> Homo sapiens

<400> 1594
 Ser Ile Pro Gly Gly Tyr Asn Thr Asp Ile Ser Arg Val Phe Asn Gly
 5 10 15
 Asn Asn Cys Thr Ser Cys Gln Gln Lys Leu Leu Pro Gly Pro Leu Glu
 20 25 30
 Ile Tyr Asp Ile Asp Ala Ile Thr Phe Pro Phe Ile Asp Val Leu Phe
 35 40 45
 His Leu Glu Val Lys Ile Gly Ala Thr
 50 55

<210> 1595
 <211> 78
 <212> PRT
 <213> Homo sapiens

Leu Asp Val Leu Gln Met Lys Glu Glu Asp Val Leu Lys Phe Leu Ala
5 10 15

Ala Gly Thr His Leu Gly Gly Thr Asn Leu Asp Phe Gln Met Glu Gln
20 25 30

Tyr Ile Tyr Lys Arg Lys Ser Asp Gly Ile Tyr Ile Ile Asn Leu Lys
35 40 45

Arg Thr Trp Glu Lys Leu Leu Leu Ala Ala Arg Ala Ile Val Ala Ile
50 55 60

Glu Asn Pro Ala Asp Val Ser Val Ile Ser Ser Arg Asn Thr
65 70 75

<213> Homo sapiens

<223> Xaa = Any amino acid

Tyr Lys Leu Phe Phe Phe Phe Phe Phe Phe Phe Ser Thr Lys Val
5 10 15

Tyr Xaa Xaa Glu Thr Ile Thr Ser Cys Cys Pro Xaa Trp His Thr Xaa
20 25 30

Ser Pro Arg Arg Val Phe Asn Ser Xaa Pro Xaa Ile Ile Phe Ile Pro
35 40 45

Lys Xaa Xaa Pro Xaa Thr Ile Xaa Trp Leu Gln His Xaa Pro Xaa Asn
50 55 60

Glu Val Pro Gln Xaa Ala Lys Phe Tyr Ile Gly Xaa Thr Gly Lys Phe
65 70 75 80

Lys Xaa Xaa Asp Gly Xaa Thr Ile Gly Ser Xaa Ile Met Ser Gly Gly
85 90 95

Xaa Lys Xaa Trp Xaa Gly Met Val Pro Ser Leu Ser Xaa Asn Leu Leu
100 105 110

Leu Thr Trp Xaa Gly Ser Cys Arg Ile Leu Pro Leu Gly Asn Xaa Xaa
115 120 125

Ser Xaa
130

<213> Homo sapiens

<220>

553

<221> variant

<222> (1)...(73)

<223> Xaa = Any amino acid

<400> 1597

```

Thr Ser Phe Phe Phe Phe Phe Phe Phe Phe Phe Pro Pro Lys Phe
          5                      10                      15

Ile Xaa Xaa Lys Gln Ser Pro Val Ala Val Xaa Xaa Gly Thr Leu Xaa
          20                      25                      30

Ala Pro Gly Gly Ser Leu Thr Xaa Phe Leu Xaa Leu Tyr Ser Ser Gln
          35                      40                      45

Lys Xaa Xaa Xaa Gly Gln Xaa Phe Gly Tyr Ser Ile Xaa Pro Xaa Met
          50                      55                      60

Arg Ser Pro Lys Xaa Leu Ser Phe Thr
          65                      70

```

<210> 1598

<211> 57

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(57)

<223> Xaa = Any amino acid

<400> 1598

```

Pro Xaa Tyr Cys Xaa Arg Xaa Xaa Phe Trp Asp Glu Tyr Asn Xaa Arg
          5                      10                      15

Xaa Gly Val Lys Asp Pro Pro Gly Ala Xaa Ser Val Pro Xaa Arg Thr
          20                      25                      30

Ala Thr Gly Asp Cys Phe Xaa Xaa Ile Asn Phe Gly Gly Lys Lys Lys
          35                      40                      45

Lys Lys Lys Lys Lys Lys Lys Leu Val
          50                      55

```

<210> 1599

<211> 69

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(69)

<223> Xaa = Any amino acid

<400> 1599

```

Leu Val Xaa Leu Xaa Xaa Leu Xaa Pro Ile Ile Xaa Xaa Xaa Gly Xaa
          5                      10                      15

Phe Pro Arg Gly Arg Ile Leu Gln Leu Xaa Leu Gln Val Arg Arg Arg
          20                      25                      30

Phe Xaa Leu Asn Asp Gly Thr Met Pro Xaa Gln Xaa Phe Xaa Pro Pro

```


554

35 40 45
 Asp Ile Xaa Leu Asp Pro Met Val Xaa Pro Ser Xaa Xaa Leu Asn Phe
 50 55 60

Pro Xaa Ser Pro Met
 65

<210> 1600
 <211> 65
 <212> PRT
 <213> Homo sapiens

<400> 1600
 Met Leu Gln Tyr Leu Asn Met Leu Cys Gln Thr Ile Pro Leu Cys Asn
 5 10 15

Arg Leu His Ile Val Phe Met Ile Leu Ile Lys Leu Tyr Val Glu Thr
 20 25 30

Glu Cys Glu Val Lys Ser Glu His Lys Lys Ile Met His Asp Glu Ile
 35 40 45

Ala Tyr His Phe Ile Gly Tyr Leu Leu Cys Ile Tyr Thr Leu Arg Pro
 50 55 60

Leu
 65

<210> 1601
 <211> 64
 <212> PRT
 <213> Homo sapiens

<400> 1601
 Leu Thr His Leu Phe Leu Leu Lys Arg Tyr Cys Pro Leu Gly Gly Glu
 5 10 15

Trp Glu Ser Leu Leu His Cys Cys Ser His Ser Glu Arg Thr Phe Pro
 20 25 30

Cys Thr Tyr Leu Ser Thr Cys Phe Asn Leu Ile Asn Ala Thr Phe Cys
 35 40 45

Ile Phe Gln Thr Ser Ile Asn Ser Ala Ile Lys Arg Cys Ser Phe Phe
 50 55 60

<210> 1602
 <211> 174
 <212> PRT
 <213> Homo sapiens

<400> 1602
 Ala Leu Ala Pro Gly Pro Val Leu Phe Ser Ser Met Val Cys Leu Arg
 5 10 15

Leu Pro Gly Gly Ser Cys Met Ala Val Leu Thr Val Thr Leu Met Val
 20 25 30

Leu Ser Ser Pro Leu Ala Leu Ala Gly Asp Thr Arg Pro Arg Phe Leu

555

35 40 45
 Glu Tyr Ser Thr Ser Glu Cys His Phe Phe Asn Gly Thr Glu Arg Val
 50 55 60
 Arg Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu Tyr Val Arg Phe
 65 70 75 80
 Asp Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu Leu Gly Arg Pro
 85 90 95
 Asp Glu Glu Tyr Trp Asn Ser Gln Lys Asp Phe Leu Glu Asp Arg Arg
 100 105 110
 Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly Val Val Glu Ser
 115 120 125
 Phe Thr Val Gln Arg Arg Val His Pro Lys Val Thr Val Tyr Pro Ser
 130 135 140
 Lys Thr Gln Pro Leu Gln His His Asn Leu Leu Val Cys Ser Val Ser
 145 150 155 160
 Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp Phe Arg Asn
 165 170

<210> 1603
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 1603
 Ala Pro His Trp Leu Trp Leu Gly Thr Pro Asp His Val Ser Trp Ser
 5 10 15
 Thr Leu Arg Leu Ser Val Ile Ser Ser Met Gly Arg Ser Gly Cys Gly
 20 25 30
 Ser Trp Thr Asp Thr Ser Ile Thr Lys Arg Ser Thr Cys Ala Ser Thr
 35 40 45
 Ala Thr Trp Gly Ser Ser Gly Arg
 50 55

<210> 1604
 <211> 52
 <212> PRT
 <213> Homo sapiens

<400> 1604
 Ser Gly Pro Trp Ser Cys Pro Val Leu Gln His Gly Val Ser Glu Ala
 5 10 15
 Pro Trp Arg Leu Leu His Gly Ser Ser Asp Ser Asp Thr Asp Gly Ala
 20 25 30
 Glu Leu Pro Thr Gly Phe Gly Trp Gly His Gln Thr Thr Phe Leu Gly
 35 40 45
 Val Leu Tyr Val
 50

<210> 1605
<211> 54
<212> PRT
<213> Homo sapiens

<400> 1605
His Ser Asp Val Glu Tyr Ser Lys Lys Arg Gly Leu Val Ser Pro Ala
5 10 15
Lys Ala Ser Gly Glu Leu Ser Thr Ile Ser Val Thr Val Arg Thr Ala
20 25 30
Met Gln Glu Pro Pro Gly Ser Leu Arg His Thr Met Leu Glu Asn Arg
35 40 45
Thr Gly Pro Gly Ala Arg
50

<210> 1606
<211> 70
<212> PRT
<213> Homo sapiens

<400> 1606
Ser Ser Pro Gln Pro Arg Ser Cys Val Cys Ser Arg Cys Pro Arg
5 10 15
Pro Ala Cys Leu Pro Gly Ser Pro Ser Gly Cys Ser Ser Thr Pro His
20 25 30
Gln Ala Ala Pro Ala Pro Ser Pro Pro Gly Thr Pro Pro Arg Arg Cys
35 40 45
Arg Ser Ala Arg Thr Pro Leu Gly Tyr Arg Ser Ile Cys Pro Gly Thr
50 55 60
Ala Pro Ala Pro Ser His
65 70

<210> 1607
<211> 50
<212> PRT
<213> Homo sapiens

<400> 1607
Ser Thr Pro Arg Asn Val Val Trp Cys Pro Gln Pro Lys Pro Val Gly
5 10 15
Ser Ser Ala Pro Ser Val Ser Leu Ser Glu Leu Pro Cys Arg Ser Leu
20 25 30
Gln Gly Ala Ser Asp Thr Pro Cys Trp Arg Thr Gly Gln Asp Gln Gly
35 40 45
Pro Glu
50

<210> 1608

<211> 143
 <212> PRT
 <213> Homo sapiens

<400> 1608
 Arg Ile His Ser His Leu Arg Met Asp Ser Pro Leu His Cys Glu Ala
 5 10 15
 Leu His Asn Pro Val Val Val Ser Ala Val Gly Val His Arg Gly Pro
 20 25 30
 Pro Val Phe Gln Glu Val Leu Leu Ala Val Pro Val Leu Leu Ile Arg
 35 40 45
 Pro Pro Gln Leu Arg His Arg Pro Glu Leu Pro His Val Ala Val Glu
 50 55 60
 Ala His Val Leu Leu Leu Val Ile Glu Val Ser Val Gln Glu Pro His
 65 70 75 80
 Pro Leu Arg Pro Ile Glu Glu Met Thr Leu Arg Arg Arg Val Leu Gln
 85 90 95
 Glu Thr Trp Ser Gly Val Pro Ser Gln Ser Gln Trp Gly Ala Gln His
 100 105 110
 His Gln Cys His Cys Gln Asn Cys His Ala Gly Ala Ser Arg Glu Pro
 115 120 125
 Gln Thr His His Ala Gly Glu Gln Asp Arg Thr Arg Gly Gln Ser
 130 135 140

<210> 1609
 <211> 79
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(79)
 <223> Xaa = Any amino acid

<400> 1609
 Leu Lys Gln Arg Asn Thr Leu Lys Asp Gly Ile Ile Met Ile Xaa Thr
 5 10 15
 Leu Leu Ile Ile Xaa Xaa Xaa Ile Val Pro Ile Phe Leu Leu Leu Asp
 20 25 30
 Lys Asp Asp Ser Lys Ala Gly Met Glu Glu Asp His Thr Tyr Glu Gly
 35 40 45
 Leu Asp Ile Asp Gln Thr Ala Thr Tyr Glu Asp Ile Val Thr Leu Arg
 50 55 60
 Thr Gly Glu Val Lys Trp Ser Val Gly Glu His Pro Gly Gln Glu
 65 70 75

<210> 1610
 <211> 87
 <212> PRT

<213> Homo sapiens

<400> 1610

```

Leu Gly Gly Pro Gly Lys Gly Leu Gly His Glu Pro Gly Ser Ser Glu
      5              10              15

Ala Val Thr Glu Ala Arg Glu Pro Ala Pro Arg Ser Trp Gly Asp Leu
      20              25              30

Ala Leu Thr Pro Gly Leu Gly Ala His Leu Gln Thr Thr Ser Leu Pro
      35              40              45

Leu Ser Ala Ala Ser Leu Cys Pro His Arg Trp Leu Ser Gly Gln Cys
      50              55              60

Pro Gly Pro Arg Arg Cys Asp Leu Pro Pro Cys Gln Pro Cys Cys His
      65              70              75              80

Pro Cys Pro Ala Ala Gly Arg
      85

```

<210> 1611

<211> 113

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(113)

<223> Xaa = Any amino acid

<400> 1611

```

Trp Gly Val Arg Glu Arg Gly Trp Ala Met Ser Gln Ala Ala Pro Lys
      5              10              15

Gln Ser Leu Arg Pro Gly Ser Leu His Pro Gly His Gly Ala Thr Trp
      20              25              30

Leu Ser Leu Leu Ala Trp Val Leu Thr Tyr Arg Pro Leu His Phe Pro
      35              40              45

Cys Pro Gln Arg His Tyr Val Leu Ile Gly Gly Cys Leu Val Asn Val
      50              55              60

Gln Ala Leu Val Gly Val Ile Phe Leu His Ala Ser Leu Ala Val Ile
      65              70              75              80

Leu Val Gln Gln Gln Glu Asp Arg His Asp Xaa Xaa Xaa Asp Asp Gln
      85              90              95

Gln Arg Xaa Asp His Asp Asp Thr Ile Leu Gln Arg Val Pro Leu Leu
      100             105             110

Gln

```

<210> 1612

<211> 115

<212> PRT

<213> Homo sapiens

<400> 1612

Thr Leu Pro Pro Asp Arg Met Lys Phe Ile Ser Thr Ser Leu Leu Leu
 5 10 15

Met Leu Leu Val Ser Ser Leu Ser Pro Val Gln Gly Val Leu Glu Val
 20 25 30

Tyr Tyr Thr Ser Leu Arg Cys Arg Cys Val Gln Glu Ser Ser Val Phe
 35 40 45

Ile Pro Arg Arg Phe Ile Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn
 50 55 60

Gly Cys Pro Arg Lys Glu Ile Ile Val Trp Lys Lys Asn Lys Ser Ile
 65 70 75 80

Val Cys Val Asp Pro Gln Ala Glu Trp Ile Gln Arg Met Met Glu Val
 85 90 95

Leu Arg Lys Arg Ser Ser Ser Thr Leu Pro Val Pro Val Phe Lys Arg
 100 105 110

Lys Ile Pro
 115

<210> 1613

<211> 55

<212> PRT

<213> Homo sapiens

<400> 1613

Glu Lys Glu Val Leu Gln Leu Tyr Gln Phe Gln Cys Leu Arg Glu Arg
 5 10 15

Phe Pro Asp Ala Asp Ile Ser Thr Lys Asn Thr Cys Ile Leu Pro Leu
 20 25 30

Ser Leu Leu Trp Ile Leu Val Leu Cys Leu Val Lys Ser Phe Pro Gly
 35 40 45

Lys Arg Thr Ser Pro Tyr Lys
 50 55

<210> 1614

<211> 51

<212> PRT

<213> Homo sapiens

<400> 1614

Ser His Ala Tyr Leu Tyr Gly Glu Val Leu Phe Pro Gly Lys Asp Leu
 5 10 15

Thr Lys His Lys Thr Lys Ile Gln Ser Arg Asp Lys Gly Arg Met Gln
 20 25 30

Val Phe Leu Val Glu Ile Ser Ala Ser Gly Asn Leu Ser Leu Lys His
 35 40 45

Trp Asn Trp
 50

<210> 1615

<211> 136

<212> PRT

<213> Homo sapiens

<400> 1615

Tyr Leu Lys Val Ile Val Ala Leu Gly Met Pro Gly Gln Glu Asp Glu
 5 10 15

Gly Ala Leu Trp Thr Gln Gln Ser Ala Glu Phe Arg Ser Gly Lys Pro
 20 25 30

Met Val Ala Gly Thr Pro Cys Phe Leu Pro Leu Leu Ser Ala Cys Val
 35 40 45

Thr His Ile Asn Gly Asn Asn Phe Phe Gln Leu Leu Ala Glu Val Gly
 50 55 60

Glu Ala Gly Ser Leu His Arg Glu Gly Leu Ser Ser Leu Leu Leu Pro
 65 70 75 80

Ala Ser Phe Cys Phe Gly Cys Arg Glu Trp Phe Ile His Thr Leu Ile
 85 90 95

Pro Ser Pro Pro Leu Val Asp Gly Gly Leu Ala Phe Ser Ile Pro Val
 100 105 110

Phe Trp Cys Leu Pro Leu Ser Ala Thr Leu Asn His Leu Pro Trp Ser
 115 120 125

Cys Cys Val Met Gly Thr Cys Leu
 130 135

<210> 1616

<211> 79

<212> PRT

<213> Homo sapiens

<400> 1616

Thr Arg Pro Thr Lys Ala Arg Ser Met Ser Pro Gln Val Ser Ser Gln
 5 10 15

Ser Arg Leu Thr Leu Ser Ser Gly Arg Val Tyr Ile Ala Val Phe Asn
 20 25 30

Thr Ser Arg Ser Leu Trp Leu Trp Gly Cys Arg Gly Arg Arg Thr Arg
 35 40 45

Val Arg Cys Gly His Ser Ser Pro Arg Asn Ser Val Leu Gly Ser Gln
 50 55 60

Trp Ser Pro Ala Pro Leu Ala Ser Ser Leu Cys Cys Leu Pro Val
 65 70 75

<210> 1617

<211> 73

<212> PRT

<213> Homo sapiens

<400> 1617

His Thr Ser Met Ala Ile Thr Ser Ser Asn Ser Ser Gln Lys Trp Glu
 5 10 15
 Arg Pro Ala Ala Cys Thr Glu Arg Gly Phe Pro Leu Ser Cys Ser Pro
 20 25 30
 Leu Arg Ser Val Leu Ala Ala Glu Ser Gly Ser Ser Ile Leu Ser Phe
 35 40 45
 Pro Arg Leu Pro Leu Trp Thr Gly Val Leu Pro Phe Gln Phe Leu Cys
 50 55 60
 Phe Gly Val Phe Pro Tyr Leu Leu Pro
 65 70

<210> 1618
 <211> 57
 <212> PRT
 <213> Homo sapiens

<400> 1618
 Leu Tyr Leu Ile Pro Gln Gly His Cys Gly Ser Gly Asp Ala Gly Ala
 5 10 15
 Gly Gly Arg Gly Cys Ala Val Asp Thr Ala Val Arg Gly Ile Pro Phe
 20 25 30
 Trp Glu Ala Asn Gly Arg Arg His Pro Leu Leu Pro Pro Ser Val Val
 35 40 45
 Cys Leu Cys Asp Thr His Gln Trp Gln
 50 55

<210> 1619
 <211> 89
 <212> PRT
 <213> Homo sapiens

<400> 1619
 Leu Leu Pro Thr Pro Arg Arg Ser Gly Arg Gly Arg Gln Pro Ala Pro
 5 10 15
 Arg Gly Ala Phe Leu Ser Leu Ala Pro Arg Phe Val Leu Phe Trp Leu
 20 25 30
 Gln Arg Val Val His Pro Tyr Ser His Ser Leu Ala Ser Pro Cys Gly
 35 40 45
 Arg Gly Ser Cys Leu Phe Asn Ser Cys Val Leu Val Ser Ser Leu Ile
 50 55 60
 Cys Tyr Pro Glu Ser Pro Ala Leu Val Leu Leu Cys Asp Gly Asn Met
 65 70 75 80
 Leu Val Asn Cys Val Thr Asn Leu Leu
 85

<210> 1620
 <211> 124
 <212> PRT

<213> Homo sapiens

<400> 1620

Lys Gly Lys Thr Pro Val His Lys Gly Arg Arg Gly Asn Glu Ser Met
5 10 15

Asp Glu Pro Leu Ser Ala Ala Lys Thr Glu Arg Ser Gly Glu Gln Glu
20 25 30

Arg Gly Lys Pro Leu Ser Val Gln Ala Ala Gly Leu Ser His Phe Cys
35 40 45

Glu Glu Leu Glu Glu Val Ile Ala Ile Asp Val Cys His Thr Gly Arg
50 55 60

Gln Gln Arg Glu Glu Ala Arg Gly Ala Gly Asp His Trp Leu Pro Arg
65 70 75 80

Thr Glu Phe Arg Gly Leu Leu Cys Pro Gln Arg Thr Leu Val Leu Leu
85 90 95

Pro	Arg	His	Pro	Gln	Ser	His	Asn	Asp	Leu	Glu	Val	Leu	Asn	Thr	Ala
			100					105					110		

Ile Tyr Thr Arg Pro Glu Leu Arg Val Asn Leu Asp
115 120

<210> 1621

<211> 123

<212> PRT

<213> Homo sapiens

<400> 1621

Phe Arg Val Ala Asp Lys Gly Arg His Gln Asn Thr Gly Ile Glu Lys
5 10 15

Ala Arg Pro Pro Ser Thr Arg Gly Gly Glu Gly Met Arg Val Trp Met
20 25 30

Asn His Ser Leu Gln Pro Lys Gln Asn Glu Ala Gly Ser Lys Arg Glu
35 40 45

Glu Ser Pro Ser Arg Cys Arg Leu Pro Ala Ser Pro Thr Ser Ala Arg
50 55 60

Ser Trp Lys Lys Leu Leu Pro Leu Met Cys Val Thr Gln Ala Asp Asn
65 70 75 80

Arg Gly Arg Lys Gln Gly Val Pro Ala Thr Ile Gly Phe Pro Glu Arg
85 90 95

Asn Ser Ala Asp Cys Cys Val His Ser Ala Pro Ser Ser Ser Cys Pro
100 105 110

Gly Ile Pro Arg Ala Thr Met Thr Leu Arg Tyr
115 120

<210> 1622

<211> 117

<212> PRT

<213> Homo sapiens

<400> 1622

Ala Ala Met Ala Arg Gly Pro Lys Lys His Leu Lys Arg Val Ala Ala
 5 10 15

Pro Lys His Trp Met Leu Asp Lys Leu Thr Gly Val Phe Ala Pro Arg
 20 25 30

Pro Ser Thr Gly Pro His Lys Leu Arg Glu Cys Leu Pro Leu Ile Ile
 35 40 45

Phe Leu Arg Asn Arg Leu Lys Tyr Ala Leu Thr Gly Asp Glu Val Lys
 50 55 60

Lys Ile Cys Met Gln Arg Phe Ile Lys Ile Asp Gly Lys Val Arg Thr
 65 70 75 80

Asp Ile Thr Tyr Pro Ala Gly Phe Met Asp Val Ile Ser Ile Asp Lys
 85 90 95

Thr Gly Glu Asn Phe Arg Leu Ile Tyr Asp Thr Lys Gly Arg Phe Ala
 100 105 110

Val His Arg Ile Thr
 115

<210> 1623

<211> 117

<212> PRT

<213> Homo sapiens

<400> 1623

Cys Asn Thr Met Tyr Ser Lys Ala Thr Leu Gly Val Ile Asp Gln Thr
 5 10 15

Glu Ile Leu Ser Arg Leu Val Asn Ala Asp Asp Ile His Glu Ser Ser
 20 25 30

Arg Val Gly Tyr Ile Ser Ser Asp Leu Ala Ile Asp Phe Asn Glu Pro
 35 40 45

Leu His Ala Asn Leu Leu Tyr Phe Ile Ser Cys Gln Gly Ile Leu Lys
 50 55 60

Ser Val Pro Gln Glu Asn Asp Glu Gly Glu Thr Leu Ser Gln Leu Val
 65 70 75 80

Gly Thr Gly Gly Trp Thr Arg Ser Lys His Thr Gly Gln Phe Ile Gln
 85 90 95

His Pro Met Leu Trp Ser Cys His Pro Leu Gln Met Leu Leu Gly Thr
 100 105 110

Thr Ser His Gly Cys
 115

<210> 1624

<211> 83

<212> PRT

<213> Homo sapiens

```

<210> 1625
<211> 67
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(67)
<223> Xaa = Any amino acid

<400> 1625
Leu Lys Gln Arg Asn Thr Leu Lys Asp Gly Ile Ile Met Ile Xaa Thr
      5                                10                                15

Leu Leu Ile Ile Leu Phe Ile Ile Val Pro Ile Phe Leu Leu Leu Asp
      20                                25                                30

Lys Asp Asp Ser Lys Ala Gly Met Glu Glu Asp His Xaa Tyr Glu Gly
      35                                40                                45

Leu Asp Ile Asp Gln Thr Ala Thr Tyr Glu Asp Ile Val Thr Leu Arg
      50                                55                                60

Thr Gly Glu
      65

```

```
<210> 1626  
<211> 52  
<212> PRT  
<213> Homo sapiens  
  
<220>  
<221> variant  
<222> (1)...(52)  
<223> Xaa = Any amino acid  
  
<400> 1626  
Ile Thr Asn Trp Val Thr Leu Asn Glu Leu Ile Lys Phe Gln Ala Ile  
          5                      10                      15  
  
Val His Ala Thr Asn Ser Gln Arg Pro Arg Lys Leu Leu Ala Glu Lys  
      20                      25                      30
```

Val Val Tyr Val Gly Xaa Trp Ile Pro Ala Leu Leu Leu Thr Ile Xaa
35 40 45

Asp Phe Ile Phe
50

```
<210> 1627
<211> 102
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> variant
<222> (1)...(102)
<223> Xaa = Any amino acid
```

<400> 1627
Leu Gln Val Leu Gln Asp Ala Phe Cys Xaa Xaa Xaa Tyr Tyr Ile His
5 10 15

Leu Ile Ile Asn Phe Leu Leu Arg Leu Cys Arg Leu Gly Ile Phe Xaa
20 25 30

Xaa Lys Glu Lys Ile Trp Pro Leu Leu Lys Val Cys Ala Cys Gln Asn
35 40 45

Phe Lys Lys Ile Pro His Val Lys Val Pro Ser Ala Ser Ala Gly Asp
50 55 60

Ser Val Leu Val Leu Leu Ser Leu Asp Trp Arg Ser Leu Phe Pro Ser
65 70 75 80

Ser Leu Val Pro Val Leu Gln Leu Leu Phe Leu Ala Asn Arg Cys Ala
85 90 95

Asn Glu Leu Pro Thr Gly
100

```
<210> 1628
<211> 86
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> variant  
<222> (1)...(86)  
<223> Xaa = Any amino acid
```

<400> 1628
Ile Ser Phe Ser Asp Ser Val Gly Trp Ala Phe Ser Xaa Ser Arg Lys
 5 10 15

Lys Phe Gly Pro Cys Ser Arg Ser Val His Val Lys Thr Leu Arg Arg
20 25 30

Phe Pro Met Leu Arg Tyr Leu Gln Pro Val Leu Val Ile Leu Ser Leu
35 40 45

Ser Phe Tyr Pro Trp Ile Gly Val Pro Ser Phe Leu Val His Leu Phe
50 55 60

Gln Ser Phe Asn Phe Cys Phe Leu Leu Thr Gly Val Gln Met Asn Tyr
 65 70 75 80

Gln Leu Gly Asn Leu Glu
 85

<210> 1629

<211> 62

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(62)

<223> Xaa = Any amino acid

<400> 1629

Arg Tyr Leu Asn Met Gly Asn Leu Leu Lys Val Leu Thr Cys Thr Asp
 5 10 15

Leu Glu Gln Gly Pro Asn Phe Phe Leu Xaa Xaa Glu Asn Ala Gln Pro
 20 25 30

Thr Glu Ser Glu Lys Glu Ile Tyr Asn Gln Val Asn Val Val Xaa Xaa
 35 40 45

Xaa Ala Glu Gly Ile Leu Glu Asp Leu Gln Ser Tyr Xaa Gly
 50 55 60

<210> 1630

<211> 99

<212> PRT

<213> Homo sapiens

<400> 1630

Leu Ser Phe Leu Glu Val Leu Cys Thr Tyr Ala Pro His Leu Tyr Leu
 5 10 15

Ala Phe Ala Trp Ser Asp His Ser Ser Phe Ser Leu Thr Leu Asn Val
 20 25 30

Glu Asn Val Ala Ile Val Ala Ala Cys Val Val Thr Leu Leu Leu
 35 40 45

Ser Asn Phe Leu Thr Leu Lys Lys Gly Arg Met Ser Ala Ser Glu Cys
 50 55 60

Asp Phe Leu Leu Thr Cys Ser Leu Asp Arg Leu Phe Ser Ile Val Phe
 65 70 75 80

Phe Leu Ser Phe Ser Pro Ser Thr Thr Arg Glu Thr Ala Pro Asp Gly
 85 90 95

Lys Asp Ile

<210> 1631

<211> 57

<212> PRT

<213> Homo sapiens

<400> 1631

Tyr Phe Phe Cys His Phe Leu His Gln Gln Pro Gly Arg Leu His Leu
5 10 15
Met Glu Lys Ile Tyr Asp Cys Phe Met Thr Phe Leu Asn Tyr Leu Phe
20 25 30
Phe Ile Pro His Leu Arg Phe Trp Trp Ser Pro Phe Cys Ile Ile Val
35 40 45
Leu Arg Met Ile Lys Lys Asn Asn Asn
50 55

<210> 1632

<211> 87

<212> PRT

<213> Homo sapiens

<400> 1632

Ser Ser His Ile Ser Phe Pro Ser Gly Ala Val Ser Leu Val Val Asp
5 10 15
Gly Glu Asn Asp Lys Lys Asn Thr Ile Leu Lys Ser Leu Ser Lys Glu
20 25 30
Gln Val Ser Arg Lys Ser His Ser Glu Ala Leu Ile Leu Pro Phe Phe
35 40 45
Ser Val Arg Lys Leu Leu Lys Arg Arg Ser Val Thr Thr Gln Ala Ala
50 55 60
Thr Met Ala Thr Phe Ser Thr Phe Asn Val Arg Glu Lys Glu Leu Trp
65 70 75 80
Ser Leu His Ala Lys Ala Arg
85

<210> 1633

<211> 53

<212> PRT

<213> Homo sapiens

<400> 1633

Ala Met Leu Phe Leu Gln Lys Thr Asp Gly Cys Trp Leu Phe Arg Ala
5 10 15
Ser Leu Met Gly Cys Gly Asn Ser Lys Asn Val Pro Gln Cys Gln Pro
20 25 30
Cys Arg Lys Ile Asn Gly Met Gly Ser Val Leu Ser Leu Val Val Ile
35 40 45
Phe Phe Tyr His Pro
50

<210> 1634

<211> 59

<212> PRT

<213> Homo sapiens

<400> 1634'

Ser Thr His Ser Ala Phe Leu Gln Cys Lys Lys Val Ala Gln Lys Lys
5 10 15

Lys Arg Asp Asn Thr Ser Cys Tyr Asn Gly Tyr Ile Leu Tyr Ile Gln
20 25 30

Cys Lys Arg Glu Gly Ala Met Val Thr Pro Cys Lys Gly Gln Ile Glu
35 40 45

Met Trp Cys Val Cys Ala Glu Tyr Leu Lys Lys
50 55

<210> 1635

<211> 98

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1) . . . (98)

<223> Xaa = Any amino acid

<400> 1635

Pro Asn Cys Leu Ser Asn Val Cys Ile Asn Cys Glu Ser Gln Xaa Xaa
5 10 15

Gln Leu Leu Ser Arg Ile Tyr Ser Leu Thr Ser Asn Lys Gln Ala Leu
20 25 30

Arg Asp Thr Glu Ser Gln Ile Gln Ile Leu Pro Met Gly Ile Lys Arg
35 40 45

Leu Arg Leu Ser Pro His Leu Glu Asn Tyr Leu His His Lys Tyr Ile
50 55 60

Ile Thr Gly Ser Leu Tyr Glu Ala Asp Thr Lys Cys Tyr Arg His Ser
65 70 75 80

Gln Asn Ile Ile Leu Gly Asn Asn Val Ile Lys Met Pro Asn Leu Ser
85 90 95

Gln Gln

<210> 1636

<211> 66

<212> PRT

<213> Homo sapiens

<400> 1636

Lys Asp Gly Ile Ile Met Ile Gln Thr Leu Leu Ile Ile Leu Phe Ile
5 10 15

Ile Val Pro Ile Phe Leu Leu Leu Asp Lys Asp Asp Ser Lys Ala Gly
20 25 30

Met Glu Glu Asp His Thr Tyr Glu Gly Leu Asp Ile Asp Gln Thr Ala
35 40 45

Thr Tyr Glu Asp Ile Val Thr Leu Arg Thr Gly Glu Val Lys Trp Phe
 50 55 60

Cys Arg
 65

<210> 1637
 <211> 84
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(84)
 <223> Xaa = Any amino acid

<400> 1637
 Pro Ala Pro Arg Ser Trp Gly Asp Leu Ala Leu Thr Pro Gly Leu Gly
 5 10 15

Xaa Ser Pro Thr Glu Pro Leu His Phe Pro Cys Pro Gln Arg His Tyr
 20 25 30

Val Leu Ile Gly Gly Cys Leu Val Asn Val Gln Ala Leu Val Gly Val
 35 40 45

Ile Phe Leu His Ala Ser Leu Ala Val Ile Leu Val Gln Gln Gln Glu
 50 55 60

Asp Arg His Asp Asp Glu Glu Asp Asp Gln Gln Arg Leu Asp His Asp
 65 70 75 80

Asp Thr Ile Leu

<210> 1638
 <211> 64
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(64)
 <223> Xaa = Any amino acid

<400> 1638
 Cys Thr Gln Val Met Gly Arg Pro Gly Ser His Ser Trp Pro Gly Cys
 5 10 15

Xaa Thr Tyr Arg Thr Thr Ser Leu Pro Leu Ser Ala Ala Ser Leu Cys
 20 25 30

Pro His Arg Trp Leu Ser Gly Gln Cys Pro Gly Pro Arg Arg Cys Asp
 35 40 45

Leu Pro Pro Cys Gln Pro Cys Cys His Pro Cys Pro Ala Ala Gly Arg
 50 55 60

<210> 1639

<211> 59
<212> PRT
<213> Homo sapiens

<400> 1639
Pro Cys Leu Arg Ser Lys Val Thr Arg Lys Arg Pro Cys Leu Pro Ser
 5 10 15
Met Thr Leu Met Glu Glu Met Leu Arg Glu Ala Phe Arg Cys Met Thr
 20 25 30
Gln Gly Lys Thr Ala Lys Asn Leu Val Leu Ala Leu Leu Ile Leu Leu
 35 40 45
Phe Val Leu Phe Leu Gly Val Leu Arg Ala Lys
 50 55

<210> 1640
<211> 51
<212> PRT
<213> Homo sapiens

<400> 1640
Glu Gln Asn Asp Asn Thr Gln Lys Phe Ser Lys Trp Asp Phe Pro Gly
 5 10 15
Arg Ala Asn Glu Arg Pro Tyr Cys Tyr Ala Ile Trp Ser Lys Thr Thr
 20 25 30
Leu Gln Glu Asp Val Phe Thr Gly Gly Pro Arg Ala Lys Leu Leu His
 35 40 45
Glu Gly Ile
 50

<210> 1641
<211> 82
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(82)
<223> Xaa = Any amino acid

<400> 1641
Asp Phe Gly Gly Cys Pro Asp Tyr Glu Trp Ala Leu Pro His Cys Pro
 5 10 15
Gly Gly Ser Ser Asp Asp Ser Ser Arg Asp Leu Cys Thr His Leu Cys
 20 25 30
Asp Cys Val Val Pro Ser Leu Gly Arg His Tyr Val Tyr Tyr Phe Arg
 35 40 45
Ile Thr Pro Gly Ser Asn Gly Glu Lys Leu Gln Glu Val Leu Gly Gln
 50 55 60
Arg Lys Asn Asp Asn Glu Phe Ile Xaa Pro Xaa Cys Cys His Phe Trp
 65 70 75 80

Asn Asp

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<210> 1642
<211> 155
<212> PRT
<213> Homo sapiens
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<220>
<221> variant
<222> (1)...(155)
<223> Xaa = Any amino acid
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<400> 1642
Asp Cys Gln Lys Ser Cys Ser Cys Ser Pro His Phe Val Ile Cys Phe
      5                      10                      15

Ile Phe Arg Ser Phe Glu Ser Lys Met Thr Thr Pro Arg Asn Ser Val
      20                      25                      30

Asn Gly Thr Phe Pro Ala Glu Pro Met Lys Gly Pro Ile Ala Met Gln
      35                      40                      45

Ser Gly Pro Lys Pro Leu Phe Arg Arg Met Ser Ser Leu Val Gly Pro
      50                      55                      60

Ala Gln Ser Phe Phe Met Arg Glu Ser Lys Thr Leu Gly Ala Val Gln
      65                      70                      75                      80

Ile Met Asn Gly Leu Phe His Ile Ala Leu Gly Gly Leu Leu Met Ile
      85                      90                      95

Pro Ala Gly Ile Tyr Ala Pro Ile Cys Val Thr Val Trp Tyr Pro Leu
      100                     105                     110

Trp Gly Gly Ile Met Tyr Ile Ile Ser Gly Ser Leu Leu Ala Ala Thr
      115                     120                     125

Glu Lys Asn Ser Arg Lys Cys Trp Val Lys Gly Lys Met Ile Met Asn
      130                     135                     140

Ser Leu Xaa Xaa Phe Ala Ala Ile Ser Gly Met
      145                     150                     155

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<210> 1643
<211> 55
<212> PRT
<213> Homo sapiens
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<220>  
<221> variant  
<222> (1)...(55)  
<223> Xaa = Any amino acid
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<400> 1643
Ile Ile Pro Glu Met Ala Ala Xaa Arg Xaa Asn Glu Phe Ile Ile Ile
5 10 15
Phe Pro Leu Thr Gln His Phe Leu Glu Phe Phe Ser Val Ala Ala Arg
20 25 30

Ser Asp Pro Glu Ile Ile Tyr Ile Met Pro Pro Gln Arg Gly Tyr His
35 40 45

Thr Val Thr Gln Met Gly Ala
50 55

<210> 1644
<211> 89
<212> PRT
<213> Homo sapiens

<400> 1644
Ile Pro Ala Gly Ile Ile Arg Arg Pro Pro Arg Ala Met Trp Lys Ser
5 10 15

Pro Phe Ile Ile Trp Thr Ala Pro Lys Val Leu Asp Ser Leu Met Lys
20 25 30

Lys Leu Cys Ala Gly Pro Thr Ser Glu Asp Ile Leu Leu Lys Ser Gly
35 40 45

Phe Gly Pro Asp Cys Ile Ala Ile Gly Pro Phe Ile Gly Ser Ala Gly
50 55 60

Lys Val Pro Phe Thr Glu Phe Leu Gly Val Val Ile Leu Leu Ser Lys
65 70 75 80

Leu Leu Lys Ile Lys Gln Ile Thr Lys
85

<210> 1645
<211> 62
<212> PRT
<213> Homo sapiens

<400> 1645
Ser Gly Asn Asn Ile His Asn Ala Ser Pro Glu Arg Val Pro His Ser
5 10 15

His Thr Asp Gly Cys Ile Asp Pro Cys Trp Asn His Gln Lys Thr Pro
20 25 30

Gln Gly Asn Val Glu Glu Pro Ile His Asn Leu Asp Ser Pro Gln Ser
35 40 45

Leu Arg Phe Pro His Glu Glu Ala Leu Arg Gly Ala His Gln
50 55 60

<210> 1646
<211> 64
<212> PRT
<213> Homo sapiens

<400> 1646
Ile Ser Gly Cys Cys His Phe Ala Leu Lys Thr Pro Lys Asn Lys Thr
5 10 15

Asn Asn Lys Met Arg Arg Ala Arg Thr Arg Phe Leu Ala Val Leu Pro
20 25 30

Cys Val Met His Leu Asn Ala Ser Leu Ser Ile Ser Ser Met Ser Val
35 40 45

Ile Glu Gly Arg His Gly Leu Phe Arg Val Thr Leu Asp Leu Arg Gln
50 55 60

<210> 1647

<211> 58

<212> PRT

<213> Homo sapiens

<400> 1647

Cys Pro Ser Ala Ile Thr Ile Gln Gln Leu Gln Ala Gly Leu Ala Asp
5 10 15

Arg Glu Tyr Gly Arg Arg Thr Arg Ser Asp Glu Asn Met His Ala Thr
20 25 30

Ile Phe Thr Thr Glu His Thr Val Phe Cys Asp Arg Asn Cys Arg Pro
35 40 45

Cys Trp Gly Thr Arg Tyr Ser Arg Pro His
50 55

<210> 1648

<211> 71

<212> PRT

<213> Homo sapiens

<400> 1648

Lys Ser Arg Pro Thr Cys Ser His Trp Thr Asp Val Gln Val Gln Ser
5 10 15

Pro Tyr Ser Ser Tyr Arg Gln Gly Trp Leu Ile Gly Ser Met Gly Glu
20 25 30

Gly His Ala Gln Met Lys Thr Cys Met Gln Arg Phe Ser Pro Leu Asn
35 40 45

Thr Leu Phe Ser Val Ile Glu Thr Val Gly Pro Ala Gly Gly Gln Asp
50 55 60

Ile His Gly Leu Thr Ser Gln
65 70

<210> 1649

<211> 73

<212> PRT

<213> Homo sapiens

<400> 1649

Gly Arg Glu Tyr Leu Val Pro Gln Gln Gly Arg Gln Phe Leu Ser Gln
5 10 15

Lys Thr Val Cys Ser Val Val Lys Ile Val Ala Cys Met Phe Ser Ser
20 25 30

Glu Arg Val Leu Leu Pro Tyr Ser Leu Ser Ala Ser Pro Ala Cys Ser
35 40 45

Cys Cys Met Val Ile Ala Leu Gly His Gln Ser Asn Asp Cys Lys Ser
 50 55 60

Ala Trp Ile Phe Thr Cys Arg Gly Tyr
 65 70

<210> 1650
 <211> 88
 <212> PRT
 <213> Homo sapiens

<400> 1650
 Ser Arg Leu Leu Glu Gln Leu Ala Trp Ala Gly Phe Ser His Pro Gly
 5 10 15

Cys Pro Leu Asp Cys Ser Thr Gln Ala Phe Pro Trp Gly Leu Gly Ser
 20 25 30

Leu His Lys Val Arg Cys Leu Leu Pro Tyr Gly Pro Ser Leu Ala Gly
 35 40 45

Asn Lys Gly Ala Ser Gly Ala Gly Arg Pro Gly Gly Ile Ser Leu Ala
 50 55 60

Ser Glu Ala Val Asn Ile Leu Ser Pro Ser Arg Ala Asp Ser Phe Tyr
 65 70 75 80

His Arg Lys Gln Cys Val Gln Trp
 85

<210> 1651
 <211> 69
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(69)
 <223> Xaa = Any amino acid

<400> 1651
 Leu Leu Leu Pro Asp Thr Leu His Arg Leu Val Asp Phe Gly Met Ser
 5 10 15

Gly Leu Arg Leu His Ala Arg Gly Cys Asn Thr Met Tyr Ser Lys Ala
 20 25 30

Thr Leu Gly Val Ile Asp Gln Thr Glu Ile Leu Ser Arg Leu Xaa Asn
 35 40 45

Ala Asp Asp Ile His Glu Ser Ser Xaa Gly Arg Xaa Tyr Gln Phe Gly
 50 55 60

Pro Cys His Xaa Phe
 65

<210> 1652
 <211> 57
 <212> PRT
 <213> Homo sapiens

<400> 1652

Ala Thr Cys Phe Ser Phe Gly Arg Asn Ser Leu Pro Thr Gly Ile Thr
 5 10 15

Thr Gly Ser Tyr Ser Phe Cys Phe Gln Thr His Ser Ile Ala Leu Ser
 20 25 30

Ile Leu Glu Cys Leu Gly Ser Asp Phe Met Leu Val Gly Val Ile Arg
 35 40 45

Cys Thr Ala Lys Arg Pro Leu Val Ser
 50 55

<210> 1653

<211> 66

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(66)

<223> Xaa = Any amino acid

<400> 1653

Ile Arg Arg Lys Phe Ser Pro Val Leu Xaa Met Leu Met Thr Ser Met
 5 10 15

Asn Pro Ala Xaa Val Gly Xaa Ile Ser Ser Asp Leu Ala Ile Xaa Phe
 20 25 30

Asn Glu Pro Leu His Ala Asn Leu Leu Tyr Phe Ile Xaa Xaa Gln Gly
 35 40 45

Ile Leu Lys Ser Val Pro Gln Glu Asn Asp Glu Gly Glu Thr Leu Ser
 50 55 60

Xaa Leu
 65

<210> 1654

<211> 67

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(67)

<223> Xaa = Any amino acid

<400> 1654

Lys Xaa Arg Glu Cys Leu Pro Leu Ile Ile Phe Leu Arg Asn Arg Leu
 5 10 15

Lys Tyr Ala Leu Xaa Xaa Asp Glu Val Lys Lys Ile Cys Met Gln Arg
 20 25 30

Phe Ile Lys Xaa Asp Gly Lys Val Arg Thr Asp Xaa Thr Tyr Xaa Cys
 35 40 45

Trp Ile His Gly Cys His Gln His Xaa Gln Asp Gly Arg Glu Phe Pro

50 55 60

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<210> 1655
<211> 99
<212> PRT
<213> Homo sapiens
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<220>  
<221> variant  
<222> (1)...(99)  
<223> Xaa = Any amino acid
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<400> 1655
Arg Arg Phe Ala Cys Ser Gly Ser Leu Lys Xaa Met Ala Arg Ser Glu
 5 10 15

Leu Ile Xaa Pro Thr Xaa Ala Gly Phe Met Asp Val Ile Ser Ile Xaa
20 25 30

Lys Thr Gly Glu Asn Phe Arg Leu Ile Tyr Asp Thr Lys Gly Arg Phe
35 40 45

Ala Val His Arg Ile Thr Pro Thr Ser Met Lys Ser Glu Pro Arg His
50 55 60

Ser Lys Ile Asp Lys Ala Met Glu Cys Val Trp Lys Gln Lys Leu Tyr
65 70 75 80

Glu Pro Val Val Ile Pro Val Gly Arg Leu Phe Arg Pro Asn Glu Lys
85 90 95

Gln Val Ala

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<210> 1656
<211> 115
<212> PRT
<213> Homo sapiens
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<220>
<221> variant
<222> (1)...(115)
<223> Xaa = Any amino acid
```

<400> 1656
Thr Leu Pro Pro Asp Arg Met Lys Phe Ile Ser Thr Ser Leu Leu Leu
 5 10 15

Met Leu Leu Val Ser Ser Leu Ser Pro Val Gln Gly Val Leu Glu Val
20 25 30

Tyr Tyr Thr Ser Leu Arg Cys Arg Cys Val Gln Xaa Ser Ser Val Phe
35 40 45

Ile Pro Xaa Arg Phe Ile Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn
50 55 60

Gly Cys Pro Arg Lys Glu Ile Ile Val Trp Lys Lys Asn Lys Ser Ile

65		70		75		80
Val Cys Val Asp	Pro Gln Ala Glu Trp	Ile Gln Arg Met Met	Glu Val			
	85	90	95			
Leu Arg Lys Arg	Ser Ser Ser Thr	Leu Pro Val Pro Val	Phe Lys Arg			
	100	105	110			
Lys Ile Pro						
	115					

<210> 1657
 <211> 70
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(70)
 <223> Xaa = Any amino acid

<400> 1657
Leu Pro Pro Phe Leu Ser Glu Leu Phe Leu Leu His Ile Thr Ala Ala
5 10 15
Thr Thr Ala Pro Val Ile Thr Ala Pro Arg Arg Thr Arg Pro Ala Met
20 25 30
Met Pro Thr Met Gly Met Val Gly Trp Glu Asp Ser Ser His Leu Xaa
35 40 45
Val Arg Gly Leu Gly Arg Pro Ser Cys Cys Thr Trp Gln Val Tyr Leu
50 55 60
Cys Ser Ser Pro Glu Gly
65 70

<210> 1658
 <211> 63
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(63)
 <223> Xaa = Any amino acid

<400> 1658
Ala Leu Pro Pro Pro His His Gly Ser Asp His Ser Ser Ser Asp His
5 10 15
Ser Ser Lys Glu Asn Gln Ala Ser Asn Asp Ala His Asp Gly Asp Gly
20 25 30
Gly Leu Gly Arg Gln Leu Pro Ser Xaa Gly Glu Gly Leu Gly Gln Thr
35 40 45
Leu Met Leu His Met Ala Gly Val Ser Leu Leu Leu Ser Arg Arg
50 55 60

<210> 1659
 <211> 50
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(50)
 <223> Xaa = Any amino acid

<400> 1659
 Gly Ser Ala Gln Ala Pro His Xaa Glu Met Gly Ala Val Phe Pro Ala
 5 10 15
 His His Pro His Arg Gly His His Cys Trp Pro Gly Ser Pro Trp Ser
 20 25 30
 Cys Asp His Trp Ser Cys Gly Arg Cys Arg Asp Val Glu Glu Glu Glu
 35 40 45
 Leu Arg
 50

<210> 1660
 <211> 92
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(92)
 <223> Xaa = Any amino acid

<400> 1660
 Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys His Val Gln His Glu Gly
 5 10 15
 Leu Pro Lys Pro Leu Thr Xaa Arg Trp Glu Leu Ser Ser Gln Pro Thr
 20 25 30
 Ile Pro Ile Val Gly Ile Ile Ala Gly Leu Val Leu Leu Gly Ala Val
 35 40 45
 Ile Thr Gly Ala Val Val Ala Val Met Trp Arg Arg Lys Ser Ser
 50 55 60
 Asp Arg Lys Gly Gly Ser Tyr Thr Gln Ala Ala Ser Ser Asp Ser Ala
 65 70 75 80
 Gln Gly Ser Asp Val Ser Leu Thr Ala Cys Lys Val
 85 90

<210> 1661
 <211> 55
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(55)
 <223> Xaa = Any amino acid

<400> 1661

Glu Lys Glu Val Leu Gln Leu Tyr Gln Phe Gln Cys Leu Arg Glu Arg
5 10 15
Phe Pro Asp Ala Asp Ile Ser Thr Lys Asn Thr Cys Ile Leu Pro Leu
20 25 30
Ser Leu Leu Trp Ile Leu Val Leu Xaa Leu Val Lys Ser Phe Pro Gly
35 40 45
Lys Arg Thr Ser Pro Tyr Lys
50 55

<210> 1662

<211> 115

<212> PRT

<213> Homo sapiens

<400> 1662

Thr Leu Pro Pro Asp Arg Met Lys Phe Ile Ser Thr Ser Leu Leu Leu
5 10 15
Met Leu Leu Val Ser Ser Leu Ser Pro Val Gln Gly Val Leu Glu Val
20 25 30
Tyr Tyr Thr Ser Leu Arg Cys Arg Cys Val Gln Glu Ser Ser Val Phe
35 40 45
Ile Pro Arg Arg Phe Ile Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn
50 55 60
Gly Cys Pro Arg Lys Glu Ile Ile Val Trp Lys Lys Asn Lys Ser Ile
65 70 75 80
Val Cys Val Asp Pro Gln Ala Glu Trp Ile Gln Arg Met Met Glu Val
85 90 95
Leu Arg Lys Arg Ser Ser Ser Thr Leu Pro Val Pro Val Phe Lys Arg
100 105 110
Lys Ile Pro
115

<210> 1663

<211> 51

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(51)

<223> Xaa = Any amino acid

<400> 1663

Ser His Ala Tyr Leu Tyr Gly Glu Val Leu Phe Pro Gly Lys Asp Leu
5 10 15
Thr Lys Xaa Lys Thr Lys Ile Gln Ser Arg Asp Lys Gly Arg Met Gln
20 25 30

580

Val Phe Leu Val Glu Ile Ser Ala Ser Gly Asn Leu Ser Leu Lys His
 35 40 45

Trp Asn Trp
 50

<210> 1664
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 1664
 Thr Leu Pro Pro Asp Arg Met Lys Phe Ile Ser Thr Ser Leu Leu Leu
 5 10 15

Met Leu Leu Val Ser Ser Leu Ser Pro Val Gln Gly Val Leu Glu Val
 20 25 30

Tyr Tyr Thr Ser Leu Arg Cys Arg Cys Val Gln Glu Ser Ser Val Phe
 35 40 45

Ile Pro Arg Arg Phe Ile Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn
 50 55 60

Gly Cys Pro Arg Lys Glu Ile Ile Val Trp Lys Lys Asn Lys Ser Ile
 65 70 75 80

Val Cys Val Asp Pro Gln Ala Glu Trp Ile Gln Arg Met Met Glu Val
 85 90 95

Leu Arg Lys Arg Ser Ser Ser Thr Leu Pro Val Pro Val Phe Lys Arg
 100 105 110

Lys Ile Pro
 115

<210> 1665
 <211> 55
 <212> PRT
 <213> Homo sapiens

<400> 1665
 Glu Lys Glu Val Leu Gln Leu Tyr Gln Phe Gln Cys Leu Arg Glu Arg
 5 10 15

Phe Pro Asp Ala Asp Ile Ser Thr Lys Asn Thr Cys Ile Leu Pro Leu
 20 25 30

Ser Leu Leu Trp Ile Leu Val Leu Cys Leu Val Lys Ser Phe Pro Gly
 35 40 45

Lys Arg Thr Ser Pro Tyr Lys
 50 55

<210> 1666
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 1666

581

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<400> 1668
Glu Pro Ser Gln Gln Xaa Leu Ser Arg Ile Tyr Ser Leu Thr Ser Asn
          5                      10                      15

Lys Gln Ala Leu Arg Asp Thr Glu Ser Gln Ile Gln Ile Leu Pro Met
          20                      25                      30

Gly Ile Lys Arg Leu Arg Leu Xaa Pro His Leu Glu Xaa Tyr Leu His
          35                      40                      45

His Lys Tyr Ile Ile Thr Gly Ser Leu Tyr Glu Ala Asp Thr Lys Cys
          50                      55                      60

Tyr Arg His Ser Gln Asn Ile Ile Leu Gly Asn Asn Val Ile Lys Met
          65                      70                      75                      80

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Pro Asn Xaa Ser Gln Gln
85

<210> 1669

<211> 70

<212> PRT

<213> Homo sapiens

<400> 1669

Arg Asp Asn Val Ile Cys Thr Pro Tyr Asp Ile Ser Thr Phe Leu Ala
5 10 15

Thr Thr Ser Gly Arg His Ser Pro Lys Leu Glu Lys Lys Glu Ile Glu
20 25 30

Asp Phe Cys Leu Cys Lys Val Leu Lys Ile Cys Ser Lys Leu Ile Lys
35 40 45

Leu Ser Leu Cys Ser Phe Leu Gln Gln Met Ile Gln Lys Lys Lys Lys
50 55 60

Lys Lys Lys Lys Ser Leu
65 70

<210> 1670

<211> 50

<212> PRT

<213> Homo sapiens

<400> 1670

Ile Ile Cys Cys Arg Lys Glu His Lys Asp Ser Phe Ile Asn Leu Glu
5 10 15

Gln Ile Leu Arg Thr Leu His Arg Gln Lys Ser Ser Ile Ser Phe Phe
20 25 30

Ser Asn Phe Gly Glu Cys Leu Pro Leu Val Val Ala Lys Asn Val Glu
35 40 45

Ile Ser
50

<210> 1671

<211> 115

<212> PRT

<213> Homo sapiens

<400> 1671

Tyr Asp Glu Asp Arg Leu Phe Phe Phe Asp Phe Ser Gln Asn Thr Arg
5 10 15

Val Pro Cys Leu Pro Glu Phe Ala Asp Trp Ala Gln Glu Gln Gly Asp
20 25 30

Ala Pro Ala Ile Leu Phe Asp Lys Glu Phe Cys Glu Trp Met Ile Gln
35 40 45

Gln Ile Gly Pro Lys Leu Asp Gly Lys Ile Pro Val Ser Arg Gly Phe
50 55 60

583

Pro Ile Ala Glu Val Phe Thr Leu Lys Pro Leu Glu Phe Gly Lys Pro
65 70 75 80

Asn Thr Leu Val Cys Phe Val Ser Asn Leu Phe Pro Pro Met Leu Thr
85 90 95

Val Asn Trp Gln His His Ser Val Pro Val Glu Gly Phe Gly Pro Thr
100 105 110

Phe Val Ser
115

<210> 1672
<211> 65
<212> PRT
<213> Homo sapiens

<400> 1672
Glu Thr Leu Trp Thr Pro Gly Phe Ser His Gln Val Leu Ala Leu Phe
5 10 15

Ala Gly Ser Ser Thr Arg Arg Thr Leu Cys Gln Ile Lys Trp Gln Glu
20 25 30

His Leu Pro Val Pro Glu Pro Ser Gln Gln Ile Arg Ala Gly Lys Ala
35 40 45

Pro Glu Cys Ser Gly Lys Ser Arg Arg Arg Lys Ala Gly Pro Arg Arg
50 55 60

Arg
65

<210> 1673
<211> 77
<212> PRT
<213> Homo sapiens

<400> 1673
Asp Lys Ser Arg Pro Lys Ser Phe His Arg Asp Gly Met Met Leu Pro
5 10 15

Val His Cys Gln His Gly Trp Glu Glu Ile Thr Asp Lys Thr Asp Gln
20 25 30

Ser Val Gly Leu Ala Lys Leu Gln Gly Leu Gln Arg Glu His Phe Ser
35 40 45

Asp Arg Lys Pro Ser Gly His Arg Asp Phe Pro Ile Lys Phe Trp Pro
50 55 60

Tyr Leu Leu Asp His Pro Leu Ala Glu Leu Phe Val Lys
65 70 75

<210> 1674
<211> 73
<212> PRT
<213> Homo sapiens

<400> 1674

Cys Cys Gln Phe Thr Val Ser Met Gly Gly Lys Arg Leu Leu Thr Lys
 5 10 15

Gln Thr Lys Val Leu Gly Leu Pro Asn Ser Arg Gly Phe Ser Val Asn
 20 25 30

Thr Ser Ala Ile Gly Asn Pro Leu Asp Thr Gly Ile Phe Pro Ser Ser
 35 40 45

Phe Gly Pro Ile Cys Trp Ile Ile His Ser Gln Asn Ser Leu Ser Asn
 50 55 60

Lys Met Ala Gly Ala Ser Pro Cys Ser
 65 70

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<210> 1675
<211> 199
<212> PRT
<213> Homo sapiens
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<400> 1675
His Leu Ile Tyr Lys Cys Gly Gly Ile Asp Lys Arg Thr Ile Glu Lys
      5              10              15

Phe Gly Lys Glu Ala Ala Glu Met Gly Lys Gly Ser Phe Lys Tyr Ala
      20              25              30

Trp Val Leu Asp Lys Leu Lys Ala Glu Arg Glu Arg Gly Ile Thr Ile
      35              40              45

Asp Ile Ser Leu Trp Lys Phe Glu Thr Ser Lys Tyr Tyr Val Thr Ile
      50              55              60

Ile Asp Ala Pro Gly His Arg Asp Phe Ile Lys Asn Met Ile Thr Gly
      65              70              75              80

Thr Ser Gln Ala Asp Cys Ala Val Leu Ile Val Ala Ala Gly Val Gly
      85              90              95

Glu Phe Glu Ala Gly Ile Ser Lys Asn Gly Gln Thr Arg Glu His Ala
      100              105              110

Leu Leu Ala Tyr Thr Leu Gly Val Lys Gln Leu Ile Val Gly Val Asn
      115              120              125

Lys Met Asp Ser Thr Glu Pro Pro Tyr Ser Gln Lys Arg Tyr Glu Glu
      130              135              140

Ile Val Lys Glu Val Ser Thr Tyr Ile Lys Lys Ile Gly Tyr Asn Pro
      145              150              155              160

Asp Thr Val Ala Phe Val Pro Ile Ser Gly Trp Asn Gly Asp Asn Met
      165              170              175

Leu Glu Pro Ser Ala Asn Met Pro Trp Phe Lys Gly Trp Lys Val Thr
      180              185              190

Arg Lys Asp Gly Asn Ala Ser
      195

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<210> 1676

<211> 76
<212> PRT
<213> Homo sapiens

<400> 1676
Thr Gly Ile Ala Ile Leu Thr Gly Asp Phe Pro Ser Leu Glu Pro Arg
 5 10 15
His Val Ser Thr Trp Leu Gln His Val Val Thr Ile Pro Thr Arg Asn
 20 25 30
Trp His Lys Cys Tyr Cys Val Gly Val Val Ala Asn Phe Leu Asn Val
 35 40 45
Ser Ala Asp Phe Leu Asn Asn Phe Leu Ile Ser Leu Leu Ala Val Gly
 50 55 60
Trp Leu Ser Gly Ile His Phe Val Asn Thr Asp Asn
 65 70 75

<210> 1677
<211> 122
<212> PRT
<213> Homo sapiens

<400> 1677
Leu Phe His Thr Gln Cys Val Ser Gln Lys Gly Met Leu Ser Gly Leu
 5 10 15
Pro Ile Leu Gly Asp Thr Ser Phe Lys Phe Thr Asn Thr Ser Ser Asn
 20 25 30
Asn Gln Asp Ser Thr Val Ser Leu Arg Cys Pro Cys Asn His Val Phe
 35 40 45
Asp Lys Val Ser Val Ser Trp Gly Ile Asn Asp Ser His Ile Val Leu
 50 55 60
Ala Gly Leu Lys Phe Pro Gln Gly Asp Ile Asn Gly Asp Thr Thr Phe
 65 70 75 80
Thr Leu Ser Phe Gln Phe Ile Gln Asp Pro Gly Ile Leu Glu Gly Ala
 85 90 95
Leu Ser His Leu Ser Ser Leu Leu Pro Lys Phe Phe Asn Gly Ser Phe
 100 105 110
Val Asp Ala Thr Ala Phe Ile Asp Gln Met
 115 120

<210> 1678
<211> 56
<212> PRT
<213> Homo sapiens

<400> 1678
Tyr Leu Leu Val Ser Asn Phe His Lys Glu Ile Ser Met Val Ile Pro
 5 10 15
Arg Ser Arg Ser Ala Phe Ser Leu Ser Lys Thr Gln Ala Tyr Leu Lys
 20 25 30

Glu Pro Phe Pro Ile Ser Ala Ala Ser Phe Pro Asn Phe Ser Met Val
 35 40 45

Leu Leu Ser Met Pro Pro His Leu
 50 55

<210> 1679

<211> 87

<212> PRT

<213> Homo sapiens

<400> 1679

Ile Leu Thr Leu Tyr Ser Glu Pro Ser Phe Asn Thr Met Val Ser Phe
 5 10 15

Leu Arg Ala Ser Arg Ser Pro Val Arg Ser Met Val Ile Gly Pro Gly
 20 25 30

Ala Leu Ser Gln Thr Arg Val Ser Arg Val Thr Thr Thr Leu Gly Ala
 35 40 45

Phe Gly Ser Val Thr Thr Gly Pro Ser Pro Ser Ser Val Phe Leu Tyr
 50 55 60

Leu Ile Arg Leu Ser Ser Leu Ser Ile Ser Cys Ser Ser Phe Arg
 65 70 75 80

Asp Phe Cys Gly Gly Gly Leu
 85

<210> 1680

<211> 55

<212> PRT

<213> Homo sapiens

<400> 1680

His Asn Gly Phe Leu Phe Glu Gly Phe Gln Ile Ser Ser Lys Val His
 5 10 15

Gly Asp Trp Ser Arg Gly Thr Leu Thr Asn Gln Gly Glu Pro Gly Asp
 20 25 30

Asn Asp Ile Gly Gly Phe Arg Ile Cys His His Arg Thr Ile Ser Gln
 35 40 45

Gln Arg Phe Leu Val Leu Asn
 50 55

<210> 1681

<211> 123

<212> PRT

<213> Homo sapiens

<400> 1681

Ile Arg Met Thr Glu Lys Ala Pro Glu Pro His Val Glu Glu Asp Asp
 5 10 15

Asp Asp Glu Leu Asp Ser Lys Leu Asn Tyr Lys Pro Pro Pro Gln Lys
 20 25 30

Ser	Leu	Lys	Glu	Leu	Gln	Glu	Met	Asp	Lys	Asp	Asp	Glu	Ser	Leu	Ile	
35			40					45								
Lys	Tyr	Lys	Lys	Thr	Leu	Leu	Gly	Asp	Gly	Pro	Val	Val	Thr	Asp	Pro	
50		55					60									
Lys	Ala	Pro	Asn	Val	Val	Val	Thr	Arg	Leu	Thr	Leu	Val	Cys	Glu	Ser	
65			70					75					80			
Ala	Pro	Gly	Pro	Ile	Thr	Met	Asp	Leu	Thr	Gly	Asp	Leu	Glu	Ala	Leu	
				85			90					95				
Lys	Lys	Glu	Thr	Ile	Val	Leu	Lys	Glu	Gly	Ser	Glu	Tyr	Arg	Val	Lys	
			100				105				110					
Ile	His	Phe	Lys	Val	Asn	Arg	Asp	Ile	Val	Ser						
115		120														

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<210> 1682
<211> 191
<212> PRT
<213> Homo sapiens
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<400> 1682																	
Pro	Lys	Glu	Val	Arg	Gln	Leu	Ala	Glu	Asp	Phe	Leu	Lys	Asp	Tyr	Ile		
				5					10					15			
His	Ile	Asn	Ile	Gly	Ala	Leu	Glu	Leu	Ser	Ala	Asn	His	Asn	Ile	Leu		
			20					25					30				
Gln	Ile	Val	Asp	Val	Cys	His	Asp	Val	Glu	Lys	Asp	Glu	Lys	Leu	Ile		
		35					40					45					
Arg	Leu	Met	Glu	Glu	Ile	Met	Ser	Glu	Lys	Glu	Asn	Lys	Thr	Ile	Val		
	50					55						60					
Phe	Val	Glu	Thr	Lys	Arg	Arg	Cys	Asp	Glu	Leu	Thr	Arg	Lys	Met	Arg		
65					70					75					80		
Arg	Asp	Gly	Trp	Pro	Ala	Met	Gly	Ile	His	Gly	Asp	Lys	Ser	Gln	Gln		
				85					90					95			
Glu	Arg	Asp	Trp	Val	Leu	Asn	Glu	Phe	Lys	His	Gly	Lys	Ala	Pro	Ile		
		100						105					110				
Leu	Ile	Ala	Thr	Asp	Val	Ala	Ser	Arg	Gly	Leu	Asp	Val	Glu	Asp	Val		
		115					120					125					
Lys	Phe	Val	Ile	Asn	Tyr	Asp	Tyr	Pro	Asn	Ser	Ser	Glu	Asp	Tyr	Ile		
	130					135					140						
His	Arg	Ile	Gly	Arg	Thr	Ala	Arg	Ser	Thr	Lys	Thr	Gly	Thr	Ala	Tyr		
145					150					155					160		
Thr	Phe	Phe	Thr	Pro	Asn	Asn	Ile	Lys	Gln	Val	Ser	Asp	Leu	Ile	Ser		
				165					170					175			
Val	Leu	Arg	Glu	Ala	Asn	Gln	Ala	Ile	Asn	Pro	Lys	Leu	Leu	Gln			
			180					185					190				

<210> 1683
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 1683
 Leu Lys Gln Leu Gly Ile Asn Cys Leu Ile Ser Phe Thr Lys His Arg
 5 10 15
 Asp Lys Val Ala His Leu Leu Tyr Val Ile Arg Cys Lys Glu Ser Val
 20 25 30
 Cys Cys Ala Cys Phe Gly Thr Ala Ser Ser Ser Ser Asn Ser Met Asn
 35 40 45
 Ile Ile Leu
 50

<210> 1684
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 1684
 Asn Pro Val Thr Leu Leu Leu Thr Leu Val Thr Met Asp Thr His Gly
 5 10 15
 Arg Pro Pro Ile Ser Pro His Phe Ser Gly Lys Leu Ile Thr Ser Ser
 20 25 30
 Phe Gly Phe His Lys Asn Asn Gly Phe Ile Leu Leu Leu Thr His Asp
 35 40 45
 Leu Phe His
 50

<210> 1685
 <211> 55
 <212> PRT
 <213> Homo sapiens

<400> 1685
 Leu Leu Ser Pro Trp Ile Pro Met Ala Gly His Pro Ser Leu Leu Ile
 5 10 15
 Phe Leu Val Ser Ser Ser His Leu Leu Leu Val Ser Thr Lys Thr Met
 20 25 30
 Val Leu Phe Ser Phe Ser Leu Met Ile Ser Ser Ile Arg Arg Ile Ser
 35 40 45
 Phe Ser Ser Phe Ser Thr Ser
 50 55

<210> 1686
 <211> 62
 <212> PRT
 <213> Homo sapiens
 .
 <400> 1686

Val	Phe	Leu	Ser	Pro	Trp	Val	Lys	Ser	Glu	Ser	Gly	Ser	Leu	Cys	Leu
				5					10					15	
Ser	Val	Leu	Val	Tyr	Cys	Trp	Ser	Glu	Ser	Lys	Phe	Leu	Ile	Lys	Ala
			20					25					30		
Val	Asp	Leu	Ala	Leu	Thr	Val	Tyr	Ala	Asp	Ile	Gly	Glu	Thr	Ile	Trp
		35					40					45			
Leu	Phe	Gln	Thr	Ser	Gln	Asp	Leu	Ser	Lys	Lys	Thr	Trp	Leu		
	50					55					60				

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<210> 1687
<211> 86
<212> PRT
<213> Homo sapiens
```

```
<400> 1687
Glu Pro Ser Gln Gln Leu Leu Ser Arg Ile Tyr Ser Leu Thr Ser Asn
      5                                10                        15

Lys Gln Ala Leu Arg Asp Thr Glu Ser Gln Ile Gln Ile Leu Pro Met
      20                                25                        30

Gly Ile Lys Arg Leu Arg Leu Ser Pro His Leu Glu Asn Tyr Leu His
      35                                40                        45

His Lys Tyr Ile Ile Thr Gly Ser Leu Tyr Glu Ala Asp Thr Lys Cys
      50                                55                        60

Tyr Arg His Ser Gln Asn Ile Ile Leu Gly Asn Asn Val Ile Lys Met
      65                                75                        80

Pro Asn Leu Ser Gln Gln
      85
```

```
<210> 1688
<211> 95
<212> PRT
<213> Homo sapiens
```

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<220>
<221> variant
<222> (1)...(95)
<223> Xaa = Any amino acid
```

```
<400> 1688
Pro Leu Xaa Val Ala Leu Ala Gln Arg Lys Glu Glu Arg Gln Ala His
      5                                10                        15

Leu Thr Asn Gln Tyr Met Gln Arg Met Ala Ser Val Arg Ala Val Pro
      20                                25                        30

Asn Pro Val Ile Asn Pro Tyr Gln Pro Ala Pro Pro Ser Gly Tyr Phe
      35                                40                        45

Met Ala Ala Ile Pro Gln Thr Gln Asn Xaa Ala Ala Tyr Tyr Pro Pro
      50                                55                        60

Ser Gln Ile Ala Gln Leu Arg Pro Ser Pro Arg Trp Thr Ala Gln Gly
      65                                70                        75                        80
```

Ala Arg Pro His Pro Phe Gln Asn Met Pro Gly Ala Ile Arg Pro
85 90 95

```
<210> 1689
<211> 50
<212> PRT
<213> Homo sapiens
```

<400> 1689
Tyr Ser Ile Phe Phe Cys His Phe Leu His Gln Gln Pro Gly Arg Leu
 5 10 15

His Leu Met Glu Lys Ile Tyr Asp Cys Phe Met Thr Phe Leu Asn Tyr
20 25 30

Leu Phe Leu Phe His Ile Tyr Val Phe Gly Gly Val Pro Phe Ala Ser
35 40 45

Leu Phe
50

```
<210> 1690
<211> 94
<212> PRT
<213> Homo sapiens
```

<400> 1690
Leu Ser Phe Leu Glu Val Leu Cys Thr Tyr Ala Pro His Leu Tyr Leu
 5 10 15

Ala Phe Ala Trp Ser Asp His Ser Ser Phe Ser Leu Thr Leu Asn Val
20 25 30

Glu Asn Val Ala Ile Val Ala Ala Cys Val Val Thr Leu Leu Leu Leu
35 40 45

Ser Asn Phe Leu Thr Leu Lys Lys Gly Arg Met Ser Ala Ser Glu Cys
50 55 60

Asp Phe Leu Leu Thr Cys Ser Leu Asp Arg Leu Phe Ser Ile Val Phe
65 70 75 80

Phe Phe Val Ile Phe Ser Ile Asn Asn Gln Gly Asp Cys Thr
85 90

```
<210> 1691
<211> 53
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> variant  
<222> (1)...(53)  
<223> Xaa = Any amino acid
```

<400> 1691
Xaa Met Leu Phe Leu Gln Lys Thr Asp Gly Cys Trp Leu Phe Arg Ala
 5 10 15

Ser Leu Met Gly Cys Gly Asn Ser Lys Asn Val Pro Gln Cys Gln Pro
 20 25 30

Cys Arg Lys Ile Asn Gly Met Gly Ser Val Leu Ser Leu Val Val Ile
 35 40 45

Phe Phe Tyr His Pro
 50

<210> 1692

<211> 59

<212> PRT

<213> Homo sapiens

<400> 1692

Ser Thr His Ser Ala Phe Leu Gln Cys Lys Lys Val Ala Gln Lys Lys
 5 10 15

Lys Arg Asp Asn Thr Ser Cys Tyr Asn Gly Tyr Ile Leu Tyr Ile Gln
 20 25 30

Cys Lys Arg Glu Gly Ala Met Val Thr Pro Cys Lys Gly Gln Ile Glu
 35 40 45

Met Trp Cys Val Cys Ala Glu Tyr Leu Lys Lys
 50 55

<210> 1693

<211> 91

<212> PRT

<213> Homo sapiens

<400> 1693

Glu Cys His Glu Ala Val Ile Tyr Leu Phe His Gln Val Gln Ser Pro
 5 10 15

Trp Leu Leu Met Glu Lys Met Thr Lys Lys Asn Thr Ile Leu Lys Ser
 20 25 30

Leu Ser Lys Glu Gln Val Ser Arg Lys Ser His Ser Glu Ala Leu Ile
 35 40 45

Leu Pro Phe Phe Ser Val Arg Lys Leu Leu Lys Arg Arg Ser Val Thr
 50 55 60

Thr Gln Ala Ala Thr Met Ala Thr Phe Ser Thr Phe Asn Val Arg Glu
 65 70 75 80

Lys Glu Leu Trp Ser Leu His Ala Lys Ala Arg
 85 90

<210> 1694

<211> 55

<212> PRT

<213> Homo sapiens

<400> 1694

Pro Arg Leu Leu Pro Ala Pro Pro Trp Arg Arg Ala Thr Ser Cys Leu
 5 10 15

592

Thr Ala Arg Ser Ser Pro Leu Ala Met Ser Gly Ser Ala Ala Leu Arg
 20 25 30

His Ser Ser Ser Leu Pro Ser Trp Ala Trp Ser Pro Val Ala Ser Thr
 35 40 45

Lys Leu Pro Ser Thr Pro Ser
 50 55

<210> 1695
 <211> 54
 <212> PRT
 <213> Homo sapiens

<400> 1695
 Arg Ser Arg Ser Leu Leu Leu Leu Ser Ala Ser Thr Pro Cys Gly Ser
 5 10 15

Ala Ala Pro Ser Trp Pro Arg Cys Pro Pro Ser Ser Arg Cys Gly Ser
 20 25 30

Ala Ser Arg Ser Met Thr Ser Pro Ala Pro Pro Ser Ser Thr Ala Asn
 35 40 45

Ala Ser Arg Arg Thr Met
 50

<210> 1696
 <211> 147
 <212> PRT
 <213> Homo sapiens

<400> 1696
 Thr Ala Ala Ser Ser Ser Ser Leu Glu Lys Ser Tyr Glu Leu Pro Asp
 5 10 15

Gly Gln Val Ile Thr Ile Gly Asn Glu Arg Phe Arg Cys Pro Glu Ala
 20 25 30

Leu Phe Gln Pro Ser Phe Leu Gly Met Glu Ser Cys Gly Ile His Glu
 35 40 45

Thr Thr Phe Asn Ser Ile Met Lys Cys Asp Val Asp Ile Arg Lys Asp
 50 55 60

Leu Tyr Ala Asn Thr Val Leu Ser Gly Gly Thr Thr Met Tyr Pro Gly
 65 70 75 80

Ile Ala Asp Arg Met Gln Lys Glu Ile Thr Ala Leu Ala Pro Ser Thr
 85 90 95

Met Lys Ile Lys Ile Ile Ala Pro Pro Glu Arg Lys Tyr Ser Val Trp
 100 105 110

Ile Gly Gly Ser Ile Leu Ala Ser Leu Ser Thr Phe Gln Gln Met Trp
 115 120 125

Ile Ser Lys Gln Glu Tyr Asp Glu Ser Gly Pro Ser Ile Val His Arg
 130 135 140

Lys Cys Phe

Gln Glu Gly Arg Leu Glu Glu Cys Leu Arg Ala Ala Glu Pro Leu Ile
 115 120 125

Ala Asn Gly Asp Asp Leu Ala Val Arg Gln Leu Val Ala Leu Leu Gln
 130 135 140

Gly Gly Ala Gly Ser Ser Arg
 145 150

<210> 1699
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 1699
 Pro Gly Phe Pro Leu Trp Glu Val Leu Phe Leu Ala Gly Gln Leu Gly
 5 10 15

Arg Glu Trp Arg Thr Glu Lys Arg Val Glu Ile Thr Cys Ser Leu Glu
 20 25 30

Leu Ser Trp Gly Thr Ser Pro His Ser Val His Lys Ser Leu Pro Leu
 35 40 45

Glu Met Glu Cys Ser Phe Tyr His Gly Lys Arg Ile
 50 55 60

<210> 1700
 <211> 57
 <212> PRT
 <213> Homo sapiens

<400> 1700
 Val Gly His Asp Ser Glu Gln Asp Arg Pro Lys Glu Val Gln Gly Leu
 5 10 15

Trp Ser Gly Met Glu Thr Ser Ser Glu Arg Thr His Gly Arg Ser Arg
 20 25 30

Cys Arg Arg Tyr Thr Ser Ser Arg Ile Thr His Arg Met Asp Pro Leu
 35 40 45

Glu Val Lys Thr Cys Gly Lys Thr Val
 50 55

<210> 1701
 <211> 50
 <212> PRT
 <213> Homo sapiens

<400> 1701
 Cys Cys Asn Gln Val Ser Pro Cys Gly Lys Cys Cys Phe Leu Leu Gly
 5 10 15

Ser Trp Glu Gly Asn Gly Glu Gln Arg Arg Glu Trp Lys Ser His Ala
 20 25 30

His Leu Asn Phe Pro Gly Glu Arg Leu Leu Thr Ala Tyr Thr Arg Ala
 35 40 45

Ser Leu
50

<210> 1702
<211> 53
<212> PRT
<213> Homo sapiens

<400> 1702
Lys Trp Ser Val His Phe Ile Met Gly Lys Glu Ser Glu Trp Asp Met
5 10 15
Ile Gln Asn Arg Thr Gly Pro Arg Lys Cys Arg Gly Cys Gly Val Gly
20 25 30
Trp Arg Gln Ala Leu Lys Gly His Met Gly Asp Leu Asp Val Glu Gly
35 40 45
Thr Gln Val Val Gly
50

<210> 1703
<211> 65
<212> PRT
<213> Homo sapiens

<400> 1703
His Pro Gly Phe Gln Val Leu Ser Asn Thr Val Gly Pro Leu Lys Ala
5 10 15
Ser Ser Phe Leu Pro Leu Pro Gln Ser His Pro Tyr Gln Asp Lys Gly
20 25 30
Leu Leu Thr Val Leu Ser Ile Ala Pro Thr Val Thr Met Phe Ala Ser
35 40 45
Leu Leu Ser Pro Thr Glu Gln Leu Pro Ile Thr Leu Ser Tyr His Met
50 55 60
Ser
65

<210> 1704
<211> 64
<212> PRT
<213> Homo sapiens

<400> 1704
Ile Ser His Val Ser Phe Gln Ser Leu Ser Pro Ser His Ser Thr Ala
5 10 15
Pro Ala Leu Pro Trp Ala Gly Pro Val Leu Asn His Val Pro Leu Arg
20 25 30
Phe Phe Ser His Asp Lys Met Asn Thr Pro Phe Leu Lys Gly Gly Ser
35 40 45
Cys Val Arg Cys Glu Glu Thr Phe Pro Arg Lys Val Gln Val Ser Met
50 55 60

<210> 1705
<211> 52
<212> PRT
<213> Homo sapiens

<400> 1705
Ala Trp Gly Ile His Leu Pro Arg Ile Ser Ile Leu Ala Ser Arg Ser
5 10 15
Ser Leu Ile Gln Trp Gly Leu Ser Arg His Pro Leu Ser Phe Leu Tyr
20 25 30
Leu Lys Ala Thr Leu Ile Arg Ile Lys Gly Ser Ser Leu Ser Ser Pro
35 40 45
Leu Pro Pro Arg
50

<210> 1706
<211> 67
<212> PRT
<213> Homo sapiens

<400> 1706
Gln Cys Leu Leu Pro Tyr Phe Leu Gln Leu Ser Ser Phe Leu Leu His
5 10 15
Cys Leu Thr Thr Cys Leu Asn Leu Gln Trp Ile His Pro Val Ser Tyr
20 25 30
Pro Thr Thr Cys Val Pro Ser Thr Ser Arg Ser Pro Met Cys Pro Phe
35 40 45
Arg Ala Cys Leu His Pro Thr Pro Gln Pro Leu His Phe Leu Gly Pro
50 55 60
Val Leu Phe
65

<210> 1707
<211> 115
<212> PRT
<213> Homo sapiens

<400> 1707
Thr Leu Pro Pro Asp Arg Met Lys Phe Ile Ser Thr Ser Leu Leu Leu
5 10 15
Met Leu Leu Val Ser Ser Leu Ser Pro Val Gln Gly Val Leu Glu Val
20 25 30
Tyr Tyr Thr Ser Leu Arg Cys Arg Cys Val Gln Glu Ser Ser Val Phe
35 40 45
Ile Pro Arg Arg Phe Ile Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn
50 55 60
Gly Cys Pro Arg Lys Glu Ile Ile Val Trp Lys Lys Asn Lys Ser Ile
65 70 75 80

Val Cys Val Asp Pro Gln Ala Glu Trp Ile Gln Arg Met Met Glu Val
85 90 95

Leu Arg Lys Arg Ser Ser Ser Thr Leu Pro Val Pro Val Phe Lys Arg
100 105 110

Lys Ile Pro
115

<210> 1708
<211> 55
<212> PRT
<213> Homo sapiens

<400> 1708
Glu Lys Glu Val Leu Gln Leu Tyr Gln Phe Gln Cys Leu Arg Glu Arg
5 10 15

Phe Pro Asp Ala Asp Ile Ser Thr Lys Asn Thr Cys Ile Leu Pro Leu
20 25 30

Ser Leu Leu Trp Ile Leu Val Leu Cys Leu Val Lys Ser Phe Pro Gly
35 40 45

Lys Arg Thr Ser Pro Tyr Lys
50 55

<210> 1709
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(51)
<223> Xaa = Any amino acid

<400> 1709
Xaa His Ala Tyr Leu Tyr Gly Glu Val Leu Phe Pro Gly Lys Asp Leu
5 10 15

Thr Lys His Lys Thr Lys Ile Gln Ser Arg Asp Lys Gly Arg Met Gln
20 25 30

Val Phe Leu Val Glu Ile Ser Ala Ser Gly Asn Leu Ser Leu Lys His
35 40 45

Trp Asn Trp
50

<210> 1710
<211> 58
<212> PRT
<213> Homo sapiens

<400> 1710
Leu Thr Arg Gly Leu Thr Pro Arg Glu Phe Ile Gln Phe Leu Asn Val
5 10 15

Arg Ser Ser Leu Val Ser Pro Ser Arg Ala Pro Gln Ser Met Ser Trp
 20 25 30

Phe Ser Gly Leu Cys Arg Ala Gly Tyr Leu Leu Lys Arg Leu Ala Ile
 35 40 45

Lys Ala Lys Phe Asn Leu Gly Phe Pro Arg
 50 55

<210> 1711
 <211> 76
 <212> PRT
 <213> Homo sapiens

<400> 1711
 Leu Pro Asn Gln Gly Gln Cys Glu Ser Ala Val Ser Phe Ile Glu Ile
 5 10 15

Leu Ser Thr Asp Ala Asn Gln Gly Glu Leu Arg Leu Ile Leu Pro Gln
 20 25 30

Phe Tyr Arg Val Val Thr Ile Leu Lys Leu Leu His Ile Ala Ser Gln
 35 40 45

Phe Gly Val Trp Arg Phe Val Tyr Ser Val Pro Val Asn Arg Asn Phe
 50 55 60

Asp Leu Phe Ile Glu Leu Glu Asp Asp Gln Gly Ile
 65 70 75

<210> 1712
 <211> 63
 <212> PRT
 <213> Homo sapiens

<400> 1712
 Val Thr Val Gln Met Ile Asp Ser Arg Val Asn Thr Gln Gly Val His
 5 10 15

Pro Val Pro Lys Cys Pro Leu Phe Ser Arg Leu Thr Phe Lys Ser Pro
 20 25 30

Pro Val Asn Val Leu Val Leu Trp Phe Val Gln Gly Arg Val Ser Val
 35 40 45

Lys Glu Val Gly Asn Lys Ser Gln Val Gln Leu Gly Val Pro Ser
 50 55 60

<210> 1713
 <211> 156
 <212> PRT
 <213> Homo sapiens

<400> 1713
 Arg Gly Asn Pro Lys Leu Asn Leu Ala Phe Ile Ala Asn Leu Phe Asn
 5 10 15

Arg Tyr Pro Ala Leu His Lys Pro Glu Asn Gln Asp Ile Asp Trp Gly
 20 25 30

<400> 1715
Glu Pro Ser Gln Gln Leu Leu Ser Arg Ile Tyr Ser Leu Thr Ser Asn
 5 10 15

Lys	Gln	Ala	Leu	Xaa	Asp	Thr	Glu	Ser	Gln	Ile	Gln	Ile	Leu	Pro	Met			
			20							25							30	
Gly	Ile	Lys	Arg	Leu	Arg	Leu	Ser	Pro	His	Leu	Glu	Asn	Tyr	Leu	His			
			35							40							45	
His	Lys	Tyr	Ile	Ile	Thr	Gly	Ser	Leu	Tyr	Glu	Ala	Asp	Thr	Lys	Cys			
			50							55							60	
Tyr	Arg	His	Ser	Gln	Asn	Ile	Ile	Leu	Gly	Asn	Asn	Val	Ile	Lys	Met			
			65							70							75	80
Pro	Asn	Leu	Ser	Gln	Gln													
						85												

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<210> 1716
<211> 69
<212> PRT
<213> Homo sapiens
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```
<400> 1716
Leu Cys Leu Arg Ala Leu Ala Gly Gln Glu Gln Asp Ser Trp Asp Gly
      5                                10                        15

Ala Ala Gln Ala Trp Phe Leu Leu Pro Val Ala Ala Asp Asn Leu Gly
      20                                25                        30

Gly Asn Leu Pro Leu Ala Val Leu Glu Ala Thr Val Leu Ser Pro Ser
      35                                40                        45

Ile Thr Ala Leu Gly Pro Gly Asp Ala Lys Gly Gln Asn Gln Asp Lys
      50                                55                        60

Glu Ala Gln Ser Gln
      65
```

```
<210> 1717
<211> 102
<212> PRT
<213> Homo sapiens
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```

<400> 1717
Leu Pro Thr Ser Pro Ser Ala Leu Ala Ser Tyr Ser Pro Ser Thr Thr
                    5                      10                      15

Asp Met Ala Gln Ser Leu Ala Leu Ser Leu Leu Ile Leu Val Leu Ala
                20                      25                      30

Phe Gly Ile Pro Arg Thr Gln Gly Ser Asp Gly Gly Ala Gln Asp Cys
                35                      40                      45

Cys Leu Lys Tyr Ser Gln Arg Lys Ile Pro Ala Lys Val Val Arg Ser
                50                      55                      60

Tyr Arg Lys Gln Glu Pro Ser Leu Gly Cys Ser Ile Pro Ala Ile Leu
                65                      70                      75                      80

Phe Leu Pro Arg Lys Arg Ser Gln Ala Glu Leu Cys Ala Asp Pro Lys
                85                      90                      95

Glu Leu Trp Val Gln Gln

```

100

<210> 1718
<211> 77
<212> PRT
<213> Homo sapiens

<400> 1718
Ala Ser Leu Ser Trp Phe Trp Pro Leu Ala Ser Pro Gly Pro Lys Ala
5 10 15
Val Met Glu Gly Leu Arg Thr Val Ala Ser Ser Thr Ala Lys Gly Arg
20 25 30
Phe Pro Pro Arg Leu Ser Ala Ala Thr Gly Ser Arg Asn Gln Ala Trp
35 40 45
Ala Ala Pro Ser Gln Leu Ser Cys Ser Cys Pro Ala Ser Ala Leu Arg
50 55 60
Gln Ser Tyr Val Gln Thr Gln Arg Ser Ser Gly Cys Ser
65 70 75

<210> 1719
<211> 60
<212> PRT
<213> Homo sapiens

<400> 1719
Trp Arg Gly Ser Gly Leu Leu Pro Gln Val Gln Pro Lys Glu Asp Ser
5 10 15
Arg Gln Gly Cys Pro Gln Leu Pro Glu Ala Gly Thr Lys Leu Gly Leu
20 25 30
Leu His Pro Ser Tyr Pro Val Leu Ala Pro Gln Ala Leu Ser Gly Arg
35 40 45
Ala Met Cys Arg Pro Lys Gly Ala Leu Gly Ala Ala
50 55 60

<210> 1720
<211> 115
<212> PRT
<213> Homo sapiens

<400> 1720
Thr Leu Pro Pro Asp Arg Met Lys Phe Ile Ser Thr Ser Leu Leu Leu
5 10 15
Met Leu Leu Val Ser Ser Leu Ser Pro Val Gln Gly Val Leu Glu Val
20 25 30
Tyr Tyr Thr Ser Leu Arg Cys Arg Cys Val Gln Glu Ser Ser Val Phe
35 40 45
Ile Pro Arg Arg Phe Ile Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn
50 55 60
Gly Cys Pro Arg Lys Glu Ile Ile Val Trp Lys Lys Asn Lys Ser Ile

602

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65              70              75              80
Val Cys Val Asp Pro Gln Ala Glu Trp Ile Gln Arg Met Met Glu Val
      85              90              95
Leu Arg Lys Arg Ser Ser Ser Thr Leu Pro Val Pro Val Phe Lys Arg
      100             105             110
Lys Ile Pro
      115
```

```
<210> 1721
<211> 55
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> variant
<222> (1)...(55)
<223> Xaa = Any amino acid
```

```

<400> 1721
Glu Lys Glu Val Leu Gln Leu Tyr Gln Phe Gln Cys Leu Arg Glu Arg
      5                                10                                15

Phe Pro Asp Ala Asp Ile Ser Thr Lys Asn Thr Cys Ile Leu Pro Leu
      20                                25                                30

Ser Leu Leu Trp Ile Leu Val Leu Cys Leu Val Lys Ser Phe Pro Gly
      35                                40                                45

Lys Arg Xaa Ser Pro Tyr Lys
      50                                55

```

```
<210> 1722
<211> 51
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> variant  
<222> (1)...(51)  
<223> Xaa = Any amino acid
```

```

<400> 1722
Ser His Ala Tyr Leu Tyr Gly Glu Xaa Leu Phe Pro Gly Lys Asp Leu
          5                      10                      15

Thr Lys His Lys Thr Lys Ile Gln Ser Arg Asp Lys Gly Arg Met Gln
          20                      25                      30

Val Phe Leu Val Glu Ile Ser Ala Ser Gly Asn Leu Ser Leu Lys His
          35                      40                      45

Trp Asn Trp
          50

```

```
<210> 1723
<211> 62
<212> PRT
```

<213> Homo sapiens

<400> 1723

Leu Cys Gln Gly Ala Glu Ser His Asp Ser Gln Leu Cys Ala Ala Ala
 5 10 15
Leu Val Asp Leu Arg Gly Val Val Ala Leu Leu Leu Ala Glu Val Asp
 20 25 30
Ala Ile Val Leu Lys Pro Asp Ala Leu Asp Gly Glu Gly Gly Glu Arg
 35 40 45
Phe Val Leu Gly Leu Phe His Ala Ala Leu Phe Gln Leu Gln
 50 55 60

<210> 1724

<211> 62

<212> PRT

<213> Homo sapiens

<400> 1724

Leu Lys Leu Glu Lys Gly Arg Met Glu Glu Ser Gln Asn Glu Ser Leu
 5 10 15
Ala Thr Leu Thr Ile Gln Gly Ile Arg Phe Glu Asp Asn Gly Ile Tyr
 20 25 30
Phe Cys Gln Gln Lys Cys Asn Asn Thr Ser Glu Val Tyr Gln Gly Cys
 35 40 45
Gly Thr Glu Leu Arg Val Met Gly Phe Ser Thr Leu Ala Gln
 50 55 60

<210> 1725

<211> 60

<212> PRT

<213> Homo sapiens

<400> 1725

Ser Trp Lys Arg Ala Ala Trp Lys Ser Pro Arg Thr Asn Leu Ser Pro
 5 10 15
Pro Ser Pro Ser Lys Ala Ser Gly Leu Arg Thr Met Ala Ser Thr Ser
 20 25 30
Ala Ser Arg Ser Ala Thr Thr Pro Arg Arg Ser Thr Arg Ala Ala Ala
 35 40 45
Gln Ser Cys Glu Ser Trp Asp Ser Ala Pro Trp His
 50 55 60

<210> 1726

<211> 88

<212> PRT

<213> Homo sapiens

<400> 1726

Thr Leu Pro Pro Asp Arg Met Lys Phe Ile Ser Thr Ser Leu Leu Leu
 5 10 15

Met Leu Leu Val Ser Ser Leu Ser Pro Val Gln Gly Val Leu Glu Val
 20 25 30
 Tyr Tyr Thr Ser Leu Arg Cys Arg Cys Val Gln Glu Ser Ser Val Phe
 35 40 45
 Ile Pro Arg Arg Phe Ile Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn
 50 55 60
 Gly Cys Pro Arg Lys Glu Ile Ile Val Trp Lys Lys Asn Lys Ser Ile
 65 70 75 80
 Val Cys Val Asp Pro Gln Ala Glu
 85

<210> 1727
 <211> 57
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(57)
 <223> Xaa = Any amino acid

<400> 1727
 Ile Gln Gly Gln Asn Gln Gln Gln Xaa Leu Gln Ser Ser Ala Asp Ile
 5 10 15
 Lys Tyr Lys Leu Gln Gly Gln Phe Leu Phe Glu Gly Leu Phe Xaa Phe
 20 25 30
 Xaa Glu Ala Ser Met Arg Cys Xaa His Leu Pro Gly Ala Asn Phe Tyr
 35 40 45
 Ser Gln Leu Thr His Ala Xaa Asn Ala
 50 55

<210> 1728
 <211> 65
 <212> PRT
 <213> Homo sapiens

<400> 1728
 Arg Asp Asn Val Ile Cys Thr Pro Tyr Asp Ile Ser Thr Phe Leu Ala
 5 10 15
 Thr Thr Ser Gly Arg His Ser Pro Lys Leu Glu Lys Lys Glu Ile Glu
 20 25 30
 Asp Phe Cys Leu Cys Lys Val Leu Lys Ile Cys Ser Lys Leu Ile Lys
 35 40 45
 Leu Ser Leu Cys Ser Phe Leu Gln Lys Lys Lys Lys Lys Lys Lys
 50 55 60
 Arg
 65

<210> 1729

```

<400> 1731
Ser Phe Gln Xaa Ala Gln Glu Pro Cys Leu Cys Xaa Ser Ser Xaa Asn
          5              10              15

Phe Leu Ala Pro Pro Val His Glu Asp Ala His Ser Thr Xaa Asp Glu
          20              25              30

Pro Gln His Xaa Ala Pro Ser Ser Arg Gln Cys Leu Thr Pro Gly Xaa

```

35 40 45

Ile Arg Leu Xaa
50

<210> 1732
<211> 64
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(64)
<223> Xaa = Any amino acid

<400> 1732
His Leu Ala Pro Gly Gln Thr Phe Asn Phe Gln Ile Gly Tyr Cys Cys
5 10 15

Gln Xaa Val Ala Xaa Lys Ser Val Ser Ile Ile Xaa Leu Phe Asp Ser
20 25 30

Xaa His Cys Xaa Ser His Trp Ala Ser Asn His Val Pro Xaa Phe Leu
35 40 45

Xaa Xaa Gln Ile Xaa Lys Thr Xaa Lys Lys Lys Lys Lys Lys Lys Lys
50 55 60

<210> 1733
<211> 52
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(52)
<223> Xaa = Any amino acid

<400> 1733
Thr Gly Phe Leu Ser Xaa Leu Lys Arg Leu Leu Cys Leu Arg Lys Ser
5 10 15

Ile Cys Cys Val Ser Leu Ala Ser Gly Ser Arg Thr Asp Leu Gln Leu
20 25 30

Pro Asn Trp Ile Leu Leu Pro Xaa Ser Cys Xaa Glu Val Ser Phe Tyr
35 40 45

His Xaa Ala Leu
50

<210> 1734
<211> 59
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(59)
<223> Xaa = Any amino acid

<400> 1734

Pro Cys Leu Xaa Ser Lys Val Thr Arg Lys Arg Pro Cys Leu Pro Ser
 5 10 15

Met Thr Leu Met Glu Glu Met Leu Xaa Xaa Ala Phe Arg Cys Met Thr
 20 25 30

Gln Gly Lys Thr Ala Lys Asn Leu Val Leu Ala Leu Leu Ile Leu Leu
 35 40 45

Phe Val Leu Phe Leu Gly Val Xaa Arg Ala Lys
 50 55

<210> 1735

<211> 54

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(54)

<223> Xaa = Any amino acid

<400> 1735

Glu Phe Xaa Glu Gln Asn Asp Xaa Thr Gln Lys Phe Ser Lys Trp Asp
 5 10 15

Phe Pro Gly Arg Thr Asn Glu Arg Pro Tyr Cys Tyr Ala Ile Trp Xaa
 20 25 30

Lys Thr Thr Leu Xaa Glu Asp Val Phe Thr Gly Gly Pro His Xaa Lys
 35 40 45

Leu Leu Xaa Glu Gly Ile
 50

<210> 1736

<211> 119

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(119)

<223> Xaa = Any amino acid

<400> 1736

Asp Cys Gln Lys Ser Cys Ser Cys Ser Pro His Phe Val Ile Cys Phe
 5 10 15

Ile Phe Arg Ser Xaa Glu Ser Lys Met Xaa Thr Pro Arg Asn Ser Val
 20 25 30

Asn Gly Thr Phe Pro Ala Glu Pro Met Lys Gly Pro Ile Ala Met Gln
 35 40 45

Ser Gly Xaa Lys Pro Leu Xaa Xaa Arg Met Ser Ser Leu Val Gly Pro
 50 55 60

Xaa Gln Ser Phe Phe Xaa Arg Glu Ser Xaa Thr Leu Gly Ala Xaa Gln

608

65	70	75	80
Ile Xaa Asn Gly	Leu Phe His Ile Ala Leu Gly Gly	Leu Xaa Met Ile	
	85	90	95
Pro Xaa Gly Ile Tyr Ala Pro Ile Cys Val Thr Val Trp Xaa Pro Leu			
	100	105	110
Trp Gly Gly Ile Met Tyr Ile			
	115		

<210> 1737
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(59)
 <223> Xaa = Any amino acid

<400> 1737
Asn Ile His Asn Ala Ser Pro Glu Arg Xaa Pro His Ser His Thr Asp
5 10 15
Gly Cys Ile Asp Pro Xaa Trp Asp His Xaa Lys Thr Pro Gln Gly Asn
20 25 30
Val Glu Glu Pro Ile Xaa Asn Leu Xaa Ser Pro Gln Ser Xaa Arg Phe
35 40 45
Pro Xaa Glu Glu Ala Leu Xaa Gly Ala His Gln
50 55

<210> 1738
 <211> 64
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(64)
 <223> Xaa = Any amino acid

<400> 1738
Ile Ser Gly Cys Xaa His Phe Ala Leu Xaa Thr Pro Lys Asn Lys Thr
5 10 15
Asn Asn Lys Met Arg Arg Ala Arg Thr Arg Phe Leu Ala Val Leu Pro
20 25 30
Cys Val Met His Leu Asn Xaa Ser Xaa Ser Ile Ser Ser Met Ser Val
35 40 45
Ile Glu Gly Arg His Gly Leu Phe Arg Val Thr Leu Asp Xaa Arg Gln
50 55 60

<210> 1739
 <211> 89
 <212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(89)

<223> Xaa = Any amino acid

<400> 1739

Ile Xaa Xaa Gly Ile Ile Xaa Arg Pro Pro Arg Ala Met Trp Lys Ser
5 10 15

Pro Xaa Ile Ile Trp Xaa Ala Pro Lys Xaa Leu Asp Ser Leu Xaa Lys
20 25 30

Lys Leu Xaa Val Gly Pro Thr Ser Glu Asp Ile Leu Xaa Lys Ser Gly
35 40 45

Phe Xaa Pro Asp Cys Ile Ala Ile Gly Pro Phe Ile Gly Ser Ala Gly
50 55 60

Lys Val Pro Phe Thr Glu Phe Leu Gly Xaa Val Ile Leu Leu Xaa Lys
65 70 75 80

Leu Leu Lys Ile Lys Gln Ile Thr Lys
85

<210> 1740

<211> 58

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(58)

<223> Xaa = Any amino acid

<400> 1740

Leu Val His Phe Leu Asn Phe Pro His Ser Glu Phe Gln Ser Leu Leu
5 10 15

Leu His His Val Cys Arg Asn Leu Val Leu Phe Ser Val Tyr Leu His
20 25 30

Ile Thr Leu Lys Thr Leu Leu Phe Glu Asn Phe Ser Ile Ser Gln Ile
35 40 45

Asn Ile His Phe His Asn Leu Pro Leu Xaa
50 55

<210> 1741

<211> 94

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(94)

<223> Xaa = Any amino acid

<400> 1741

Gln Gln Lys Gln Asn Phe Arg Phe Gln Asn Leu Leu Leu Ala Lys Phe

610

	5		10		15
Ile Leu Ile Ile Pro Ala Ser Tyr Gly Tyr Ile Thr Ile Lys Thr Glu					
	20		25		30
Tyr His Arg Val Ile Ala Leu Phe Glu Asn Ser Xaa Ile Leu Gln Cys					
	35		40		45
Thr Ser Pro Met Lys Gln Xaa Ile Ser Ile Leu Lys Ile Lys Arg Lys					
	50		55		60
Gln His Arg Glu Val Lys Cys Gly Val Ala Lys Leu Trp Gly Leu Leu					
	65		70		75
					80
Glu Gly Thr Asn Leu Asn Arg Leu Phe Leu Leu Ser Leu Glu					
	85		90		

<210> 1742

<211> 93

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(93)

<223> Xaa = Any amino acid

<400> 1742

Val Asn Leu Tyr Phe His Gly Tyr Ser Lys Glu Arg Arg Asn Asn Leu					
	5		10		15
Leu Arg Leu Val Pro Ser Ser Arg Pro His Asn Phe Ala Thr Pro His					
	20		25		30
Leu Thr Ser Leu Cys Cys Phe Leu Leu Ile Phe Lys Met Glu Ile Xaa					
	35		40		45
Cys Phe Ile Gly Glu Val His Cys Lys Met Xaa Glu Phe Ser Asn Asn					
	50		55		60
Ala Ile Thr Leu Trp Tyr Ser Val Leu Ile Val Ile Tyr Pro Tyr Glu					
	65		70		75
					80
Ala Gly Ile Met Arg Ile Asn Phe Ala Asn Asn Lys Phe					
	85		90		

<210> 1743

<211> 62

<212> PRT

<213> Homo sapiens

<400> 1743

Val Phe Leu Ser Pro Trp Val Lys Ser Glu Ser Gly Ser Leu Cys Leu					
	5		10		15
Ser Val Leu Val Tyr Cys Trp Ser Glu Ser Lys Phe Leu Ile Lys Ala					
	20		25		30
Val Asp Leu Ala Pro Thr Val Tyr Ala Asp Ile Gly Glu Thr Ile Trp					
	35		40		45

611

Leu Phe Gln Thr Ser Gln Asp Leu Ser Lys Lys Thr Trp Leu
 50 55 60

<210> 1744
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 1744
 Glu Pro Cys Phe Ile Thr Arg Ser Ser Tyr Ser Asn Pro Val Met Phe
 5 10 15
 Glu Ile Thr Lys Leu Ser Leu Gln Cys Leu His Lys Leu Trp Glu Pro
 20 25 30
 Ser Gln Gln Leu Leu Ser Arg Ile Tyr Ser Leu Thr Ser Asn Lys Gln
 35 40 45
 Ala Leu Arg Asp Thr Glu Ser Gln Ile Gln Ile Leu Pro Met Gly Ile
 50 55 60
 Lys Arg Leu Arg Leu Ser Pro His Leu Glu Asn Tyr Leu His His Lys
 65 70 75 80
 Tyr Ile Ile Thr Gly Ser Leu Tyr Glu Ala Asp Thr Lys Cys Tyr Arg
 85 90 95
 His Ser Gln Asn Ile Ile Leu Gly Asn Asn Val Ile Lys Met Pro Asn
 100 105 110
 Leu Ser Gln Gln
 115

<210> 1745
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 1745
 Leu Gly Gly Pro Gly Lys Gly Leu Gly His Glu Pro Gly Ser Ser Glu
 5 10 15
 Ala Val Thr Glu Ala Arg Glu Pro Ala Pro Arg Ser Trp Gly Asp Leu
 20 25 30
 Ala Leu Thr Pro Gly Leu Gly Ala His Leu Gln Thr Thr Ser Leu Pro
 35 40 45
 Leu Ser Ala Ala Ser Leu Cys Pro His Arg Trp Leu Ser Gly Gln Cys
 50 55 60
 Pro Gly Pro Arg Arg Cys Asp Leu Pro Pro Cys Gln Pro Cys Cys His
 65 70 75 80
 Pro Cys Pro Ala Ala Gly Arg
 85

<210> 1746
 <211> 113
 <212> PRT

<213> Homo sapiens

<400> 1746

Trp Gly Val Arg Glu Arg Gly Trp Ala Met Ser Gln Ala Ala Pro Lys
 5 10 15

 Gln Ser Leu Arg Pro Gly Ser Leu His Pro Gly His Gly Ala Thr Trp
 20 25 30

 Leu Ser Leu Leu Ala Trp Val Leu Thr Tyr Arg Pro Leu His Phe Pro
 35 40 45

 Cys Pro Gln Arg His Tyr Val Leu Ile Gly Gly Cys Leu Val Asn Val
 50 55 60

 Gln Ala Leu Val Gly Val Ile Phe Leu His Ala Ser Leu Ala Val Ile
 65 70 75 80

 Leu Val Gln Gln Gln Glu Asp Arg His Asp Asp Glu Glu Asp Asp Gln
 85 90 95

 Gln Arg Leu Asp His Asp Asp Thr Ile Leu Gln Arg Val Pro Leu Leu
 100 105 110

Gln

<210> 1747

<211> 79

<212> PRT

<213> Homo sapiens

<400> 1747

Leu Lys Gln Arg Asn Thr Leu Lys Asp Gly Ile Ile Met Ile Gln Thr
 5 10 15

 Leu Leu Ile Ile Leu Phe Ile Ile Val Pro Ile Phe Leu Leu Leu Asp
 20 25 30

 Lys Asp Asp Ser Lys Ala Gly Met Glu Glu Asp His Thr Tyr Glu Gly
 35 40 45

 Leu Asp Ile Asp Gln Thr Ala Thr Tyr Glu Asp Ile Val Thr Leu Arg
 50 55 60

 Thr Gly Glu Val Lys Trp Ser Val Gly Glu His Pro Gly Gln Glu
 65 70 75

<210> 1748

<211> 52

<212> PRT

<213> Homo sapiens

<400> 1748

Arg Thr Ile Gly Gly Cys Arg His Val Leu Leu Glu Gln Leu Pro Arg
 5 10 15

 Thr Thr Leu Leu Arg Ser Gly Phe Gln Arg Pro Pro Asn Phe Val Ser
 20 25 30

 Phe Asn Ser Phe Arg Pro Asp Leu Leu Phe Gly Ser Val Thr Gly Arg

613

35 40 45

Gln Val Ser Thr
50

<210> 1749
<211> 115
<212> PRT
<213> Homo sapiens

<400> 1749
His Met Pro Asp Trp Leu Phe Ala Thr His Leu Lys Asp Thr Thr Gln
5 10 15
Ser Met Glu Ala Phe Asn Arg Thr Ala Leu Pro Ile Ser Gly Leu Leu
20 25 30
Ala Asp Ala Asp Met Phe Tyr Ser Ser Ser Tyr Gln Gly Pro Leu Tyr
35 40 45
Cys Asp Gln Asp Ser Asn Asp His Leu Ile Ser Tyr Leu Ser Thr Leu
50 55 60
Phe Asp Arg Thr Ser Tyr Ser Glu Ala Leu Gln Glu Asp Arg Ser Gln
65 70 75 80
Leu Arg Asp Gln Ile Thr Leu Ser Thr Leu Trp Asp Arg Cys Asn Leu
85 90 95
Ala Leu Gln Gly Ser Ala Pro Ile Thr Ser Arg Pro Ala Asn Thr Asp
100 105 110
Leu Glu Val
115

<210> 1750
<211> 52
<212> PRT
<213> Homo sapiens

<400> 1750
Val Glu Thr Cys Leu Pro Val Thr Leu Pro Asn Lys Arg Ser Gly Arg
5 10 15
Lys Glu Leu Lys Asp Thr Lys Leu Gly Gly Arg Trp Asn Pro Asp Arg
20 25 30
Ser Lys Val Val Leu Gly Asn Cys Ser Ser Arg Thr Cys Leu His Pro
35 40 45
Pro Ile Val Arg
50

<210> 1751
<211> 56
<212> PRT
<213> Homo sapiens

<400> 1751
Asn Met Ser Ser Ala Ser Ala Asn Ser Pro Leu Ile Gly Arg Ala Val Arg

5 10 15
 Leu Lys Ala Ser Ile Asp Trp Val Val Ser Phe Lys Trp Val Ala Lys
 20 25 30
 Ser Gln Ser Gly Ile Cys His Glu Gly Phe Ser Asp Arg Leu Met Val
 35 40 45
 Cys Cys Leu Thr Ser Leu Gly Lys
 50 55

<210> 1752
 <211> 86
 <212> PRT
 <213> Homo sapiens

<400> 1752
 Glu Pro Ser Gln Gln Leu Leu Ser Arg Ile Tyr Ser Leu Thr Ser Asn
 5 10 15
 Lys Gln Ala Leu Arg Asp Thr Glu Ser Gln Ile Gln Ile Leu Pro Met
 20 25 30
 Gly Ile Lys Arg Leu Arg Leu Ser Pro His Leu Glu Asn Tyr Leu His
 35 40 45
 His Lys Tyr Ile Ile Thr Gly Ser Leu Tyr Glu Ala Asp Thr Lys Cys
 50 55 60
 Tyr Arg His Ser Gln Asn Ile Ile Leu Gly Asn Asn Val Ile Lys Met
 65 70 75 80
 Pro Asn Leu Ser Gln Gln
 85

<210> 1753
 <211> 62
 <212> PRT
 <213> Homo sapiens

<400> 1753
 Val Phe Leu Ser Pro Trp Val Lys Ser Glu Ser Gly Ser Leu Cys Leu
 5 10 15
 Ser Val Leu Val Tyr Cys Trp Ser Glu Ser Lys Phe Leu Ile Lys Ala
 20 25 30
 Val Asp Leu Ala Leu Thr Val Tyr Ala Asp Ile Gly Glu Thr Ile Trp
 35 40 45
 Leu Phe Gln Thr Ser Gln Asp Leu Ser Lys Lys Thr Trp Leu
 50 55 60

<210> 1754
 <211> 191
 <212> PRT
 <213> Homo sapiens

<400> 1754
 Pro Lys Glu Val Arg Gln Leu Ala Glu Asp Phe Leu Lys Asp Tyr Ile

615

5					10					15					
His	Ile	Asn	Ile	Gly	Ala	Leu	Glu	Leu	Ser	Ala	Asn	His	Asn	Ile	Leu
			20					25					30		
Gln	Ile	Val	Asp	Val	Cys	His	Asp	Val	Glu	Lys	Asp	Glu	Lys	Leu	Ile
			35					40					45		
Arg	Leu	Met	Glu	Glu	Ile	Met	Ser	Glu	Lys	Glu	Asn	Lys	Thr	Ile	Val
			50					55					60		
Phe	Val	Glu	Thr	Lys	Arg	Arg	Cys	Asp	Glu	Leu	Thr	Arg	Lys	Met	Arg
			65					70					75		
Arg	Asp	Gly	Trp	Pro	Ala	Met	Gly	Ile	His	Gly	Asp	Lys	Ser	Gln	Gln
				85					90					95	
Glu	Arg	Asp	Trp	Val	Leu	Asn	Glu	Phe	Lys	His	Gly	Lys	Ala	Pro	Ile
			100					105					110		
Leu	Ile	Ala	Thr	Asp	Val	Ala	Ser	Arg	Gly	Leu	Asp	Val	Glu	Asp	Val
			115					120					125		
Lys	Phe	Val	Ile	Asn	Tyr	Asp	Tyr	Pro	Asn	Ser	Ser	Glu	Asp	Tyr	Ile
			130					135					140		
His	Arg	Ile	Gly	Arg	Thr	Ala	Arg	Ser	Thr	Lys	Thr	Gly	Thr	Ala	Tyr
				145				150					155		
Thr	Phe	Phe	Thr	Pro	Asn	Asn	Ile	Lys	Gln	Val	Ser	Asp	Leu	Ile	Ser
				165				170					175		
Val	Leu	Arg	Glu	Ala	Asn	Gln	Ala	Ile	Asn	Pro	Lys	Leu	Leu	Gln	
			180					185					190		

<210> 1755

<211> 51

<212> PRT

<213> Homo sapiens

<400> 1755

Leu	Lys	Gln	Leu	Gly	Ile	Asn	Cys	Leu	Ile	Ser	Phe	Thr	Lys	His	Arg
				5					10					15	

Asp	Lys	Val	Ala	His	Leu	Leu	Tyr	Val	Ile	Arg	Cys	Lys	Glu	Ser	Val
			20					25					30		

Cys	Cys	Ala	Cys	Phe	Gly	Thr	Ala	Ser	Ser	Ser	Ser	Asn	Ser	Met	Asn
			35					40					45		

Ile	Ile	Leu
		50

<210> 1756

<211> 51

<212> PRT

<213> Homo sapiens

<400> 1756

Asn	Pro	Val	Thr	Leu	Leu	Leu	Thr	Leu	Val	Thr	Met	Asp	Thr	His	Gly
				5				10						15	

Arg Pro Pro Ile Ser Pro His Phe Ser Gly Lys Leu Ile Thr Ser Ser
 20 25 30

Phe Gly Phe His Lys Asn Asn Gly Phe Ile Leu Leu Leu Thr His Asp
 35 40 45

Leu Phe His
 50

<210> 1757
 <211> 55
 <212> PRT
 <213> Homo sapiens

<400> 1757
 Leu Leu Ser Pro Trp Ile Pro Met Ala Gly His Pro Ser Leu Leu Ile
 5 10 15

Phe Leu Val Ser Ser Ser His Leu Leu Leu Val Ser Thr Lys Thr Met
 20 25 30

Val Leu Phe Ser Phe Ser Leu Met Ile Ser Ser Ile Arg Arg Ile Ser
 35 40 45

Phe Ser Ser Phe Ser Thr Ser
 50 55

<210> 1758
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 1758
 Leu Gly Gly Pro Gly Lys Gly Leu Gly His Glu Pro Gly Ser Ser Glu
 5 10 15

Ala Val Thr Glu Ala Arg Glu Pro Ala Pro Arg Ser Trp Gly Asp Leu
 20 25 30

Ala Leu Thr Pro Gly Leu Gly Ala His Leu Gln Thr Thr Ser Leu Pro
 35 40 45

Leu Ser Ala Ala Ser Leu Cys Pro His Arg Trp Leu Ser Gly Gln Cys
 50 55 60

Pro Gly Pro Arg Arg Cys Asp Leu Pro Pro Cys Gln Pro Cys Cys His
 65 70 75 80

Pro Cys Pro Ala Ala Gly Arg
 85

<210> 1759
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 1759
 Trp Gly Val Arg Glu Arg Gly Trp Ala Met Ser Gln Ala Ala Pro Lys
 5 10 15

Gln Ser Leu Arg Pro Gly Ser Leu His Pro Gly His Gly Ala Thr Trp
 20 25 30
 Leu Ser Leu Leu Ala Trp Val Leu Thr Tyr Arg Pro Leu His Phe Pro
 35 40 45
 Cys Pro Gln Arg His Tyr Val Leu Ile Gly Gly Cys Leu Val Asn Val
 50 55 60
 Gln Ala Leu Val Gly Val Ile Phe Leu His Ala Ser Leu Ala Val Ile
 65 70 75 80
 Leu Val Gln Gln Gln Glu Asp Arg His Asp Asp Glu Glu Asp Asp Gln
 85 90 95
 Gln Arg Leu Asp His Asp Asp Thr Ile Leu Gln Arg Val Pro Leu Leu
 100 105 110
 Gln

<210> 1760
 <211> 79
 <212> PRT
 <213> Homo sapiens

<400> 1760
 Leu Lys Gln Arg Asn Thr Leu Lys Asp Gly Ile Ile Met Ile Gln Thr
 5 10 15
 Leu Leu Ile Ile Leu Phe Ile Ile Val Pro Ile Phe Leu Leu Leu Asp
 20 25 30
 Lys Asp Asp Ser Lys Ala Gly Met Glu Glu Asp His Thr Tyr Glu Gly
 35 40 45
 Leu Asp Ile Asp Gln Thr Ala Thr Tyr Glu Asp Ile Val Thr Leu Arg
 50 55 60
 Thr Gly Glu Val Lys Trp Ser Val Gly Glu His Pro Gly Gln Glu
 65 70 75

<210> 1761
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 1761
 Ile Ser Thr Ser Leu Leu Leu Met Leu Leu Val Ser Ser Leu Ser Pro
 5 10 15
 Val Gln Gly Val Leu Glu Val Tyr Tyr Thr Ser Leu Arg Cys Arg Cys
 20 25 30
 Val Gln Glu Ser Ser Val Phe Ile Pro Arg Arg Phe Ile Asp Arg Ile
 35 40 45
 Gln Ile Leu Pro Arg Gly Asn Gly Cys Pro Arg Lys Glu Ile Ile Val
 50 55 60

618

Trp Lys Lys Asn Lys Ser Ile Val Cys Val Asp Pro Gln Ala Glu Trp
 65 70 75 80

Ile Gln Arg Met Met Glu Val Leu Arg Lys Arg Ser Ser Ser Thr Leu
 85 90 95

Pro Val Pro Val Phe Lys Arg Lys Ile Pro
 100 105

<210> 1762
 <211> 53
 <212> PRT
 <213> Homo sapiens

<400> 1762
 Ile Phe Ser Arg Lys Lys Asn Phe Pro Ile Gln Ile Ser Met Arg Leu
 5 10 15

Cys Lys Asn Asn Leu Ala Glu Ala Asp Gly Ala Asn Ser Ser Phe Phe
 20 25 30

Thr His Ser Thr Leu Tyr Thr Leu Gly Val Cys Ile Leu Ile His Arg
 35 40 45

Gly Gly Lys Phe Leu
 50

<210> 1763
 <211> 55
 <212> PRT
 <213> Homo sapiens

<400> 1763
 Glu Lys Glu Val Leu Gln Leu Tyr Gln Phe Gln Cys Leu Arg Glu Arg
 5 10 15

Phe Pro Asp Ala Asp Ile Ser Thr Lys Asn Thr Cys Ile Leu Pro Leu
 20 25 30

Ser Leu Leu Trp Ile Leu Val Leu Cys Leu Val Lys Ser Phe Pro Gly
 35 40 45

Lys Arg Thr Ser Pro Tyr Lys
 50 55

<210> 1764
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 1764
 Asp Tyr Val Lys Ile Thr Leu Gln Lys Leu Met Gly Gln Thr Gln Ala
 5 10 15

Ser Ser Leu Thr Ala Pro Tyr Ile His Leu Glu Phe Ala Phe Leu Phe
 20 25 30

Ile Gly Glu Glu Ser Phe Phe Glu Asn Ser Tyr Ser Val Ile Ser Asn
 35 40 45

Thr Gly Leu
50

<210> 1765
<211> 51
<212> PRT
<213> Homo sapiens

<400> 1765
Ser His Ala Tyr Leu Tyr Gly Glu Val Leu Phe Pro Gly Lys Asp Leu
5 10 15

Thr Lys His Lys Thr Lys Ile Gln Ser Arg Asp Lys Gly Arg Met Gln
20 25 30

Val Phe Leu Val Glu Ile Ser Ala Ser Gly Asn Leu Ser Leu Lys His
35 40 45

Trp Asn Trp
50

<210> 1766
<211> 101
<212> PRT
<213> Homo sapiens

<400> 1766
Ser His Leu Leu Glu Gly Gly Gln Arg Gly Gln Asp Gly Ala Ala Asp
5 10 15

Pro His Gly Val Leu Ala Leu Arg Arg Ser Asn Asp Leu Asp Leu His
20 25 30

Cys Ala Gly Cys Gln Gly Ser Asp Leu Leu Leu His Pro Val Gly Asn
35 40 45

Ala Arg Val His Gly Gly Ala Ala Arg Gln His Cys Val Gly Val Gln
50 55 60

Val Phe Ala Asp Val His Val Thr Leu His Asp Gly Val Glu Gly Ser
65 70 75 80

Phe Val Asp Ala Thr Gly Leu His Ala Gln Glu Gly Arg Leu Glu Glu
85 90 95

Cys Leu Arg Ala Ala
100

<210> 1767
<211> 124
<212> PRT
<213> Homo sapiens

<400> 1767
Val Ile Val Arg Leu Glu Ala Phe Ala Val Asp Asp Gly Gly Ala Gly
5 10 15

Leu Val Ile Leu Leu Leu Ala Asp His Ile Cys Trp Lys Val Asp Ser
20 25 30

620

Glu Ala Arg Met Glu Pro Pro Ile His Thr Glu Tyr Leu Arg/ Ser Gly
 35 40 45
 Gly Ala Met Ile Leu Ile Phe Ile Val Leu Gly Ala Arg Ala Val Ile
 50 55 60
 Ser Phe Cys Ile Leu Ser Ala Met Pro Gly Tyr Met Val Val Pro Pro
 65 70 75 80
 Asp Ser Thr Val Leu Ala Tyr Arg Ser Leu Arg Met Ser Thr Ser His
 85 90 95
 Phe Met Met Glu Leu Lys Val Val Ser Trp Met Pro Gln Asp Ser Met
 100 105 110
 Pro Arg Lys Glu Gly Trp Lys Ser Ala Ser Gly Gln
 115 120

<210> 1768
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 1768
 Arg Cys Pro Glu Ala Leu Phe Gln Pro Ser Phe Leu Gly Met Glu Ser
 5 10 15
 Cys Gly Ile His Glu Thr Thr Phe Asn Ser Ile Met Lys Cys Asp Val
 20 25 30
 Asp Ile Arg Lys Asp Leu Tyr Ala Asn Thr Val Leu Ser Gly Gly Thr
 35 40 45
 Thr Met Tyr Pro Gly Ile Ala Asp Arg Met Gln Lys Glu Ile Thr Ala
 50 55 60
 Leu Ala Pro Ser Thr Met Lys Ile Lys Ile Ile Ala Pro Pro Glu Arg
 65 70 75 80
 Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser Leu Ser Thr
 85 90 95
 Phe Gln Gln Met
 100

<210> 1769
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 1769
 Thr Leu Pro Pro Asp Arg Met Lys Phe Ile Ser Thr Ser Leu Leu Leu
 5 10 15
 Met Leu Leu Val Ser Ser Leu Ser Pro Val Gln Gly Val Leu Glu Val
 20 25 30
 Tyr Tyr Thr Ser Leu Arg Cys Arg Cys Val Gln Glu Ser Ser Val Phe
 35 40 45
 Ile Pro Arg Arg Phe Ile Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn

50 55 60
 Gly Cys Pro Arg Lys Glu Ile Ile Val Trp Lys Lys Asn Lys Ser Ile
 65 70 75 80
 Ala Cys Val Asp Pro Gln Ala Glu Trp Ile Gln Arg Met Met Glu Val
 85 90 95
 Leu Arg Lys Arg Ser Ser Ser Thr Pro Pro Val Pro Val Phe Lys Arg
 100 105 110
 Lys Ile Pro
 115

<210> 1770
 <211> 53
 <212> PRT
 <213> Homo sapiens

<400> 1770
 Ile Phe Ser Arg Lys Lys Asn Phe Pro Ile Gln Ile Ser Met Arg Leu
 5 10 15
 Cys Lys Asn Asn Leu Ala Glu Ala Asp Gly Ala Asn Ser Ser Phe Phe
 20 25 30
 Thr His Ser Thr Leu Tyr Thr Leu Gly Val Cys Ile Leu Ile His Gln
 35 40 45
 Gly Gly Lys Phe Leu
 50

<210> 1771
 <211> 55
 <212> PRT
 <213> Homo sapiens

<400> 1771
 Glu Lys Glu Val Leu Gln Leu His Gln Phe Gln Cys Leu Arg Glu Arg
 5 10 15
 Phe Pro Asp Ala Asp Ile Ser Thr Lys Asn Thr Cys Ile Leu Pro Leu
 20 25 30
 Ser Leu Leu Trp Ile Leu Val Leu Cys Leu Val Lys Ser Phe Pro Gly
 35 40 45
 Lys Arg Thr Ser Pro Tyr Lys
 50 55

<210> 1772
 <211> 53
 <212> PRT
 <213> Homo sapiens

<400> 1772
 Ser His Ala Tyr Leu Tyr Gly Glu Val Leu Phe Pro Gly Lys Asp Leu
 5 10 15
 Thr Lys His Lys Thr Lys Ile Gln Ser Arg Asp Lys Gly Arg Met Gln

20 25 30
 Val Phe Leu Val Glu Ile Ser Ala Ser Gly Asn Leu Ser Leu Lys His
 35 40 45

Trp Asn Trp Trp Ser
 50

<210> 1773
 <211> 54
 <212> PRT
 <213> Homo sapiens

<400> 1773
 Leu Gly Gln Glu Leu Cys Pro Val Pro Ala Ala Phe Ile Ser Thr His
 5 10 15

Val His Ser Leu Leu Arg Pro Arg Pro Pro Gly Ile Cys Pro Gly Leu
 20 25 30

Pro His Pro Thr Ser Ile Arg Ser Cys Pro Arg Cys Met Ser Ser Ile
 35 40 45

Gly Arg Ile Ala Arg Trp
 50

<210> 1774
 <211> 63
 <212> PRT
 <213> Homo sapiens

<400> 1774
 Gly Pro Gly Ala Val Pro Ser Ala Cys Ser Leu His Lys His Thr Arg
 5 10 15

Pro Phe Pro Thr Lys Ala Gln Thr Ser Trp Tyr Leu Pro Arg Ala Pro
 20 25 30

Ser Ser His Leu His Pro Glu Leu Pro Lys Met His Val Gln His Arg
 35 40 45

Gln Asp Cys Ser Val Val Arg Arg Leu Gly Pro Ala Gln Thr Glu
 50 55 60

<210> 1775
 <211> 68
 <212> PRT
 <213> Homo sapiens

<400> 1775
 Gly Glu Arg Pro Arg Val Gly Thr Gly Asn Leu Arg Arg Ala Gly Asn
 5 10 15

Gly Ser Leu Arg Phe Arg Lys Leu Leu Cys Lys Leu Arg Gly Trp Leu
 20 25 30

Gly Pro Lys Gly Cys Ser Ala Arg Arg Ala Ser Cys Glu Leu Ser Lys
 35 40 45

Ala Leu Gly Ser Gln His Pro Lys Ser Leu Trp Leu Gln Ser Cys Val

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50              55              60

Cys Thr Thr His
65

<210> 1776
<211> 72
<212> PRT
<213> Homo sapiens

<400> 1776
Gly Ile Arg Ser Gln Leu Ser Leu Asn Ser Gln Ser Pro Pro Trp Ala
              5              10              15
Ser Leu Pro Asn Asp Leu Val Ala Leu Gly Ala Pro Glu Val Asn Pro
              20              25              30
Glu Ile Leu Pro Pro Ser Thr Leu Gly Ser Asp Leu Cys Pro Ser Leu
              35              40              45
Cys His Lys Glu Ile Ser Val Lys Arg Val Gly Thr Gly Gly Phe Arg
              50              55              60
Pro Cys Ser Lys Ala Thr Ala Arg
65              70

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<210> 1777
<211> 52
<212> PRT
<213> Homo sapiens

<400> 1777
Val Leu Arg Gln Ile Leu Ser Leu Leu Ile Gln Ser Glu Pro Asp Leu
              5                                10                    15

Thr Phe Ser Pro Pro Ser Asn Pro Ala Tyr Ala Gly His Ala Ser Trp
              20                                25                    30

Ala Thr Pro Asp Gly Gly Gly Met Arg Glu Pro Gly Ala Asp Thr Arg
              35                                40                    45

Arg Ser Gly Pro
              50

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<210> 1778
<211> 60
<212> PRT
<213> Homo sapiens

<400> 1778
Ser His Arg Leu Leu Gly Cys Cys Glu Pro Arg Ala Leu Leu Ser Ser
          5                                10                                15
Gln Leu Ala Arg Arg Ala Glu Gln Pro Phe Gly Pro Ser His Pro Arg
          20                                25                                30
Ser Leu His Arg Ser Phe Leu Asn Leu Arg Asp Pro Phe Pro Ala Leu
          35                                40                                45
Leu Lys Phe Pro Val Pro Thr Leu Gly Leu Ser Pro

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50

55

60

<210> 1779

<211> 52

<212> PRT

<213> Homo sapiens

<400> 1779

Asn Thr Pro Ser Val Asn Ser Gly Leu Arg Pro Leu Pro Phe Ser Val
 5 10 15

Ser Gln Gly Asn Phe Gly Gln Glu Gly Gly Asn Arg Trp Phe Gln Thr
 20 25 30

Val Gln Gln Ser His Cys Gln Val Ser Phe Lys Ala Asn Phe Ile Ser
 35 40 45

Ser Tyr Ser Val
 50

<210> 1780

<211> 78

<212> PRT

<213> Homo sapiens

<400> 1780

Cys Pro Arg Trp Gly Thr Pro Arg Tyr Trp Leu Gly Ala Leu Tyr Arg
 5 10 15

Asn Gln Gln Ser Ser Pro Thr Ala Pro Pro Gly Leu Leu Pro Leu Glu
 20 25 30

Tyr Phe Pro Ala Ala Pro His Cys Ser His Ser Arg Gln Trp Arg Cys
 35 40 45

Ser Gln Thr His Arg Ile His His His Pro Gln Met Leu Gly Pro Cys
 50 55 60

Arg Gln Glu Ile Cys Gly Glu Ile Gln Gly Cys Gly Trp Phe
 65 70 75

<210> 1781

<211> 134

<212> PRT

<213> Homo sapiens

<400> 1781

Asn Leu Leu Ile Glu Pro Gln Gln Gly Ala Asp Asn Cys Asp Val Asn
 5 10 15

Gln Cys His Ser Phe Ala His Gln Lys Ser Pro Arg Leu Gln Val Ser
 20 25 30

Ile Gln Gln Pro Gln Asn Ser Pro His Phe Leu Leu Cys Ile Leu Ser
 35 40 45

Gly Leu Phe Val Val Val His Asp Ala Gln Gly Gly Glu His Pro Gly
 50 55 60

Thr Gly Trp Gly His Tyr Ile Gly Ile Ser Lys Ala His Pro Leu His

65						70						75						80
His	Leu	Gly	Cys	Cys	Leu	Trp	Ser	Thr	Ser	Pro	Gln	Leu	Leu	Ile	Ala			
				85					90					95				
His	Ile	Val	Gly	Asn	Gly	Val	Ala	Leu	Lys	His	Thr	Glu	Ser	Ile	Ile			
				100					105					110				
Thr	Leu	Lys	Cys	Trp	Asp	Leu	Ala	Gly	Arg	Lys	Phe	Ala	Glu	Lys	Phe			
				115					120					125				
Arg	Gly	Ala	Val	Gly	Leu													
						130												

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<210> 1782
<211> 66
<212> PRT
<213> Homo sapiens
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<400> 1782
Ala Ser Ser Ser Pro Arg Ile Arg Leu Thr Ser Ser Phe Ala Phe Ser
      5                      10                      15

Val Ala Cys Leu Leu Trp Cys Met Met Pro Lys Val Gly Asn Thr Gln
      20                      25                      30

Val Leu Ala Gly Gly Thr Ile Ser Glu Ser Ala Lys Leu Thr His Cys
      35                      40                      45

Thr Thr Trp Ala Ala Ala Ser Gly Val Leu Pro Arg Ser Ser Ser Leu
      50                      55                      60

Leu Thr
      65

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<210> 1783
<211> 141
<212> PRT
<213> Homo sapiens
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<400> 1783
Gln Thr Asn Arg Thr Pro Glu Phe Leu Arg Lys Phe Pro Ala Gly Lys
      5                      10                      15

Val Pro Ala Phe Glu Gly Asp Asp Gly Phe Cys Val Phe Glu Ser Asn
      20                      25                      30

Ala Ile Ala Ala Tyr Tyr Val Ser Asn Glu Glu Leu Arg Gly Ser Thr Pro
      35                      40                      45

Glu Ala Ala Ala Gln Val Val Gln Trp Val Ser Phe Ala Asp Ser Asp
      50                      55                      60

Ile Val Pro Pro Ala Ser Thr Trp Val Phe Pro Thr Leu Gly Ile Met
      65                      70                      75                      80

His His Asn Lys Gln Ala Thr Glu Asn Ala Lys Glu Glu Val Arg Arg
      85                      90                      95

Ile Leu Gly Leu Leu Asp Ala Tyr Leu Lys Thr Arg Thr Phe Leu Val
      100                      105                      110

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Gly Glu Arg Val Thr Leu Val Asp Ile Thr Val Val Cys Thr Leu Leu
 115 120 125

Trp Leu Tyr Lys Gln Val Leu Glu Pro Ser Phe His Gln
 130 135 140

<210> 1784
 <211> 53
 <212> PRT
 <213> Homo sapiens

<400> 1784
 Phe Phe Phe Leu His Arg Ile Gly Arg Gly Gly Arg Phe Gly Arg Lys
 5 10 15

Gly Val Ala Ile Asn Phe Val Thr Glu Glu Asp Lys Arg Ile Leu Arg
 20 25 30

Asp Ile Glu Thr Phe Tyr Asn Thr Thr Val Glu Glu Met Pro Met Asn
 35 40 45

Val Ala Asp Leu Ile
 50

<210> 1785
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(51)
 <223> Xaa = Any amino acid

<400> 1785
 Lys Met Gly Ser Val Lys Ser Phe Phe Leu Arg Asn Leu Phe Pro Ser
 5 10 15

Ser Val Glu Met Xaa Xaa Leu Asp Val Leu Tyr His Leu Ile Ile Tyr
 20 25 30

Ile Xaa Thr Lys Arg Tyr Lys Cys Xaa Ile Lys Ser Ala Asn Tyr Val
 35 40 45

Lys Leu Ala
 50

<210> 1786
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 1786
 Ser Pro Ile Gln Gln Gln Arg Ala Leu His Pro Lys Leu Ser Ser Gln
 5 10 15

Glu Leu Asn Lys Val Ser His Ile His Gly His Leu Leu His Cys Ser
 20 25 30

Ile Val Glu Ser Leu Asn Val Thr Lys Asn Pro Leu Val Phe Phe Ser
35 40 45

Asn Lys Val Tyr Ser His Thr Phe Pro Pro Lys Ser Thr Pro Ser Ala
50 55 60

Asn Ser Val
65

<210> 1787

<211> 58

<212> PRT

<213> Homo sapiens

<400> 1787

Lys Val Ser Met Ser Arg Arg Ile Leu Leu Ser Ser Ser Val Thr Lys
5 10 15

Phe Ile Ala Thr Pro Phe Leu Pro Asn Arg Pro Pro Leu Pro Ile Leu
20 25 30

Cys Lys Lys Lys Asn Gln Asn Val Thr Ser His Ile Met Tyr Lys Leu
35 40 45

Leu Asn Met Thr Ile His Leu Leu Thr Thr
50 55

<210> 1788

<211> 61

<212> PRT

<213> Homo sapiens

<400> 1788

Cys His Lys Arg Ser Leu Pro Ile Cys Thr Tyr Ser Gln Glu Glu His
5 10 15

Leu Tyr Gly Lys Asp Gly Ser Pro Val Ser Leu Pro Tyr Thr Leu Gln
20 25 30

Gly Leu Ser Glu Ala Ser Leu Met Arg Cys Leu Lys Pro Gly His Gly
35 40 45

Tyr Lys Gln Leu His Gly Ser Lys Lys Phe Cys Pro Phe
50 55 60

<210> 1789

<211> 51

<212> PRT

<213> Homo sapiens

<400> 1789

Ser Ile Phe Trp Gly Tyr Asp Gly Leu Thr Phe Ile Arg Lys Tyr Gly
5 10 15

Phe Ile Leu Ile Val Ala Ser Ser Ser Gly Gly Val Asn His Phe Ile
20 25 30

Phe Thr Leu Thr Trp Phe Glu Phe Leu Ser His Tyr Cys Ile Tyr Phe
35 40 45

Ala Phe Pro
50

<210> 1790
<211> 192
<212> PRT
<213> Homo sapiens

<400> 1790
Leu Leu Trp Lys Gly Ser Phe Lys Pro Ser Glu His Val Lys Pro Arg
5 10 15
Ala Pro Gly Asn Leu Thr Val His Thr Asn Val Ser Asp Thr Leu Leu
20 25 30
Leu Thr Trp Ser Asn Pro Tyr Pro Pro Asp Asn Tyr Leu Tyr Asn His
35 40 45
Leu Thr Tyr Ala Val Asn Ile Trp Ser Glu Asn Asp Pro Ala Asp Phe
50 55 60
Arg Ile Tyr Asn Val Thr Tyr Leu Glu Pro Ser Leu Arg Ile Ala Ala
65 70 75 80
Ser Thr Leu Lys Ser Gly Ile Ser Tyr Arg Ala Arg Val Arg Ala Trp
85 90 95
Ala Gln Cys Tyr Asn Thr Thr Trp Ser Glu Trp Ser Pro Ser Thr Lys
100 105 110
Trp His Asn Ser Tyr Arg Glu Pro Phe Glu Gln His Leu Leu Leu Gly
115 120 125
Val Ser Ala Ser Cys Ile Val Ile Leu Ala Val Cys Leu Leu Cys Tyr
130 135 140
Val Ser Ile Thr Lys Ile Lys Lys Glu Trp Trp Asp Gln Ile Pro Asn
145 150 155 160
Pro Ala Arg Ser Arg Leu Val Ala Ile Ile Ile Gln Asp Ala Gln Gly
165 170 175
Ser Gln Trp Glu Lys Arg Ser Arg Gly Gln Glu Pro Ala Lys Cys Pro
180 185 190

<210> 1791
<211> 75
<212> PRT
<213> Homo sapiens

<400> 1791
Gly Pro Gly Leu Ser Ala Ile Thr Pro Pro Gly Val Ser Gly Ala Pro
5 10 15
Ala Pro Ser Gly Thr Thr Pro Thr Gly Ser Pro Ser Ser Thr Ser
20 25 30
Cys Trp Ala Ser Ala Leu Pro Ala Leu Ser Ser Trp Pro Ser Ala Cys
35 40 45
Cys Ala Met Ser Ala Ser Pro Arg Leu Arg Lys Asn Gly Gly Ile Arg

629

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      50              55              60
Phe Pro Thr Gln Pro Ala Ala Ala Ser Trp Leu
 65                70                75

<210> 1792
<211> 64
<212> PRT
<213> Homo sapiens

<400> 1792
Arg Pro Ala Gly Gly Ala Ala Arg Arg Ala Pro Cys Arg Ser Cys Ala
          5                      10
Thr Trp Cys Trp Gly Ser Thr His Ser Arg Trp Cys Tyr Ser Thr Glu
          20                      25                      30
Pro Arg Pro Ser Pro Val Pro Cys Arg Lys Ser Gln Thr Ser Gly Cys
          35                      40                      45
Trp Leu Arg Cys Gly Gly Arg Val Leu Gly Arg Ser Arg Tyr Arg Phe
  50                55                60

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<210> 1793
<211> 104
<212> PRT
<213> Homo sapiens

<400> 1793
Pro Leu Ser Ile Leu Asp Tyr Tyr Ser His Glu Ala Ala Ala Gly Trp
          5                      10                      15
Val Gly Asn Leu Ile Pro Pro Phe Phe Leu Asn Leu Gly Asp Ala Asp
          20                      25                      30
Ile Ala Gln Gln Ala Asp Gly Gln Asp Asp Asn Ala Gly Ser Ala Asp
          35                      40                      45
Ala Gln Gln Glu Val Leu Leu Glu Gly Leu Pro Val Gly Val Val Pro
          50                      55                      60
Leu Gly Ala Gly Ala Pro Leu Thr Pro Gly Gly Val Ile Ala Leu Ser
          65                      70                      75                      80
Pro Gly Pro His Pro Cys Pro Val Gly Asn Pro Arg Leu Gln Gly Ala
          85                      90                      95
Gly Cys Asp Ala Glu Gly Gly Phe
          100

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<210> 1794
<211> 71
<212> PRT
<213> Homo sapiens

<400> 1794
Val Gly His Val Ile Asp Ser Glu Ile Cys Arg Val Val Phe Thr Pro
          5                               10                               15
Asn Val Asp Cys Ile Gly Glu Met Ile Ile Gln Val Ile Val Arg Gly

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630

	20		25		30
Ile Arg Val Ala Pro Gly Gln Gln Gln Ser Val Gly Asp Ile Gly Val	35		40		45
Asn Cys Gln Val Ser Trp Gly Pro Gly Phe His Met Leu Ala Gly Leu	50		55		60
Glu Gly Ala Leu Pro Gln Gln	65		70		

<210> 1795
 <211> 115
 <212> PRT
 <213> Homo sapiens

Thr Leu Pro Pro Asp Arg Met Lys Phe Ile Ser Thr Ser Leu Leu Leu	5		10		15
Met Leu Leu Val Ser Ser Leu Ser Pro Val Gln Gly Val Leu Glu Val	20		25		30
Tyr Tyr Thr Ser Leu Arg Cys Arg Cys Val Gln Glu Ser Ser Val Phe	35		40		45
Ile Pro Arg Arg Phe Ile Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn	50		55		60
Gly Cys Pro Arg Lys Glu Ile Ile Val Trp Lys Lys Asn Lys Ser Ile	65		70		75
Val Cys Val Asp Pro Gln Ala Glu Trp Ile Gln Arg Met Met Glu Val	85		90		95
Leu Arg Lys Arg Ser Ser Ser Thr Leu Pro Val Pro Val Phe Lys Arg	100		105		110
Lys Ile Pro	115				

<210> 1796
 <211> 55
 <212> PRT
 <213> Homo sapiens

Glu Lys Glu Val Leu Gln Leu Tyr Gln Phe Gln Cys Leu Arg Glu Arg	5		10		15
Phe Pro Asp Ala Asp Ile Ser Thr Lys Asn Thr Cys Ile Leu Pro Leu	20		25		30
Ser Leu Leu Trp Ile Leu Val Leu Cys Leu Val Lys Ser Phe Pro Gly	35		40		45
Lys Arg Thr Ser Pro Tyr Lys	50		55		

<210> 1797

<211> 51
<212> PRT
<213> Homo sapiens

<400> 1797
Ser His Ala Tyr Leu Tyr Gly Glu Val Leu Phe Pro Gly Lys Asp Leu
 5 10 15
Thr Lys His Lys Thr Lys Ile Gln Ser Arg Asp Lys Gly Arg Met Gln
 20 25 30
Val Phe Leu Val Glu Ile Ser Ala Ser Gly Asn Leu Ser Leu Lys His
 35 40 45
Trp Asn Trp
 50

<210> 1798
<211> 54
<212> PRT
<213> Homo sapiens

<400> 1798
Pro Val Leu Arg Gln Ile Trp Gly Trp Gly Glu His Phe Gly Leu Lys
 5 10 15
Ala Gln Ser Ser Leu Pro Cys Phe Phe Cys Ala Tyr His Ser Pro Leu
 20 25 30
Ala Ser Thr Ser Val Arg Trp Gly Gly Asp Lys Lys Arg Ser Lys Val
 35 40 45
Lys Lys Lys Val Glu Asn
 50

<210> 1799
<211> 56
<212> PRT
<213> Homo sapiens

<400> 1799
Asp Gly Gly Gly Thr Lys Arg Glu Val Lys Leu Arg Arg Lys Trp Lys
 5 10 15
Ile Lys Lys Lys Met Ser Lys Phe Leu His Ala Tyr Ile Ser Ala Tyr
 20 25 30
Ala Glu Asp Leu Pro Val Cys Cys Thr Leu Asn His Thr Phe Arg Thr
 35 40 45
Pro Gln Lys Pro Ser Leu Ser Pro
 50 55

<210> 1800
<211> 59
<212> PRT
<213> Homo sapiens

<400> 1800
Asn Lys Lys Ala Met Leu Val Glu Cys Thr Val His Ile Gly Gly Ala

632

	5		10		15
Arg Leu Ile Thr	Ile Arg Leu Leu Ala Ser Pro Val Gln Ser Phe Leu				
20		25		30	
Trp Lys Ala Val Asp Phe Ser Leu Ala Ser Leu Ser Ser Ser Val Ser					
35		40		45	
Thr Tyr Arg Ile Ser Arg Ser Gln Pro Tyr Arg					
50		55			

<210> 1801
 <211> 64
 <212> PRT
 <213> Homo sapiens

Thr Ala Lys Arg Ser Lys Ile Arg Arg Gln Cys Leu Trp Asn Val Gln					
5		10		15	
Cys Ile Leu Ala Ala His Ala Ser Leu Arg Phe Ala Cys Leu Leu Leu					
20		25		30	
Leu Phe Asn Arg Phe Phe Gly Arg Gln Trp Ile Phe Leu Leu Arg Leu					
35		40		45	
Cys Leu Leu Gln Phe Arg Leu Ile Glu Phe Leu Asp Leu Ser His Ile					
50		55		60	

<210> 1802
 <211> 57
 <212> PRT
 <213> Homo sapiens

Glu Gly Asn Ala Cys Gly Met Tyr Ser Ala Tyr Trp Arg Arg Thr Pro					
5		10		15	
His Tyr Asp Ser Pro Ala Cys Phe Ser Cys Ser Ile Val Ser Leu Glu					
20		25		30	
Gly Ser Gly Phe Phe Ser Cys Val Ser Val Phe Phe Ser Phe Asp Leu					
35		40		45	
Ser Asn Phe Ser Ile Ser Ala Ile Ser					
50		55			

<210> 1803
 <211> 51
 <212> PRT
 <213> Homo sapiens

Arg Arg Gln Arg Arg Lys Arg Lys Ile His Cys Leu Pro Lys Lys Arg					
5		10		15	
Leu Asn Arg Arg Ser Lys Gln Ala Asn Arg Asn Glu Ala Cys Ala Ala					
20		25		30	
Asn Met His Cys Thr Phe His Lys His Cys Leu Leu Ile Leu Leu Leu					

35 40 45

Leu Ala Val
50

<210> 1804
<211> 74
<212> PRT
<213> Homo sapiens

<400> 1804
Met Asp Arg Gly Pro Lys Arg Lys Arg Tyr Leu Lys Thr Asn Gly Arg
5 10 15
Asn Leu Glu Ala His Asp Pro Glu Pro Arg Lys Asp Arg Ser Leu Lys
20 25 30
Thr Trp Gly Asn Pro Lys Met Arg Thr Leu Asn Pro Thr Ser Phe Leu
35 40 45
Leu Phe Thr Leu Leu Thr Leu Arg Tyr Phe Gln Phe Ser Cys Leu Ser
50 55 60
Leu Ser Leu Ile Leu Leu Arg Cys Thr Phe
65 70

<210> 1805
<211> 77
<212> PRT
<213> Homo sapiens

<400> 1805
Gly Ser His Leu Gly Ile Ser Pro Gly Leu Gln Ala Ser Ile Leu Pro
5 10 15
Gly Phe Trp Val Met Gly Leu Gln Ile Pro Ala Val Ser Leu Glu Ile
20 25 30
Pro Phe Ser Leu Gly Ser Ser Ile His Leu Gly Arg Leu Cys Asp Arg
35 40 45
Gly Leu Pro Ser Leu Gly Cys Arg Ser Ser Ser Tyr Asn Pro Gly Leu
50 55 60
Ile Leu Gly Arg Trp Pro Cys Val Thr Ser Leu Ser Ser
65 70 75

<210> 1806
<211> 85
<212> PRT
<213> Homo sapiens

<400> 1806
Tyr Cys Gln Ser Lys Gly Asn Arg Gln His Gln Lys Val His Leu Lys
5 10 15
Arg Ile Arg Leu Lys Asp Lys Gln Glu Asn Trp Lys Tyr Leu Arg Val
20 25 30
Arg Ser Val Asn Asn Arg Lys Glu Val Gly Phe Arg Val Leu Ile Leu

634

35 40 45
 Gly Phe Pro Gln Val Phe Lys Leu Leu Ser Phe Leu Gly Ser Gly Ser
 50 55 60
 Trp Ala Ser Arg Phe Arg Pro Leu Val Leu Arg Tyr Leu Phe Arg Leu
 65 70 75 80
 Gly Pro Leu Ser Ile
 85

<210> 1807
 <211> 50
 <212> PRT
 <213> Homo sapiens

<400> 1807
 Asp Arg Tyr Trp Tyr Ser Phe Ile Ile Glu Thr Lys Arg Ser Ala Leu
 5 10 15
 Leu Asp Phe Pro Leu Phe Val Leu Lys Gly Ile Lys Asp Cys Arg Phe
 20 25 30
 Pro Ala Leu Ser Ser Arg Gly His Tyr Glu Gln Ile Lys Trp Lys Asp
 35 40 45
 Lys Phe
 50

<210> 1808
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 1808
 Trp Pro Arg Glu Asp Arg Ala Gly Asn Leu Gln Ser Leu Ile Pro Phe
 5 10 15
 Arg Thr Lys Ser Gly Lys Ser Ser Lys Ala Asp Leu Leu Val Ser Ile
 20 25 30
 Ile Lys Glu Tyr Gln Tyr Arg Ser Gln Lys Arg Ser Val Ser Leu Gln
 35 40 45
 Gly Tyr Phe
 50

<210> 1809
 <211> 92
 <212> PRT
 <213> Homo sapiens

<400> 1809
 Arg Ala Gly Leu Glu Ala Leu Leu Ala Pro Lys Pro Leu Phe His Ala
 5 10 15
 Thr Val Leu Arg Gly Met Cys Pro Gln Cys Thr Ala Thr Arg Thr Gln
 20 25 30
 Leu Asn Glu Leu Pro Gly Lys His Tyr Ser Pro Thr Ser Thr Leu Gly

35 40 45
 Gly Cys Leu Ser Phe Pro Thr Thr Gly Ile Ser Pro Ser Ala Pro Ala
 50 55 60
 Ser Ser Leu His Pro Lys Ser Ser Val Val Ser Val Leu Glu Gly Thr
 65 70 75 80
 Val Gly Pro Leu Arg Leu Lys Phe Asn Thr Pro Gln
 85 90

<210> 1810
 <211> 50
 <212> PRT
 <213> Homo sapiens

<400> 1810
 Gly Val Leu Asn Phe Asn Leu Arg Gly Pro Thr Val Pro Ser Lys Thr
 5 10 15
 Glu Thr Thr Glu Leu Leu Gly Trp Arg Leu Glu Ala Gly Ala Glu Gly
 20 25 30
 Leu Ile Pro Val Val Gly Lys Leu Arg Gln Pro Pro Lys Val Glu Val
 35 40 45
 Gly Glu
 50

<210> 1811
 <211> 66
 <212> PRT
 <213> Homo sapiens

<400> 1811
 Val Thr Pro Phe Pro Phe Pro Glu Ile Gly Thr Ser Tyr Ser Lys Gly
 5 10 15
 Glu Arg Arg Ala Gln Arg Asp Leu Tyr Arg Thr Ser Leu Ala His Gly
 20 25 30
 Asp Trp Arg Gln Arg Val Gly Ser Trp Arg Gly Val Gln Ser Leu Gln
 35 40 45
 Gln Ile Leu Arg Ala Ser Lys Ser Ser Ser Trp Thr Phe Leu Leu Ile
 50 55 60
 Trp Ile
 65

<210> 1812
 <211> 83
 <212> PRT
 <213> Homo sapiens

<400> 1812
 Lys Ser Arg Leu Arg Glu Thr Ser Arg Lys Ser Ser Leu Lys Pro Ser
 5 10 15
 Ile Phe Val Gly Gly Thr Gly Leu Leu Ser Ser Ser Pro Pro Ser Ala

20 25 30
 Ser Ser His His Val Gln Glu Arg Ser Cys Thr Asp Leu Ser Gly Leu
 35 40 45
 Ser Phe Leu Leu Trp Asn Asn Leu Phe Leu Phe Gln Glu Arg Glu Met
 50 55 60
 Val Ser Leu Arg Pro Trp Thr Ala Ser Pro Ala Arg Leu Gly Pro Gln
 65 70 75 80
 Val Pro Leu

<210> 1813
 <211> 82
 <212> PRT
 <213> Homo sapiens

<400> 1813
 Ser Pro Gln Tyr Leu Leu Glu Gly Leu Asp Ser Ser Pro Ala Pro His
 5 10 15
 Pro Leu Pro Pro Val Thr Met Cys Lys Arg Gly Pro Val Gln Ile Ser
 20 25 30
 Leu Gly Ser Pro Phe Ser Phe Gly Ile Thr Cys Ser Tyr Phe Arg Lys
 35 40 45
 Gly Lys Trp Cys His Ser Gly Pro Gly Leu Leu Leu Gln Pro Gly Trp
 50 55 60
 Gly His Arg Ser His Ser Ser Glu Gly Gln Cys Leu Arg Ile Lys Ala
 65 70 75 80
 Val Phe

<210> 1814
 <211> 53
 <212> PRT
 <213> Homo sapiens

<400> 1814
 Ile Gln Ile Lys Arg Asn Val Gln Glu Glu Leu Phe Glu Ala Leu Asn
 5 10 15
 Ile Cys Trp Arg Asp Trp Thr Pro Leu Gln Leu Pro Thr Leu Cys Leu
 20 25 30
 Gln Ser Pro Cys Ala Arg Glu Val Leu Tyr Arg Ser Leu Trp Ala Leu
 35 40 45
 Leu Ser Pro Leu Glu
 50

<210> 1815
 <211> 116
 <212> PRT
 <213> Homo sapiens

<220>

<221> variant

<222> (1)...(116)

<223> Xaa = Any amino acid

<400> 1815

Pro Lys Glu Val Arg Gln Leu Ala Glu Asp Phe Leu Lys Asp Tyr Ile
 5 10 15

His Ile Asn Ile Gly Ala Leu Glu Leu Ser Ala Asn His Asn Ile Leu
 20 25 30

Gln Ile Val Asp Val Cys His Asp Xaa Xaa Lys Asp Glu Lys Leu Ile
 35 40 45

Xaa Leu Met Glu Glu Ile Met Ser Glu Lys Glu Asn Lys Thr Ile Val
 50 55 60

Phe Val Glu Thr Lys Arg Arg Cys Asp Glu Leu Thr Arg Lys Met Arg
 65 70 75 80

Arg Asp Gly Trp Pro Ala Met Gly Ile His Xaa Asp Lys Ser Gln Gln
 85 90 95

Glu Arg Asp Trp Ala Leu Asn Glu Ser Lys His Gly Lys Ala Pro Ile
 100 105 110

Leu Ile Xaa Thr
 115

<210> 1816

<211> 51

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(51)

<223> Xaa = Any amino acid

<400> 1816

Ser Pro Val Thr Leu Leu Leu Thr Leu Val Xaa Met Asp Thr His Gly
 5 10 15

Arg Pro Pro Ile Ser Pro His Phe Ser Gly Lys Leu Ile Thr Ser Ser
 20 25 30

Phe Gly Phe His Lys Asn Asn Gly Phe Ile Leu Leu Leu Thr His Asp
 35 40 45

Leu Phe His
 50

<210> 1817

<211> 55

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1) . . . (55)

<223> Xaa = Any amino acid

<400> 1817

Leu Leu Xaa Pro Trp Ile Pro Met Ala Gly His Pro Ser Leu Leu Ile
5 10 15

Phe Leu Val Ser Ser Ser His Leu Leu Leu Val Ser Thr Lys Thr Met
20 25 30

Val Leu Phe Ser Phe Ser Leu Met Ile Ser Ser Ile Arg Xaa Ile Ser
35 40 45

Phe Ser Ser Phe Xaa Xaa Ser
50 55

<210> 1818

<211> 63

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1) ... (63)

<223> Xaa = Any amino acid

<400> 1818

Gly Gly Lys Met Ala Val Gln Ile Ser Lys Lys Arg Lys Phe Val Ala
5 10 15

Asp Gly Ile Phe Lys Ala Glu Leu Asn Glu Phe Leu Thr Arg Glu Leu
20 25 30

Ala Glu Asp Gly Tyr Ser Gly Val Glu Gly Ala Ser Tyr Thr Asn Gln
35 40 45

Asp Arg Asn His Tyr Leu Xaa His Gln Asn Thr Xaa Cys Ser Trp
50 55 60

<210> 1819

<211> 70

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1) ... (70)

<223> Xaa = Any amino acid

<400> 1819

Met Ser Phe Leu Leu Gly Ser Trp Leu Lys Met Ala Thr Leu Glu Leu
5 10 15

Arg Val Arg Val Thr Pro Thr Arg Thr Glu Ile Ile Ile Leu Xaa Thr
20 25 30

Arg Thr Xaa Asn Val Leu Gly Glu Lys Gly Arg Arg Ile Arg Glu Leu
35 40 45

Thr Ala Val Val Gln Lys Arg Phe Gly Phe Pro Glu Gly Ser Val Glu
50 55 60

Leu Tyr Ala Xaa Lys Val
65 70

<210> 1820
<211> 76
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(76)
<223> Xaa = Any amino acid

<400> 1820
Thr Thr Ala Val Ser Ser Arg Ile Arg Arg Pro Phe Ser Pro Arg Thr
5 10 15
Xaa Cys Val Leu Val Xaa Lys Ile Met Ile Ser Val Leu Val Gly Val
20 25 30
Thr Arg Thr Leu Asn Ser Arg Val Ala Ile Phe Ser Gln Leu Pro Ser
35 40 45
Lys Lys Leu Ile Gln Phe Ser Phe Glu Asp Ala Ile Ser Asp Lys Leu
50 55 60
Pro Leu Leu Gly Tyr Leu His Cys His Leu Ala Ala
65 70 75

<210> 1821
<211> 70
<212> PRT
<213> Homo sapiens

<400> 1821
Pro Met Trp Leu Val Phe Ser Leu Gln Leu Ala Arg Phe His Thr Leu
5 10 15
Thr Ser Leu Ser Gln Pro Gln Glu Thr Met Ile Gly Leu Leu Leu Leu
20 25 30
Gly Glu Lys Arg Thr Gln Asp Thr His Ser Glu Trp Leu Ser Ser Trp
35 40 45
Thr Val Tyr Leu His Thr Pro Arg Val Phe His Ser Leu Met Val Leu
50 55 60
Ser Arg Asp Pro Lys Thr
65 70

<210> 1822
<211> 70
<212> PRT
<213> Homo sapiens

<400> 1822
Ile Val Phe Gly Ser Arg Asp Lys Thr Ile Lys Leu Trp Asn Thr Leu
5 10 15

Gly Val Cys Lys Tyr Thr Val Gln Asp Glu Ser His Ser Glu Trp Val
 20 25 30
 Ser Cys Val Arg Phe Ser Pro Asn Ser Ser Asn Pro Ile Ile Val Ser
 35 40 45
 Cys Gly Trp Asp Lys Leu Val Lys Val Trp Asn Leu Ala Asn Cys Lys
 50 55 60
 Leu Lys Thr Asn His Ile
 65 70

<210> 1823
 <211> 64
 <212> PRT
 <213> Homo sapiens

<400> 1823
 Leu Phe Leu Asp Leu Glu Ile Lys Pro Ser Ser Tyr Gly Ile Pro Trp
 5 10 15
 Val Cys Ala Asn Thr Leu Ser Arg Met Arg Ala Thr Gln Ser Gly Cys
 20 25 30
 Leu Val Ser Ala Ser Arg Pro Thr Ala Ala Thr Leu Ser Ser Ser Pro
 35 40 45
 Val Ala Gly Thr Ser Trp Ser Arg Tyr Gly Thr Trp Leu Thr Ala Ser
 50 55 60

<210> 1824
 <211> 74
 <212> PRT
 <213> Homo sapiens

<400> 1824
 Ala Ala Arg Glu Pro Val Trp Ala Gly Ser Val Cys Arg Arg Val Tyr
 5 10 15
 Gly Gln Ala Ala Phe Ala Gly Val Phe Thr Gly Arg Gln Arg Leu Gln
 20 25 30
 Ala Cys Leu His Ala Gly Val Ala Pro Cys Glu Thr Thr Gly Pro Gly
 35 40 45
 Phe Gln Arg Ser Cys Ser Gly Glu Ser Ala Val Phe Ser Gln Val His
 50 55 60
 Gly Ala Glu Trp Val Cys Asn Met Lys Tyr
 65 70

<210> 1825
 <211> 66
 <212> PRT
 <213> Homo sapiens

<400> 1825
 Leu Asp Asp Gly Leu Gln Pro Leu Ser Val Leu Ser Val Pro His Ser
 5 10 15

Thr Ser Ile Ser Cys Cys Thr Pro Thr Gln Leu Arg Glu Leu Val Arg
 20 25 30
 Thr Gln Pro Ile His Leu Ser Arg Thr Ser Glu Thr Leu Asp Gln Trp
 35 40 45
 Ser His Met Val Leu Arg Leu His Val Asn Thr Pro Ala Asn Ala Ala
 50 55 60
 Cys Arg
 65

<210> 1826
 <211> 76
 <212> PRT
 <213> Homo sapiens

<400> 1826
 Tyr Gly Asp Ser Leu Trp Lys Ser Ser Phe Pro Ser Phe Val Ser Leu
 5 10 15
 Pro Thr Met Gln Glu Ala Ser Leu Ala Val Leu Phe Tyr Tyr His Tyr
 20 25 30
 Ile Ser Pro Ile Cys Asn Lys Val Leu Tyr Arg Gln Val Arg Ser Met
 35 40 45
 Leu Ser Ser Ser Leu Ser Pro Arg Arg Leu Arg Leu Arg Tyr Arg Gly
 50 55 60
 Asn Ser Pro Val Gln Ser Leu Phe Met Leu Thr Gln
 65 70 75

<210> 1827
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 1827
 Trp Arg Gly Ser Gly Leu Leu Pro Gln Val Gln Pro Lys Glu Asp Ser
 5 10 15
 Arg Gln Gly Cys Pro Gln Leu Pro Glu Ala Gly Thr Lys Leu Arg Leu
 20 25 30
 Leu His Pro Ser Tyr Pro Val Leu Ala Pro Gln Ala Leu Ser Gly Arg
 35 40 45
 Ala Met Cys Arg Pro Lys Gly Ala Leu Gly Ala Ala
 50 55 60

<210> 1828
 <211> 95
 <212> PRT
 <213> Homo sapiens

<400> 1828
 Leu Ala Ser Tyr Ser Pro Ser Thr Thr Asp Met Ala Gln Ser Leu Ala
 5 10 15

Leu Ser Leu Leu Thr Leu Val Leu Ala Phe Gly Ile Pro Arg Thr Gln
 20 25 30
 Gly Ser Asp Gly Gly Ala Gln Asp Cys Cys Leu Lys Tyr Ser Gln Arg
 35 40 45
 Lys Ile Pro Ala Lys Val Val Arg Ser Tyr Arg Lys Gln Glu Pro Ser
 50 55 60
 Leu Gly Cys Ser Ile Pro Ala Ile Leu Phe Leu Pro Arg Lys Arg Ser
 65 70 75 80
 Gln Ala Glu Leu Cys Ala Asp Pro Lys Glu Leu Trp Val Gln Gln
 85 90 95

<210> 1829
 <211> 50
 <212> PRT
 <213> Homo sapiens

<400> 1829
 Ala Trp Phe Leu Leu Pro Val Ala Ala Asp Asn Leu Gly Gly Asn Leu
 5 10 15
 Pro Leu Ala Val Leu Glu Ala Thr Val Leu Ser Pro Ser Ile Thr Ala
 20 25 30
 Leu Gly Pro Gly Asp Ala Lys Gly Gln Asn Gln Gly Lys Glu Ala Gln
 35 40 45
 Ser Gln
 50

<210> 1830
 <211> 62
 <212> PRT
 <213> Homo sapiens

<400> 1830
 Val Ala Val Ser Ser Leu Arg His Gly Val Cys Ser Pro Thr Asp Ile
 5 10 15
 Gly Val Leu Arg Lys Gly Gly Val Ile Trp Gln Lys Cys His Phe Ala
 20 25 30
 Cys Cys Ile Gln Gly Ser Tyr Ser Thr Arg Tyr Cys Glu Leu Cys Ser
 35 40 45
 His Gln Leu Ala Gln Lys Gln Gln Thr Ala Leu Cys Cys Gln
 50 55 60

<210> 1831
 <211> 94
 <212> PRT
 <213> Homo sapiens

<400> 1831
 Trp Leu Ser Pro Leu Ser Ala Met Ala Cys Ala Arg Pro Leu Ile Ser
 5 10 15

643

Val Tyr Ser Glu Lys Gly Glu Ser Ser Gly Lys Asn Val Thr Leu Pro
 20 25 30
 Ala Val Phe Lys Ala Pro Ile Arg Pro Asp Ile Val Asn Phe Val His
 35 40 45
 Thr Asn Leu Arg Lys Asn Asn Arg Gln Pro Tyr Ala Val Ser Glu Leu
 50 55 60
 Ala Gly His Gln Thr Ser Ala Glu Ser Trp Gly Thr Gly Arg Ala Val
 65 70 75 80
 Ala Arg Ile Pro Arg Val Arg Gly Gly Gly Thr His Arg Ser
 85 90

<210> 1832
 <211> 102
 <212> PRT
 <213> Homo sapiens

<400> 1832
 Leu Pro Thr Ser Pro Ser Ala Leu Ala Ser Asp Ser Pro Ser Thr Thr
 5 10 15
 Asp Met Ala Gln Ser Leu Ala Leu Ser Leu Leu Ile Leu Val Leu Ala
 20 25 30
 Phe Gly Ile Pro Arg Thr Gln Gly Ser Asp Gly Gly Ala Gln Asp Cys
 35 40 45
 Cys Leu Lys Tyr Ser Gln Arg Lys Ile Pro Ala Lys Val Val Arg Ser
 50 55 60
 Tyr Arg Lys Gln Glu Pro Ser Leu Gly Cys Ser Ile Pro Ala Ile Leu
 65 70 75 80
 Phe Leu Pro Arg Lys Arg Ser Gln Ala Glu Leu Cys Ala Asp Pro Lys
 85 90 95
 Glu Leu Trp Val Gln Gln
 100

<210> 1833
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 1833
 Trp Arg Gly Ser Gly Leu Leu Pro Gln Val Gln Pro Lys Glu Asp Ser
 5 10 15
 Arg Gln Gly Cys Pro Gln Leu Pro Glu Ala Gly Thr Lys Leu Arg Leu
 20 25 30
 Leu His Pro Ser Tyr Pro Val Leu Ala Pro Gln Ala Leu Ser Gly Arg
 35 40 45
 Ala Met Cys Arg Pro Lys Gly Ala Leu Gly Ala Ala
 50 55 60

<210> 1834
 <211> 50
 <212> PRT
 <213> Homo sapiens

<400> 1834
 Ala Trp Phe Leu Leu Pro Val Ala Ala Asp Asn Leu Gly Gly Asn Leu
 5 10 15
 Pro Leu Ala Val Leu Glu Ala Thr Val Leu Ser Pro Ser Ile Thr Ala
 20 25 30
 Leu Gly Pro Gly Asp Ala Lys Gly Gln Asn Gln Asp Lys Glu Ala Gln
 35 40 45
 Ser Gln
 50

<210> 1835
 <211> 76
 <212> PRT
 <213> Homo sapiens

<400> 1835
 Thr Lys Leu Val Met Met Gln Lys Leu Leu Lys Cys Ser Arg Leu Val
 5 10 15
 Leu Ala Leu Ala Leu Ile Leu Val Leu Glu Ser Ser Val Gln Gly Tyr
 20 25 30
 Pro Thr Gln Arg Ala Arg Tyr Gln Trp Val Arg Cys Asn Pro Asp Ser
 35 40 45
 Asn Ser Ala Asn Cys Leu Glu Glu Lys Gly Pro Met Phe Glu Leu Leu
 50 55 60
 Pro Gly Glu Ser Asn Lys Ile Pro Arg Leu Arg Thr
 65 70 75

<210> 1836
 <211> 68
 <212> PRT
 <213> Homo sapiens

<400> 1836
 Cys Arg Ser Tyr Ser Asn Ala Val Gly Leu Ser Trp Leu Leu Pro Ser
 5 10 15
 Ser Trp Phe Trp Asn Pro Gln Phe Lys Val Ile Leu Arg Arg Glu Pro
 20 25 30
 Gly Thr Asn Gly Cys Ala Ala Ile Gln Thr Val Ile Leu Gln Thr Ala
 35 40 45
 Leu Lys Lys Lys Asp Gln Cys Ser Asn Tyr Phe Gln Val Asn Pro Thr
 50 55 60
 Arg Ser Pro Val
 65

<210> 1837
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 1837
 Ile Leu Thr Leu Tyr Ser Glu Pro Ser Phe Asn Thr Met Val Ser Phe
 5 10 15
 Leu Arg Ala Ser Arg Ser Pro Val Arg Ser Met Val Ile Gly Pro Gly
 20 25 30
 Ala Leu Ser Gln Thr Arg Val Ser Arg Val Thr Thr Thr Leu Gly Ala
 35 40 45
 Phe Gly Ser Val Thr Thr Gly Pro Ser Pro Ser Ser Val Phe Leu Tyr
 50 55 60
 Leu Ile Arg Leu Ser Ser Ser Leu Ser Ile Ser Cys Ser Ser Phe Arg
 65 70 75 80
 Asp Phe Cys Gly Gly Gly Leu
 85

<210> 1838
 <211> 55
 <212> PRT
 <213> Homo sapiens

<400> 1838
 His Asn Gly Phe Leu Phe Glu Gly Phe Gln Ile Ser Ser Lys Val His
 5 10 15
 Gly Asp Trp Ser Arg Gly Thr Leu Thr Asn Gln Gly Glu Pro Gly Asp
 20 25 30
 Asn Asp Ile Gly Gly Phe Arg Ile Cys His His Arg Thr Ile Ser Gln
 35 40 45
 Gln Arg Phe Leu Val Leu Asn
 50 55

<210> 1839
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 1839
 Leu Lys Lys Pro Gln Ser Pro His Val Glu Glu Asp Asp Asp Asp Glu
 5 10 15
 Leu Asp Ser Lys Leu Asn Tyr Lys Pro Pro Pro Gln Lys Ser Leu Lys
 20 25 30
 Glu Leu Gln Glu Met Asp Lys Asp Asp Glu Ser Leu Ile Lys Tyr Lys
 35 40 45
 Lys Thr Leu Leu Gly Asp Gly Pro Val Val Thr Asp Pro Lys Ala Pro
 50 55 60
 Asn Val Val Val Thr Arg Leu Thr Leu Val Cys Glu Ser Ala Pro Gly

646

65					70					75					80
Pro	Ile	Thr	Met	Asp	Leu	Thr	Gly	Asp	Leu	Glu	Ala	Leu	Lys	Lys	Glu
				85					90					95	
Thr	Ile	Val	Leu	Lys	Glu	Gly	Ser	Glu	Tyr	Arg	Val	Lys	Ile	His	Phe
			100					105					110		
Lys	Val	Asn	Arg	Asp	Ile	Val	Ser								
			115				120								

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<210> 1840
<211> 75
<212> PRT
<213> Homo sapiens
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<400> 1840
Glu Leu Gln Glu Glu Ser Gly Leu Glu Asp Ser Gln Arg Asn Lys Ser
      5                      10                      15

Arg Leu Asn Cys Ile Arg Tyr Ile Pro Ala Cys Trp Gln Leu His Lys
      20                      25                      30

Asn Ile Ser Asp Phe Asn Pro Asn Leu Ala Asn Glu Thr Gly Phe Leu
      35                      40                      45

Phe Phe Met Leu Cys Val Thr Glu Leu Lys Thr Gln Phe Pro Asn Pro
      50                      55                      60

Gln Phe Met Gln Pro Pro Ser Gly Ile Leu Ser
      65                      70                      75

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<210> 1841
<211> 59
<212> PRT
<213> Homo sapiens
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<400> 1841
Val Phe Ser Ser Val Thr His Asn Ile Lys Asn Lys Asn Pro Val Ser
      5                                10                                15

Leu Ala Lys Phe Gly Leu Lys Ser Glu Met Phe Leu Trp Ser Cys Gln
      20                                25                                30

Gln Ala Gly Met Tyr Leu Ile Gln Phe Asn Leu Leu Leu Phe Leu Trp
      35                                40                                45

Leu Ser Ser Lys Pro Leu Ser Ser Cys Asn Ser
      50                                55

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<210> 1842
<211> 51
<212> PRT
<213> Homo sapiens
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<400> 1842
Tyr Ser Leu Ile Cys Phe Tyr Phe Phe Gly Cys Leu Pro Asn His Phe
                    5                      10                      15
Leu Pro Val Ile Leu Lys Leu Ala Ser Pro Pro Ser Ser Glu Lys Leu

```

20 25 30
 Pro Leu Arg Ile Phe Leu Ile Val Arg Val Tyr Phe Arg Ile Glu Glu
 35 40 45

Ser Phe Gly
 50

<210> 1843
 <211> 74
 <212> PRT
 <213> Homo sapiens

<400> 1843
 Lys Lys Ser Leu Trp Tyr Phe Val Asn Val Ser Arg Leu Ser Cys Gln
 5 10 15

Cys Gln Lys Ile Leu Phe Met Asn Pro Val Gly Ile Pro Trp Tyr Leu
 20 25 30

Lys Lys Ile Pro Asn Ser Thr Ile His Glu Leu Phe Leu Ser Leu Lys
 35 40 45

Ser Lys Lys Lys Leu His His Thr Asn Tyr Lys Ile Gln Val Leu Glu
 50 55 60

Lys Ile Phe Phe Phe Ile Leu Lys Leu Phe
 65 70

<210> 1844
 <211> 50
 <212> PRT
 <213> Homo sapiens

<400> 1844
 Leu Lys Leu Thr Phe Cys Cys Leu Phe Lys Leu Met Met Tyr Phe Tyr
 5 10 15

Gln Thr Glu Thr Leu Lys Ser Ile Ile Ser Phe Asp Phe Ser Tyr His
 20 25 30

Pro Gln Ile Lys Pro Leu Leu Ser Lys Pro Leu Leu Val Lys Lys Val
 35 40 45

Leu Lys
 50

<210> 1845
 <211> 93
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(93)
 <223> Xaa = Any amino acid

<400> 1845
 Gly Asp Xaa Val Gly Xaa Gly Ala Gln Ala Ala Thr Met Ala Tyr His
 5 10 15

<210> 1848
<211> 53
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(53)
<223> Xaa = Any amino acid

<400> 1848
Ala Lys Gly Gly Phe Ile Lys Xaa Asn Gln Tyr Trp Ala Asn Pro Phe
 5 10 15

Xaa Pro Phe Phe Ser Phe Ser Met Xaa Ile Leu Phe Phe Xaa Tyr Ser
 20 25 30

Ser Ser Ser Cys Ser Lys Leu Lys Leu Gly Lys Glu Ser His Phe Xaa
 35 40 45

Leu Xaa Val Phe Leu
 50

<210> 1849
<211> 54
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(54)
<223> Xaa = Any amino acid

<400> 1849
Asn Xaa His Arg Lys Arg Glu Lys Gly Xaa Lys Gly Ile Gly Pro Ile
 5 10 15

Leu Ile Xaa Phe Tyr Lys Thr Ser Phe Gly Leu Glu Gly Met Thr Leu
 20 25 30

Ala Thr Ile Ile Xaa Ser Met Phe Lys Gln Val Pro Leu Val Val Ala
 35 40 45

Leu Asn Val Ile Xaa Leu
 50

<210> 1850
<211> 188
<212> PRT
<213> Homo sapiens

<400> 1850
Gln Val Leu Asp Ile Asn Leu Ala Ala Glu Pro Lys Val Asn Arg Gly
 5 10 15

Lys Ala Gly Val Lys Arg Ser Ala Ala Glu Met Tyr Gly Ser Val Thr
 20 25 30

Glu His Pro Ser Pro Ser Pro Leu Leu Ser Ser Ser Phe Asp Leu Asp

650

35 40 45
 Tyr Asp Phe Gln Arg Asp Tyr Tyr Asp Arg Met Tyr Ser Tyr Pro Ala
 50 55 60
 Arg Val Pro Pro Pro Pro Pro Ile Ala Arg Ala Val Val Pro Ser Lys
 65 70 75 80
 Arg Gln Arg Val Ser Gly Asn Thr Ser Arg Arg Gly Lys Ser Gly Phe
 85 90 95
 Asn Ser Lys Ser Gly Gln Arg Gly Ser Ser Lys Ser Gly Lys Leu Lys
 100 105 110
 Gly Asp Asp Leu Gln Ala Ile Lys Lys Glu Leu Thr Gln Ile Lys Gln
 115 120 125
 Lys Val Asp Ser Leu Leu Glu Asn Leu Glu Lys Ile Glu Lys Glu Gln
 130 135 140
 Ser Lys Gln Ala Val Glu Met Lys Asn Asp Lys Ser Glu Glu Glu Gln
 145 150 155 160
 Ser Ser Ser Ser Val Lys Lys Asp Glu Thr Asn Val Lys Met Glu Ser
 165 170 175
 Glu Gly Gly Ala Asp Asp Ser Ala Glu Glu Gly Asp
 180 185

<210> 1851

<211> 50

<212> PRT

<213> Homo sapiens

<400> 1851

Ser His Leu Ser Ser Arg Ser Cys Cys Ser Ala Pro Leu Leu Thr Tyr
 5 10 15
 His Ser Ser Ser Leu Leu Leu Val Cys Ser Val Pro Phe Gln Phe Phe
 20 25 30
 Pro Gly Phe Pro Gly Glu Asn Pro Leu Phe Val Leu Ser Gly Ser Ala
 35 40 45
 Pro Ser
 50

<210> 1852

<211> 66

<212> PRT

<213> Homo sapiens

<400> 1852

Leu Ile Ile Leu His Leu Tyr Cys Leu Phe Ala Leu Phe Leu Phe Asn
 5 10 15
 Phe Phe Gln Val Phe Gln Glu Arg Ile His Phe Leu Phe Tyr Leu Gly
 20 25 30
 Gln Leu Leu Leu Asn Gly Leu Lys Val Ile Ser Phe Gln Leu Ser Arg
 35 40 45

Leu Gly Arg Ser Pro Leu Ser Thr Leu Arg Ile Glu Ala Thr Phe Ala
 50 55 60

Pro Ser
 65

<210> 1853
 <211> 71
 <212> PRT
 <213> Homo sapiens

<400> 1853
 Ser Pro Ser Ser Ala Glu Ser Ser Ala Pro Pro Ser Asp Ser Ile Phe
 5 10 15

Thr Leu Val Ser Ser Phe Phe Thr Glu Leu Leu Leu Cys Ser Ser Ser
 20 25 30

Asp Leu Ser Phe Phe Ile Ser Thr Ala Cys Leu Leu Cys Ser Phe Ser
 35 40 45

Ile Phe Ser Arg Phe Ser Arg Arg Glu Ser Thr Phe Cys Phe Ile Trp
 50 55 60

Val Ser Ser Phe Leu Met Ala
 65 70

<210> 1854
 <211> 80
 <212> PRT
 <213> Homo sapiens

<400> 1854
 His Arg Gly Arg Gln Glu Ala Ile Ala Gly Gly His Leu Ser Leu Asp
 5 10 15

Gly Ser Ser Leu Val His Thr Val Pro Lys Lys Gly Leu Pro Leu Gly
 20 25 30

Pro Arg Asn Pro Ser Gln Pro Ser Gln Ala Glu Pro His Pro Gly Phe
 35 40 45

Ser Gln Arg Gly Ala Gln Glu Asp Pro Ser Cys Pro Lys Ser Glu Glu
 50 55 60

Gln Gln Glu Thr Ala Ser Glu Val Arg His Ser Ser Val Leu Leu Pro
 65 70 75 80

<210> 1855
 <211> 112
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(112)
 <223> Xaa = Any amino acid

<400> 1855

652

Met Glu Ala Pro Trp Ser Thr Gln Ser Gln Arg Lys Val Cys Leu Trp
 5 10 15

Ala His Glu Thr His Pro Ser Pro His Arg Leu Asn Leu Thr Leu Gly
 20 25 30

Phe Pro Arg Glu Val Pro Lys Lys Thr Gln Ala Ala Pro Ser Gln Arg
 35 40 45

Ser Ser Arg Lys Gln Pro Gln Lys Ser Val Thr Leu Gln Tyr Ser Ser
 50 55 60

Leu Arg Met Ser Thr Ser Cys Leu Val Thr Met Ala Thr Lys Arg Gln
 65 70 75 80

Trp Gln Cys Ser Ala Cys Gly Met Gly Glu Leu His Leu Pro Trp Val
 85 90 95

His Gly Glu Glu Thr Pro Val Thr Xaa Arg Ser Gly Glu Ser His Gly
 100 105 110

<210> 1856

<211> 127

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(127)

<223> Xaa = Any amino acid

<400> 1856

Pro Met Ala Leu Pro Ala Ser Xaa Gly His Trp Ser Leu Leu Pro Met
 5 10 15

Tyr Pro Arg Lys Met Glu Leu Pro His Pro Thr Arg Thr Ala Leu Pro
 20 25 30

Leu Ser Phe Gly Cys His Gly His Gln Thr Gly Ser Gly His Ser Lys
 35 40 45

Gly Gly Val Leu Lys Ser Asp Gly Leu Leu Arg Leu Phe Pro Ala Ala
 50 55 60

Pro Leu Thr Trp Gly Ser Leu Gly Leu Leu Gly His Leu Ser Gly Lys
 65 70 75 80

Thr Gln Gly Glu Val Gln Pro Val Arg Ala Gly Met Gly Phe Val Gly
 85 90 95

Pro Lys Ala Asp Leu Ser Leu Gly Leu Cys Gly Pro Arg Ser Phe His
 100 105 110

Leu Val Thr Ser Asp Pro Gln Leu Ser Pro Leu Ala Phe Pro Cys
 115 120 125

<210> 1857

<211> 51

<212> PRT

<213> Homo sapiens

<220>
<221> variant
<222> (1)...(51)
<223> Xaa = Any amino acid

<400> 1857
Pro Trp Leu Ser Pro Leu Leu Xaa Val Thr Gly Val Ser Ser Pro Cys
 5 10 15

Thr Gln Gly Arg Trp Ser Ser Pro Ile Pro His Ala Leu His Cys His
 20 25 30

Cys Leu Leu Val Ala Met Val Thr Lys Gln Glu Val Asp Ile Leu Arg
 35 40 45

Glu Glu Tyr
 50

<210> 1858
<211> 53
<212> PRT
<213> Homo sapiens

<400> 1858
Thr Lys Asp Tyr Leu Phe Lys Lys Ser Phe Glu Val Lys Tyr Phe Val
 5 10 15

Tyr Val Ile His Arg Cys Thr Tyr Lys His Thr His Ile Glu Ser Gln
 20 25 30

Tyr Phe Asn Thr Ser Leu Gly Ser Cys Thr Asn Ser Leu Thr Leu Arg
 35 40 45

Lys Lys Leu Arg Asn
 50

<210> 1859
<211> 57
<212> PRT
<213> Homo sapiens

<400> 1859
Tyr Ser Val Lys Leu Thr Asp Asn Leu Glu Ser Leu Ser Ser Phe Ile
 5 10 15

Phe Leu Thr Leu Gln Lys Gly Lys Glu Asp Lys His Ser Leu Pro Phe
 20 25 30

Tyr Leu Thr Asn Arg Arg Gly Thr Gln Phe Phe Ser Arg Leu Gly Thr
 35 40 45

Val Arg Glu Arg Trp Gly Lys Pro Phe
 50 55

<210> 1860
<211> 62
<212> PRT
<213> Homo sapiens

<400> 1860

Val Phe Leu Ser Pro Trp Val Lys Ser Glu Ser Gly Ser Leu Cys Leu
 5 10 15

Ser Val Leu Val Tyr Cys Trp Ser Glu Ser Lys Phe Leu Ile Lys Ala
 20 25 30

Val Asp Leu Ala Leu Thr Val Tyr Ala Asp Ile Gly Glu Thr Ile Trp
 35 40 45

Leu Phe Gln Thr Ser Gln Asp Leu Ser Lys Lys Thr Trp Leu
 50 55 60

<210> 1861
 <211> 86
 <212> PRT
 <213> Homo sapiens

<400> 1861
 Glu Pro Ser Gln Gln Leu Leu Ser Arg Ile Tyr Ser Leu Thr Ser Asn
 5 10 15

Lys Gln Ala Leu Arg Asp Thr Glu Ser Gln Ile Gln Ile Leu Pro Met
 20 25 30

Gly Ile Lys Arg Leu Arg Leu Ser Pro His Leu Glu Asn Tyr Leu His
 35 40 45

His Lys Tyr Ile Ile Thr Gly Ser Leu Tyr Glu Ala Asp Thr Lys Cys
 50 55 60

Tyr Arg His Ser Gln Asn Ile Ile Leu Gly Asn Asn Val Ile Lys Met
 65 70 75 80

Pro Asn Leu Ser Gln Gln
 85

<210> 1862
 <211> 58
 <212> PRT
 <213> Homo sapiens

<400> 1862
 Gln Arg His Cys Gln Trp Leu Arg Gly Leu His Ser His Gly Val Gly
 5 10 15

Asp Pro Gly Trp Gly Pro Asp Ala Ala Pro Ala Gly Ala Arg Arg His
 20 25 30

Pro Gly Gly Pro His Gln Ala Cys Gly His Cys Gly Leu Ala His His
 35 40 45

Ser Pro Glu Arg Ala Ala Gln Cys Arg Leu
 50 55

<210> 1863
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 1863

His	Thr	Ala	Pro	Val	Leu	Asp	Ile	Ala	Trp	Cys	Pro	His	Asn	Asp	Asn	
				5					10						15	
Val	Ile	Ala	Ser	Gly	Ser	Glu	Asp	Cys	Thr	Val	Met	Val	Trp	Glu	Ile	
			20					25					30			
Pro	Asp	Gly	Gly	Leu	Met	Leu	Pro	Leu	Arg	Glu	Pro	Val	Val	Thr	Leu	
		35					40					45				
Glu	Gly	His	Thr	Lys	Arg	Val	Gly	Ile	Val	Ala	Trp	His	Thr	Thr	Ala	
	50					55					60					
Gln	Asn	Val	Leu	Leu	Ser	Ala	Gly	Cys	Asp	Asn	Val	Ile	Met	Val	Trp	
65					70					75					80	
Asp	Val	Gly	Thr	Gly	Ala	Ala	Met	Leu	Thr	Leu	Gly	Pro	Glu	Val	His	
				85					90					95		
Pro	Asp	Thr	Ile	Tyr	Ser	Val	Asp	Trp	Ser	Arg	Asp	Gly				
			100					105								

```
<210> 1864
<211> 100
<212> PRT
<213> Homo sapiens
```

```
<400> 1864
Ile Val Ser Gly Cys Thr Ser Gly Pro Ser Val Ser Met Ala Ala Pro
                    5                                10                        15

Val Pro Thr Ser His Thr Met Ile Thr Leu Ser Gln Pro Ala Leu Ser
                20                                25                        30

Ser Thr Phe Trp Ala Val Val Cys Gln Ala Thr Met Pro Thr Arg Leu
                35                                40                        45

Val Trp Pro Ser Arg Val Thr Thr Gly Ser Arg Arg Gly Ser Ile Arg
                50                                55                        60

Pro Pro Ser Gly Ile Ser His Thr Met Thr Val Gln Ser Ser Glu Pro
        65                                70                                75                        80

Leu Ala Met Thr Leu Ser Leu Cys Gly His Gln Ala Met Ser Ser Thr
                85                                90                        95

Gly Ala Val Trp
            100
```

```
<210> 1865
<211> 103
<212> PRT
<213> Homo sapiens
```

<400> 1865
Ser Ile Ser Ala Pro Val His Thr Val Asp Arg Val Trp Val His Leu
 5 10 15
Trp Ala Gln Cys Gln His Gly Arg Pro Ser Ala His Val Pro His His
 20 25 30
Asp His Val Val Thr Thr Cys Thr Glu Gln His Val Leu Gly Cys Gly

656

```
<210> 1866
<211> 88
<212> PRT
<213> Homo sapiens
```

```
<210> 1867
<211> 157
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> variant
<222> (1)...(157)
<223> Xaa = Any amino acid
```

```
<400> 1867
Leu Xaa Xaa Lys Ala Gly Asp Gln Val Pro Gly Gly Gln Asp Ser Ala
      5                      10                    15

Leu Val Gly Pro Glu Asp Arg Gly Gly Pro Gly Ala Ser Gly Arg Glu
      20                25              30

Val Glu Gly His Arg Glu Ser Gln Glu Arg Gly His Ser Gln Asn Ser
      35                  40          45

Ser Gln Arg Leu Ala Ser Ser Pro Gly Ser Arg Ala Ala Gly Thr Ser
      50                55              60
```

Ser His Ser Gly Gly Thr Arg Trp Arg Gly Lys Thr Thr Lys Arg Val
 65 70 75 80
 Pro Val Phe Leu Arg Lys Arg Gly Cys Trp Pro Arg Val Leu Asp Arg
 85 90 95
 Gly Pro His Ala Leu Leu Ala Pro Ile Thr Pro Phe Arg Asp Cys His
 100 105 110
 Ala Glu Ser Ala Xaa Arg Lys Gly Asp Ser Lys Arg Glu Cys Gly Gln
 115 120 125
 Ala Cys Leu Arg Pro Ser Gly Arg Thr Pro Gly Leu Thr Xaa Arg Arg
 130 135 140
 Cys His His Phe Arg Phe Xaa Xaa Leu Phe Phe Phe Phe
 145 150 155

<210> 1868

<211> 156

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(156)

<223> Xaa = Any amino acid

<400> 1868

Xaa Xaa Xaa Arg Leu Val Thr Arg Ser Gln Ala Gly Lys Thr Gln Pro
 5 10 15
 Trp Trp Gly Leu Arg Thr Glu Glu Ala Gln Glu His Arg Gly Glu Arg
 20 25 30
 Trp Arg Asp Thr Gly Arg Ala Arg Ser Val Asp Thr Ala Arg Thr His
 35 40 45
 His Arg Gly Trp Arg Pro Val Pro Gly His Val Gln Gln Glu Gln Ala
 50 55 60
 Ala Thr Leu Gly Ala Pro Gly Gly Glu Ala Arg Arg Gln Arg Gly Cys
 65 70 75 80
 Pro Cys Ser Cys Glu Ser Gly Ala Ala Gly His Glu Cys Trp Thr Glu
 85 90 95
 Ala Pro Thr Leu Cys Leu Pro Pro Ser Arg Arg Ser Val Thr Val Thr
 100 105 110
 Gln Asn Leu Xaa Thr Gly Arg Glu Thr Leu Ser Gly Ser Ala Ala Lys
 115 120 125
 Pro Ala Ser Ala Arg Gln Gly Gly Leu Pro Gly Ser Leu Xaa Gly Gly
 130 135 140
 Ala Thr Ile Ser Ala Leu Xaa Ser Phe Ser Phe Ser
 145 150 155

<210> 1869

<211> 75

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(75)

<223> Xaa = Any amino acid

<400> 1869

Arg Ala Glu Ala Gly Leu Ala Ala Leu Pro Leu Arg Val Ser Leu Pro
 5 10 15

Xaa Cys Arg Phe Cys Val Thr Val Thr Glu Arg Arg Asp Gly Gly Lys
 20 25 30

Gln Ser Val Gly Ala Ser Val Gln His Ser Trp Pro Ala Ala Pro Leu
 35 40 45

Ser Gln Glu His Gly His Pro Leu Cys Arg Leu Ala Ser Pro Pro Gly
 50 55 60

Ala Pro Arg Val Ala Ala Cys Ser Cys Cys Thr
 65 70 75

<210> 1870

<211> 111

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(111)

<223> Xaa = Any amino acid

<400> 1870

Gln Ser Arg Asn Gly Val Met Gly Ala Ser Arg Ala Trp Gly Pro Leu
 5 10 15

Ser Ser Thr Arg Gly Gln Gln Pro Arg Phe Arg Lys Asn Thr Gly Thr
 20 25 30

Leu Phe Val Val Leu Pro Leu His Leu Val Pro Pro Glu Trp Leu Leu
 35 40 45

Val Pro Ala Ala Arg Asp Pro Gly Leu Asp Ala Ser Leu Cys Asp Glu
 50 55 60

Phe Trp Leu Cys Pro Arg Ser Trp Leu Ser Arg Cys Pro Ser Thr Ser
 65 70 75 80

Leu Pro Asp Ala Pro Gly Pro Pro Leu Ser Ser Gly Pro Thr Lys Ala
 85 90 95

Glu Ser Cys Pro Pro Gly Thr Trp Ser Pro Ala Phe Xaa Xaa Arg
 100 105 110

<210> 1871

<211> 104

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(104)

<223> Xaa = Any amino acid

<400> 1871

Trp Gly Gln Ala Glu Arg Gly Gly Leu Cys Pro Ala Leu Val Ala Ser
 5 10 15

 Ser Pro Ala Phe Ala Arg Thr Arg Ala Pro Ser Leu Ser Ser Cys Leu
 20 25 30

 Ser Thr Trp Cys Pro Gln Ser Gly Cys Leu Phe Leu Leu His Val Thr
 35 40 45

 Arg Asp Trp Thr Pro Ala Ser Val Met Ser Ser Gly Cys Val His Ala
 50 55 60

 Pro Gly Ser Pro Gly Val Pro Pro Pro Leu Ser Pro Met Leu Leu Gly
 65 70 75 80

 Leu Leu Cys Pro Gln Ala Pro Pro Arg Leu Ser Leu Ala Arg Leu Gly
 85 90 95

 Pro Gly His Gln Pro Xaa Xaa Xaa
 100

<210> 1872

<211> 53

<212> PRT

<213> Homo sapiens

<400> 1872

Ala Asn Thr Leu Ile Asn Gln Ser Pro Gly Lys Gln Leu Glu Cys Ile
 5 10 15

 Ile Leu Trp Ser Ser Ile Leu Cys Ser Cys Ala Asp Ile Ser Leu Ser
 20 25 30

 His Cys Val Ser Leu Ser Val Asp Thr Leu Lys Val Ala Leu Trp Lys
 35 40 45

 Met Ser Lys Phe Phe
 50

<210> 1873

<211> 67

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(67)

<223> Xaa = Any amino acid

<400> 1873

Lys Pro Pro Phe Phe Xaa Leu Leu Lys Arg Lys Gly Pro Gln Asp Thr
 5 10 15

 Ile Phe Glu Trp Leu Met Val Phe Lys Xaa Phe Arg Glu Leu Pro Ala
 20 25 30

Phe Tyr Leu Glu Thr Glu Lys Ala Arg Lys Ile Leu Ser Phe Leu Ala
 35 40 45

Cys Ile Ser Arg Val Gly Ala Asn Asp Ser Lys Leu Val Ser Lys Pro
 50 55 60

Ile Pro Leu
 65

<210> 1874
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 1874
 Pro Pro Arg Val Arg Ala Pro Ser Val Pro Gly Pro Arg Pro Ser Arg
 5 10 15

Gln Arg Ser Phe His Ser Ala Trp Asp Asp Gly Glu Glu Lys Asn Pro
 20 25 30

Asp Leu Pro His Pro Gly Pro Lys Glu Ser Ala Gly Asp Val His Gln
 35 40 45

Ala Glu Val Arg Ala Asp Glu Glu
 50 55

<210> 1875
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 1875
 Arg Arg Gly Ser Val Arg Pro Ala Ser Gln Gly Pro Gly Arg Ala Asp
 5 10 15

Lys Asp His Ser Thr Gln Pro Gly Thr Met Gly Arg Lys Lys Ile Gln
 20 25 30

Ile Ser Arg Ile Leu Asp Gln Arg Asn Arg Gln Val Thr Phe Thr Lys
 35 40 45

Arg Lys Phe Gly Leu Met Lys Lys
 50 55

<210> 1876
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 1876
 Leu Leu His Gln Pro Glu Leu Pro Leu Gly Glu Arg His Leu Pro Ile
 5 10 15

Pro Leu Val Gln Asp Ala Gly Asp Leu Asp Phe Phe Pro Pro His Arg
 20 25 30

Pro Arg Leu Ser Gly Met Ile Phe Val Cys Ser Ala Trp Ala Leu Gly
 35 40 45

Arg Trp Ala His Gly Pro Ala Ala
50 55

<210> 1877
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(51)
<223> Xaa = Any amino acid

<400> 1877
Thr Asn Gln Ser Leu Leu Arg Asn Cys Tyr Ser Leu Asn Trp Ser Ile
5 10 15

Lys Thr Ser His Gly Ser Gly Tyr Gly Val Ile Trp Cys Pro Cys Phe
20 25 30

Ser Pro Xaa Gly His Leu Ile Xaa Glu Pro Pro Xaa Glu Phe Cys Gly
35 40 45

Arg His Leu
50

<210> 1878
<211> 56
<212> PRT
<213> Homo sapiens

<400> 1878
Gly Val Phe Leu His Thr Phe Thr Ser Ser Ala Leu Ser Ile Tyr Thr
5 10 15

His Thr Gln His Pro Gln Tyr Leu Thr Ser Asn Arg Leu Tyr His Leu
20 25 30

Tyr Leu Thr Met Thr Pro Gly Arg Arg Ser Lys Phe Phe Phe Thr Ile
35 40 45

Ser Asn Ser Ser Leu Ser Leu Phe
50 55

<210> 1879
<211> 50
<212> PRT
<213> Homo sapiens

<400> 1879
Ile Ser Gln Ile Thr Lys Ser Ser Leu Arg Gln Gln Phe Lys Thr Val
5 10 15

Pro Gly Ile Lys Ile Tyr Ser His Leu Arg Ser Leu Pro Ser His Leu
20 25 30

His Leu Leu Ser Leu Lys Tyr Ile His Thr His Pro Thr Pro Ser Ile
35 40 45

Leu Asp
50

<210> 1880
<211> 70
<212> PRT
<213> Homo sapiens

<400> 1880
Arg Ser Ala Tyr Ala Ala Arg Trp Val Ala Lys Ser Leu Val Lys Gly
5 10 15
Gly Leu Cys Arg Arg Val Leu Val Gln Val Ser Tyr Ala Ile Gly Val
20 25 30
Ser His Pro Leu Ser Ile Ser Ile Phe His Tyr Gly Thr Ser Gln Lys
35 40 45
Ser Glu Arg Glu Leu Leu Glu Ile Val Lys Lys Asn Phe Asp Leu Arg
50 55 60
Pro Gly Val Ile Val Arg
65 70

<210> 1881
<211> 53
<212> PRT
<213> Homo sapiens

<400> 1881
Gly Leu Leu Met Leu Leu Val Gly Trp Gln Asn Pro Leu Leu Lys Glu
5 10 15
Val Cys Ala Gly Gly Phe Leu Phe Arg Ser Leu Met Leu Leu Glu Phe
20 25 30
Leu Ile His Tyr Leu Ser Pro Phe Ser Ile Met Val Pro Leu Arg Arg
35 40 45
Val Arg Glu Ser Tyr
50

<210> 1882
<211> 69
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(69)
<223> Xaa = Any amino acid

<400> 1882
Xaa His Lys Ile Cys Ser Ile Asp Val His Glu Ser Ser Cys Cys Xaa
5 10 15
Gly Ala Val Ser Thr Asp Xaa Trp Asn Asn Trp Pro Val Arg Lys Leu
20 25 30
Ile Lys Ala Ala Asn Ser Thr Xaa Glu Cys Asn Arg Xaa Xaa Gln Gly

35 40 45
 Leu Ile Ser Leu Ser Asp Gly Gly Leu Xaa Ile Cys Xaa Pro Gly Xaa
 50 55 60

Tyr Cys Val Ile Asn
 65

<210> 1883
 <211> 64
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(64)
 <223> Xaa = Any amino acid

<400> 1883
 Xaa Pro Xaa Gln Gln Xaa Ser Ser Pro Pro Ser Glu Arg Leu Ile Arg
 5 10 15
 Pro Cys Xaa Xaa Leu Leu His Ser Xaa Val Leu Phe Ala Ala Leu Met
 20 25 30
 Ser Phe Leu Thr Gly Gln Leu Phe Xaa Lys Ser Val Asp Thr Ala Pro
 35 40 45
 Xaa Gln Gln Glu Asp Ser Trp Thr Ser Ile Glu His Ile Leu Trp Xaa
 50 55 60

<210> 1884
 <211> 92
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(92)
 <223> Xaa = Any amino acid

<400> 1884
 Val Glu Arg Thr Arg Lys Pro Ser Leu Ser Glu Lys Lys Asn Asn Pro
 5 10 15
 Ser Lys Trp Xaa Val Ser Ser Val Tyr Asp Thr Ile Xaa Ser Trp Xaa
 20 25 30
 Thr Asn Xaa Lys Ser Ser Ile Arg Lys Ala Asn Lys Ala Leu Xaa Xaa
 35 40 45
 Ser Ile Ala Phe Xaa Cys Thr Val Cys Ser Phe Asp Glu Leu Pro His
 50 55 60
 Arg Pro Ile Ile Pro Xaa Val Cys Gly Tyr Arg Ser Xaa Thr Ala Arg
 65 70 75 80
 Gly Leu Met Asp Val Tyr Arg Thr Tyr Leu Val Xaa
 85 90

```
<210> 1885
<211> 77
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> variant
<222> (1)...(77)
<223> Xaa = Any amino acid
```

```
<400> 1885  
Gly Leu Glu Phe Arg Lys Ala Glu Arg Phe Leu Ile Trp Gln Ser Ser  
                    5                      10                      15  
  
Ser Ser Ser Arg Xaa Leu Lys Gly Leu Ser Phe Cys Arg Arg Thr Cys  
                20                      25                      30  
  
Phe Ser Ser Ser Asn Ser Ala Val Leu Phe Gly Ile His Pro Leu Gln  
        35                      40                      45  
  
Val Phe Tyr Val Xaa Asn His His Phe Asn Cys Phe Thr Asn Pro Ala  
    50                      55                      60  
  
Phe Leu Ile Asp Gly Ser Gln His Leu Ser Pro Thr Gly  
   65          70          75
```

```
<210> 1886
<211> 97
<212> PRT
<213> Homo sapiens
```

```
<400> 1886
Gly Ser Ser Thr Gly Gly Ala Ser Ala Met Ala Trp Thr Val Leu Leu
      5                                10                        15

Leu Gly Leu Leu Ser His Cys Thr Asp Ser Val Thr Ser Tyr Val Leu
      20                                25                        30

Thr Gln Thr Pro Ser Val Ser Val Ala Pro Gly Lys Thr Ala Lys Ile
      35                                40                        45

Thr Cys Gly Gly Asn Asn Ile Gly Ser Asn Asn Val His Trp Tyr Tyr
      50                                55                        60

Gln Lys Pro Gly Gln Ala Pro Val Leu Ile Ile Ser Phe Asp Asn Asp
      65                                70                        75                        80

Arg Pro Ser Gly Ile Ser Glu Arg Phe Ser Gly Phe Asn Ser Gly Asp
      85                                90                        95
```

Met

```
<210> 1887
<211> 56
<212> PRT
<213> Homo sapiens
```

<400> 1887
Lys Gln His Trp Trp Cys Leu Ser His Gly Leu Asp Arg Ser Pro Pro
 5 10 15

Arg Pro Pro Leu Ser Leu His Arg Leu Cys Asp Leu Leu Cys Val Asp
 20 25 30
 Ser Asp Thr Leu Ser Val Ser Gly Pro Arg Lys Asp Gly Gln Asp Tyr
 35 40 45
 Leu Trp Gly Lys Gln Tyr Trp Glu
 50 55

<210> 1888
 <211> 75
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(75)
 <223> Xaa = Any amino acid

<400> 1888
 Pro Phe Leu Glu Leu His Val Asn Leu Cys Gly Gln Ala Ala Phe Ala
 5 10 15
 Gly Val Phe Thr Gly Arg Gln Arg Leu Gln Ala Cys Leu Pro Ala Gly
 20 25 30
 Ser Val Cys Arg Arg Val Tyr Met Gln Ala Xaa His His Val Arg Pro
 35 40 45
 Leu Val Gln Gly Phe Arg Gly Pro Ala Gln Val Asn Arg Leu Cys Ser
 50 55 60
 His Lys Phe Thr Glu Leu Xaa Gly Cys Ala Thr
 65 70 75

<210> 1889
 <211> 74
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(74)
 <223> Xaa = Any amino acid

<400> 1889
 Ala Ala Arg Glu Pro Val Trp Ala Gly Ser Val Cys Arg Arg Val Tyr
 5 10 15
 Gly Gln Ala Ala Phe Ala Gly Val Phe Thr Gly Arg Gln Arg Leu Gln
 20 25 30
 Ala Cys Leu His Ala Gly Val Xaa Pro Cys Glu Thr Thr Gly Pro Gly
 35 40 45
 Phe Gln Arg Ser Cys Ser Gly Glu Ser Ala Val Phe Ser Gln Val His
 50 55 60
 Gly Ala Xaa Trp Val Cys Asn Met Lys Tyr
 65 70

<210> 1890
<211> 66
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(66)
<223> Xaa = Any amino acid

<400> 1890
Leu Asp Xaa Gly Leu Xaa Pro Leu Ser Val Pro Ser Val Pro His Ser
 5 10 15

Thr Ser Ile Ser Cys Cys Thr Pro Xaa Gln Leu Arg Glu Leu Val Arg
 20 25 30

Thr Gln Pro Ile His Leu Ser Arg Thr Ser Glu Thr Leu Asp Gln Trp
 35 40 45

Ser His Met Val Xaa Arg Leu His Val Asn Thr Pro Ala Asn Ala Ala
 50 55 60

Cys Arg
 65

<210> 1891
<211> 55
<212> PRT
<213> Homo sapiens

<400> 1891
Lys Leu Tyr Asn Ala Cys Ile Met Lys Lys Asp Leu Pro Phe Pro Tyr
 5 10 15

Ile Leu Ile Glu Leu His Arg Leu Ala Val His Phe Val Ile His Val
 20 25 30

Ile Arg Ile Leu Asp Ser Ile Ala Phe Glu Ile Cys Phe Phe Leu Gly
 35 40 45

Thr Lys Ser Gln Leu Ile Val
 50 55

<210> 1892
<211> 52
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(52)
<223> Xaa = Any amino acid

<400> 1892
Pro Lys Glu Val Arg Gln Leu Ala Glu Asp Phe Leu Lys Asp Tyr Ile
 5 10 15

His Ile Asn Ile Gly Ala Leu Glu Leu Xaa Ala Asn His Asn Ile Leu

20 25 30
 Xaa Xaa Val Asp Val Cys His Asp Xaa Xaa Lys Asp Glu Lys Leu Ile
 35 40 45

Arg Leu Met Glu
 50

<210> 1893
 <211> 115
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(115)
 <223> Xaa = Any amino acid

<400> 1893
 Pro Met Trp Leu Val Phe Xaa Leu Xaa Leu Ala Arg Phe His Thr Leu
 5 10 15

Thr Ser Leu Ser Gln Pro Gln Glu Thr Met Ile Gly Leu Leu Leu Leu
 20 25 30

Gly Glu Lys Arg Thr Gln Asp Thr His Ser Glu Trp Leu Ser Ser Trp
 35 40 45

Thr Val Tyr Leu His Thr Pro Arg Val Phe His Ser Leu Met Val Leu
 50 55 60

Ser Arg Asp Pro Glu Thr Ile Cys Arg Leu Ser Glu Glu Lys Ala Thr
 65 70 75 80

Leu Ser Thr Ser Leu Val Trp Pro Thr Asn Arg Leu Val Val Val Pro
 85 90 95

Val Val Arg Ser Gln Arg Arg Arg Val Pro Ser Gln Glu Pro Glu Arg
 100 105 110

Ala Asn Trp
 115

<210> 1894
 <211> 50
 <212> PRT
 <213> Homo sapiens

<400> 1894
 Leu Asp Gly Phe Ile Ser Arg Ser Arg Asp Asn Leu Pro Val Val Arg
 5 10 15

Gly Glu Gly His Thr Gln His Ile Leu Gly Met Ala His Lys Ser Pro
 20 25 30

Arg Gly Gly Ala Arg Cys Glu Ile Pro Glu Ala Gln Gly Ser Ile Pro
 35 40 45

Gly Ala
 50

```
<210> 1895
<211> 114
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> variant
<222> (1)...(114)
<223> Xaa = Any amino acid
```

```

<400> 1895
Gln Phe Ala Leu Ser Gly Ser Trp Asp Gly Thr Leu Arg Leu Trp Asp
      5              10              15

Leu Thr Thr Gly Thr Thr Thr Arg Arg Phe Val Gly His Thr Lys Asp
      20              25              30

Val Leu Ser Val Ala Phe Ser Ser Asp Asn Arg Gln Ile Val Ser Gly
      35              40              45

Ser Arg Asp Lys Thr Ile Lys Leu Trp Asn Thr Leu Gly Val Cys Lys
      50              55              60

Tyr Thr Val Gln Asp Glu Ser His Ser Glu Trp Val Ser Cys Val Arg
      65              70              75              80

Phe Ser Pro Asn Ser Ser Asn Pro Ile Ile Val Ser Cys Gly Trp Asp
      85              90              95

Lys Leu Val Lys Val Trp Asn Leu Ala Xaa Cys Lys Xaa Lys Thr Asn
      100              105              110

His Ile

```

```
<210> 1896
<211> 74
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> variant  
<222> (1)...(74)  
<223> Xaa = Any amino acid
```

```

<400> 1896
Val Trp Pro Ser Pro Leu Thr Thr Gly Arg Leu Ser Leu Asp Leu Glu
                    5                      10                      15

Ile Lys Pro Ser Ser Tyr Gly Ile Pro Trp Val Cys Ala Asn Thr Leu
                    20                      25                      30

Ser Arg Met Arg Ala Thr Gln Ser Gly Cys Leu Val Ser Ala Ser Arg
                    35                      40                      45

Pro Thr Ala Ala Thr Leu Ser Ser Ser Pro Val Ala Gly Thr Ser Trp
                    50                      55                      60

Ser Arg Tyr Gly Thr Trp Leu Xaa Ala Xaa
                    65                      70

```

```
<220>
<221> variant
<222> (1)...(60)
<223> Xaa = Any amino acid
```

```

<400> 1897
His Lys Ile Cys Ser Arg Asp Val His Glu Ser Ser Cys Cys Val Gly
      5                      10                      15

Ala Xaa Ser Thr Asp Phe Trp Asn Asn Trp Pro Val Arg Lys Pro Ile
      20                      25                      30

Lys Ala Ala Asn Ser Thr Met Asn Ala Ile Glu Ser Gln Arg Ala Leu
      35                      40                      45

Leu Ala Phe Xaa Met Glu Asp Leu Arg Phe Val Ala
      50                      55                      60

```

```
<210> 1898
<211> 60
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> variant  
<222> (1)...(60)  
<223> Xaa = Any amino acid
```

<400> 1898
Ala Thr Asn Leu Lys Ser Ser Ile Xaa Lys Ala Asn Lys Ala Leu Trp
5 10 15
Leu Ser Ile Ala Phe Ile Val Leu Phe Ala Ala Leu Met Gly Phe Leu
20 25 30
Thr Gly Gln Leu Phe Gln Lys Ser Val Asp Xaa Ala Pro Thr Gln Gln
35 40 45
Glu Asp Ser Trp Thr Ser Leu Glu His Ile Leu Trp
50 55 60

```
<210> 1899
<211> 58
<212> PRT
<213> Homo sapiens
```

```

<400> 1899
Ser Asn Ile  Lys Ala  Ile Arg Arg  His Pro Cys His His Leu Thr Gln
              5              10              15

Gly Gly Arg  Cys Trp Ser Trp Val  Gln Leu Gly Arg Arg Ser Arg Ser
              20              25              30

Arg Lys Gln Gly Asp Tyr Gly Ser  Gln Ser Val Ser Lys Trp Ala Gly
              35              40              45

```

Leu Pro Gly Arg Asp Tyr Ser Glu Gly Gln
 50 55

<210> 1900
 <211> 146
 <212> PRT
 <213> Homo sapiens

<400> 1900
 Ala Asn Gly Ser Ala Glu Thr Ser Ala Leu Asp Thr Gly Phe Ser Leu
 5 10 15
 Asn Leu Ser Glu Leu Arg Glu Tyr Thr Glu Gly Leu Thr Glu Ala Lys
 20 25 30
 Glu Asp Asp Asp Gly Asp His Ser Ser Leu Gln Ser Gly Gln Ser Val
 35 40 45
 Ile Ser Leu Leu Ser Ser Glu Glu Leu Lys Lys Leu Ile Glu Glu Val
 50 55 60
 Lys Val Leu Asp Glu Ala Thr Leu Lys Gln Leu Asp Gly Ile His Val
 65 70 75 80
 Thr Ile Leu His Lys Glu Glu Gly Ala Gly Leu Gly Phe Ser Leu Ala
 85 90 95
 Gly Gly Ala Asp Leu Glu Asn Lys Val Ile Thr Val His Arg Val Phe
 100 105 110
 Pro Asn Gly Leu Ala Ser Gln Glu Gly Thr Ile Gln Lys Gly Asn Glu
 115 120 125
 Val Leu Ser Ser Thr Ala Ser Leu Ser Arg Gly Pro Arg Thr Met Met
 130 135 140
 Pro Trp
 145

<210> 1901
 <211> 62
 <212> PRT
 <213> Homo sapiens

<400> 1901
 Thr Val Ile Thr Leu Phe Ser Arg Ser Ala Pro Pro Ala Lys Leu Asn
 5 10 15
 Pro Arg Pro Ala Pro Ser Ser Leu Cys Lys Met Val Thr Trp Met Pro
 20 25 30
 Ser Asn Cys Phe Asn Val Ala Ser Ser Arg Thr Phe Thr Ser Ser Met
 35 40 45
 Ser Phe Phe Asn Ser Ser Glu Leu Ser Arg Glu Ile Thr Asp
 50 55 60

<210> 1902
 <211> 109

<212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(109)
 <223> Xaa = Any amino acid

<400> 1902
 Ser Pro Ala Arg Pro Leu Ile Arg Ser Asp Lys Met Lys Glu Thr Ile
 5 10 15
 Met Asn Gln Glu Lys Leu Ala Lys Leu Gln Ala Gln Val Arg Ile Gly
 20 25 30
 Gly Lys Gly Thr Ala Arg Arg Lys Lys Lys Val Val His Arg Thr Ala
 35 40 45
 Thr Ala Asp Asp Lys Lys Leu Gln Phe Ser Leu Lys Lys Leu Xaa Val
 50 55 60
 Asn Asn Ile Ser Gly Ile Glu Glu Val Asn Met Phe Thr Asn Gln Gly
 65 70 75 80
 Thr Val Ile His Phe Asn Asn Pro Lys Val Gln Ala Ser Leu Ala Ala
 85 90 95
 Asn Thr Phe Thr Ile Thr Gly His Ala Glu Thr Lys Gln
 100 105

<210> 1903
 <211> 81
 <212> PRT
 <213> Homo sapiens

<400> 1903
 Gly Glu Leu Lys Phe Phe Val Ile Cys Cys Gly Cys Ser Met Asn His
 5 10 15
 Leu Leu Leu Ser Ala Ser Ser Ser Phe Pro Thr Asn Ala His Leu Cys
 20 25 30
 Leu Gln Phe Gly Glu Phe Phe Leu Val His Asp Cys Phe Phe His Leu
 35 40 45
 Val Gly Ala Asn Lys Gly Pro Arg Gly Gly Leu Gly Leu Val Leu Lys
 50 55 60
 Gly Ser Arg Val Asp His Leu Arg Leu Gly Ala His Thr Arg Gly Arg
 65 70 75 80
 Lys

<210> 1904
 <211> 59
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant

<222> (1)...(59)

<223> Xaa = Any amino acid

<400> 1904

Thr Tyr Ser Pro Leu Gln Tyr Gln Arg Tyr Cys Leu Pro Xaa Thr Ser
5 10 15

Leu Arg Arg Thr Glu Val Phe Cys His Leu Leu Trp Leu Phe Tyr Glu
20 25 30

Pro Pro Ser Ser Phe Cys Glu Gln Phe Leu Ser His Gln Cys Ala Leu
35 40 45

Val Pro Ala Val Trp Arg Val Phe Pro Gly Ser
50 55

<210> 1905

<211> 74

<212> PRT

<213> Homo sapiens

<400> 1905

Gln Thr Val Ile Gln Gln Leu Ala Pro Gly Asn Asn Ser Tyr Phe Ile
5 10 15

Ile Lys Gln Ser Leu Gln Thr His Asn Cys Ser Ala Glu Glu Leu Ser
20 25 30

Ser Thr Ile Gln Cys Ser Pro Ile Gln Leu Leu Cys Gly Gln Cys Gly
35 40 45

Cys Ile Ala Val Asp Ser Met Lys Gly Val Ile Leu Val Met Ser Cys
50 55 60

Gln Ser Ile Pro Arg Pro Gly Cys Arg Trp
65 70

<210> 1906

<211> 66

<212> PRT

<213> Homo sapiens

<400> 1906

Asp His Leu Lys Ser Cys Tyr Gln Asp Ser His Glu Asp Pro Thr Lys
5 10 15

Met Lys Arg Phe Leu Phe Leu Leu Thr Ile Ser Leu Leu Val Met
20 25 30

Val Gln Ile Gln Thr Gly Leu Ser Gly Gln Asn Asp Thr Ser Gln Thr
35 40 45

Ser Ser Pro Ser Ala Ser Ser Ser Met Ser Gly Gly Ile Phe Leu Phe
50 55 60

Phe Val

65

<210> 1907

<211> 75

<212> PRT

<213> Homo sapiens

<400> 1907

Thr Lys Arg Ser Leu Gln Thr Ala Leu Arg Ser Pro Lys Lys Leu Leu
 5 10 15

Pro Arg Gln Pro Arg Arg Ser Tyr Gln Asn Glu Ala Leu Pro Leu Pro
 20 25 30

Pro Thr His His Gln Pro Pro Gly Tyr Gly Thr Asp Thr Asn Trp Thr
 35 40 45

Leu Arg Thr Lys Arg His Gln Pro Asn Gln Gln Pro Leu Ser Ile Gln
 50 55 60

Gln His Glu Arg Arg His Phe Pro Phe Leu Arg
 65 70 75

<210> 1908

<211> 59

<212> PRT

<213> Homo sapiens

<400> 1908

Thr Lys Lys Arg Lys Met Pro Pro Leu Met Leu Leu Asp Ala Glu Gly
 5 10 15

Leu Leu Val Trp Leu Val Ser Phe Cys Pro Glu Ser Pro Val Cys Ile
 20 25 30

Cys Thr Ile Thr Arg Arg Leu Met Val Ser Arg Arg Lys Arg Lys Arg
 35 40 45

Phe Ile Leu Val Gly Ser Ser Trp Leu Ser Trp
 50 55

<210> 1909

<211> 65

<212> PRT

<213> Homo sapiens

<400> 1909

Lys Ser Gly Val Gly Ile Pro Phe His Met His Ile Asp Tyr Phe Leu
 5 10 15

Ser Phe Phe Lys Thr Cys Phe Ser Gly Phe Leu Asn Val Pro Asp Asp
 20 25 30

Ser Leu Ser Cys Arg Thr Val Asn Val Asn Leu Ser Arg Gly Leu Trp
 35 40 45

Leu Asp Val Asn Leu Ile Lys Leu Leu Cys Pro Arg Asn Ser Ala Pro
 50 55 60

Pro
 65

<210> 1910

<211> 107

<212> PRT

<213> Homo sapiens

<400> 1910

Lys Met Glu His Ser Asp Glu Asn Ile Gln Phe Trp Met Ala Cys Glu
5 10 15
Thr Tyr Lys Lys Ile Ala Ser Arg Trp Ser Arg Ile Ser Arg Ala Lys
20 25 30
Lys Leu Tyr Lys Lys Ile Tyr Ile Gln Pro Gln Ser Pro Arg Glu Ile Asn
35 40 45
Ile Asp Ser Ser Thr Arg Glu Thr Ile Ile Arg Asn Ile Gln Glu Pro
50 55 60
Thr Glu Thr Cys Phe Glu Glu Ala Gln Lys Ile Val Tyr Met His Met
65 70 75 80
Glu Arg Asp Ser Tyr Pro Arg Phe Leu Lys Ser Glu Met Tyr Gln Lys
85 90 95
Leu Leu Lys Thr Met Gln Ser Asn Asn Ser Phe
100 105

<210> 1911

<211> 74

<212> PRT

<213> Homo sapiens

<400> 1911

Lys Trp Ser Thr Val Thr Arg Ile Phe Asn Ser Gly Trp His Val Lys
5 10 15
Pro Ile Arg Lys Leu Pro His Gly Gly Ala Glu Phe Leu Gly Gln Arg
20 25 30
Ser Phe Ile Arg Phe Thr Ser Ser His Ser Pro Leu Glu Arg Leu Thr
35 40 45
Leu Thr Val Arg Gln Glu Arg Leu Ser Ser Gly Thr Phe Arg Asn Pro
50 55 60
Leu Lys His Val Leu Lys Lys Leu Arg Lys
65 70

<210> 1912

<211> 63

<212> PRT

<213> Homo sapiens

<400> 1912

Leu Leu Pro Leu Tyr Pro Glu Ile Leu Glu Met Gln Glu Trp Trp Leu
5 10 15
Gly Trp Lys Ile Met Ile Asp Ser Val Glu Gly Gln Ala Val Gly Val
20 25 30
Phe Trp Gly Gln Ser Arg Val Asn Thr Val Pro His Tyr Leu Asp Leu
35 40 45

Leu Ala Pro Ile Pro Gly Gln Met Leu Lys Lys Lys Asn Val Asn
 50 55 60

<210> 1913
 <211> 181
 <212> PRT
 <213> Homo sapiens

<400> 1913
 Ser Arg Ala Glu Met Leu Gly Ala Ile Asn Gln Glu Ser Arg Val Ser
 5 10 15

Lys Ala Val Glu Val Met Ile Gln His Val Glu Asn Leu Lys Arg Met
 20 25 30

Tyr Ala Lys Glu His Ala Glu Leu Glu Glu Leu Lys Gln Val Leu Leu
 35 40 45

Gln Asn Glu Arg Ser Phe Asn Pro Leu Glu Asp Asp Asp Asp Cys Gln
 50 55 60

Ile Lys Lys Arg Ser Ala Ser Leu Asn Ser Lys Pro Ser Ser Leu Arg
 65 70 75 80

Arg Val Thr Ile Ala Ser Leu Pro Arg Asn Ile Gly Asn Ala Gly Met
 85 90 95

Val Ala Gly Met Glu Asn Asn Asp Arg Phe Ser Arg Arg Ser Ser Ser
 100 105 110

Trp Arg Ile Leu Gly Ser Lys Gln Ser Glu His Arg Pro Ser Leu Pro
 115 120 125

Arg Phe Ile Ser Thr Tyr Ser Trp Ala Asp Ala Glu Glu Glu Lys Cys
 130 135 140

Glu Leu Lys Thr Lys Asp Asp Ser Glu Pro Ser Gly Glu Glu Thr Val
 145 150 155 160

Glu Arg Thr Arg Lys Pro Ser Leu Ser Glu Lys Lys Asn Asn Pro Ser
 165 170 175

Lys Trp Asp Val Ser
 180

<210> 1914
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 1914
 Val Leu Ile Asn Arg Gly Asn Glu Gly Arg Cys Ser Leu Cys Phe Asp
 5 10 15

Pro Lys Ile Arg Gln Leu Leu Asp Leu Leu Leu Asn Arg Ser Leu Phe
 20 25 30

Ser Ile Pro Ala Thr Ile Pro Ala Phe Pro Ile Phe Leu Gly Lys Glu
 35 40 45

Ala Ile Val Thr Leu Arg Arg Glu Asp Gly Leu Glu Phe Arg Glu Ala

50 55 60
 Glu Arg Phe Leu Ile Trp Gln Ser Ser Ser Ser Ser Arg Gly Leu Lys
 65 70 75 80
 Asp Leu Ser Phe Cys Arg Arg Thr Cys Phe Ser Ser Ser Asn Ser Ala
 85 90 95
 Cys Ser Leu Ala Tyr Ile Leu Phe Lys Phe Ser Thr Cys
 100 105

<210> 1915
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 1915
 Ile Val Ser Gly Cys Thr Ser Gly Pro Ser Val Ser Met Ala Ala Pro
 5 10 15
 Val Pro Thr Ser His Thr Met Ile Thr Leu Ser Gln Pro Ala Leu Ser
 20 25 30
 Ser Thr Phe Trp Ala Val Val Cys Gln Ala Thr Met Pro Thr Arg Leu
 35 40 45
 Val Trp Pro Ser Arg Val Thr Thr Gly Ser Arg Arg Gly Ser Ile Arg
 50 55 60
 Pro Pro Ser Gly Ile Ser His Thr Met Thr Val Gln Ser Ser Glu Pro
 65 70 75 80
 Leu Ala Met Thr Leu Ser Leu Cys Gly His Gln Ala Met Ser Ser Ala
 85 90 95
 Gly Ala Val Trp
 100

<210> 1916
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 1916
 Ser Ile Ser Ala Pro Val His Thr Val Asp Arg Val Trp Val His Leu
 5 10 15
 Trp Ala Gln Cys Gln His Gly Arg Pro Ser Ala His Val Pro His His
 20 25 30
 Asp His Val Val Thr Thr Cys Thr Glu Gln His Val Leu Gly Cys Gly
 35 40 45
 Val Pro Gly His Asn Ala His Thr Leu Gly Val Ala Leu Gln Gly Asp
 50 55 60
 Asp Gly Leu Pro Gln Gly Gln His Gln Ala Pro Ile Arg Asp Leu Pro
 65 70 75 80
 His His Asp Cys Ala Val Leu Gly Ala Thr Gly Asn Asp Val Val Ile
 85 90 95

Val Arg Ala Pro Gly Asp Val
100

<210> 1917
<211> 58
<212> PRT
<213> Homo sapiens

<400> 1917
Gln Arg His Cys Gln Trp Leu Arg Gly Leu His Ser His Gly Val Gly
5 10 15
Asp Pro Gly Trp Gly Pro Asp Ala Ala Pro Ala Gly Ala Arg Arg His
20 25 30
Pro Gly Gly Pro His Gln Ala Cys Gly His Cys Gly Leu Ala His His
35 40 45
Ser Pro Glu Arg Ala Ala Gln Cys Arg Leu
50 55

<210> 1918
<211> 109
<212> PRT
<213> Homo sapiens

<400> 1918
His Thr Ala Pro Ala Leu Asp Ile Ala Trp Cys Pro His Asn Asp Asn
5 10 15
Val Ile Ala Ser Gly Ser Glu Asp Cys Thr Val Met Val Trp Glu Ile
20 25 30
Pro Asp Gly Gly Leu Met Leu Pro Leu Arg Glu Pro Val Val Thr Leu
35 40 45
Glu Gly His Thr Lys Arg Val Gly Ile Val Ala Trp His Thr Thr Ala
50 55 60
Gln Asn Val Leu Leu Ser Ala Gly Cys Asp Asn Val Ile Met Val Trp
65 70 75 80
Asp Val Gly Thr Gly Ala Ala Met Leu Thr Leu Gly Pro Glu Val His
85 90 95
Pro Asp Thr Ile Tyr Ser Val Asp Trp Ser Arg Asp Gly
100 105

<210> 1919
<211> 78
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(78)
<223> Xaa = Any amino acid

<400> 1919

Arg	Gly	Cys	Met	Pro	Xaa	Ser	Thr	Leu	Glu	Leu	Glu	Glu	Leu	Lys	Gln
				5					10					15	
Val	Leu	Leu	His	Asn	Glu	Arg	Ser	Phe	Asn	Pro	Leu	Glu	Asp	Asp	Asp
			20					25					30		
Asp	Cys	Gln	Ile	Lys	Lys	Arg	Pro	Ala	Ser	Leu	Asn	Ser	Lys	Pro	Ser
		35					40					45			
Ser	Leu	Arg	Arg	Val	Thr	Ile	Ala	Ser	Leu	Pro	Xaa	Asn	Ile	Gly	Asn
	50					55					60				
Ala	Gly	Met	Val	Ala	Gly	Met	Glu	Asn	Asn	Asp	Pro	Ile	Xaa		
	65				70					75					

```
<210> 1920
<211> 103
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> variant
<222> (1)...(103)
<223> Xaa = Any amino acid
```

```
<400> 1920  
Xaa Ile Gly Ser Leu Phe Ser Ile Pro Ala Thr Ile Pro Ala Phe Pro  
          5              10              15  
  
Ile Phe Xaa Gly Lys Glu Ala Ile Val Thr Leu Arg Arg Glu Asp Gly  
      20          25              30  
  
Leu Glu Phe Arg Glu Ala Gly Arg Phe Leu Ile Trp Gln Ser Ser Ser  
     35          40              45  
  
Ser Ser Arg Gly Leu Lys Asp Leu Ser Leu Cys Arg Arg Thr Cys Phe  
    50          55              60  
  
Ser Ser Ser Asn Ser Ser Val Xaa Phe Gly Ile His Pro Leu Gln Val  
   65          70              75              80  
  
Xaa Tyr Val Leu Asn His His Phe Asn Cys Phe Thr Asn Pro Ala Phe  
            85              90              95  
  
Leu Ile Asp Gly Ser Gln His  
        100
```

```
<210> 1921
<211> 60
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> variant  
<222> (1)...(60)  
<223> Xaa = Any amino acid
```

<400> 1921
Thr Ser Ser Pro Ala Ala Pro Thr Ser Ala Cys Ala Ser Arg Pro Pro
 5 10 15

Gly Pro Ser Trp Thr Trp Gly Arg Ala Pro Arg Thr Glu Ser Ser Gln
 20 25 30
 Pro Arg Gly Ser Ser Ser Cys Ser Ala Arg Trp Cys Leu Gly Arg Cys
 35 40 45
 Cys Cys Xaa Gly Asn Asp Gly Lys Asn Xaa Asn Xaa
 50 55 60

<210> 1922
 <211> 60
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(60)
 <223> Xaa = Any amino acid

<400> 1922
 Pro Ala Val Leu Arg His Leu Pro Pro Arg Ala Pro Ala Ala Pro Gln
 5 10 15
 Ala Leu Pro Gly His Gly Gly Gly His Gln Glu Pro Asn His His Ser
 20 25 30
 Arg Gly Asp His Pro Pro Val Leu Arg Gly Gly Ala Trp Asp Ala Ala
 35 40 45
 Ala Val Xaa Glu Thr Met Ala Arg Thr Xaa Thr Xaa
 50 55 60

<210> 1923
 <211> 60
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(60)
 <223> Xaa = Any amino acid

<400> 1923
 Gln Gln Ser Cys Gly Thr Tyr Leu Arg Val Arg Gln Pro Pro Pro Arg
 5 10 15
 Pro Phe Leu Asp Met Gly Glu Gly Thr Lys Asn Arg Ile Ile Thr Ala
 20 25 30
 Glu Gly Ile Ile Leu Leu Phe Cys Ala Val Val Pro Gly Thr Leu Leu
 35 40 45
 Leu Xaa Arg Lys Arg Trp Gln Glu Arg Xaa Leu Xaa
 50 55 60

<210> 1924
 <211> 60
 <212> PRT
 <213> Homo sapiens

```
<220>  
<221> variant  
<222> (1)...(60)  
<223> Xaa = Any amino acid  
  
<400> 1924  
Xaa Glu Xaa Ser Phe Leu Pro Ser Phe Pro Xaa Gln Gln Gln Arg Pro  
          5                      10                      15  
Arg His His Arg Ala Glu Gln Glu Asp Asp Pro Leu Gly Cys Asp Asp  
      20              25              30  
Ser Val Leu Gly Ala Leu Pro His Val Gln Glu Gly Pro Gly Gly Arg  
    35              40              45  
Leu Ala His Ala Glu Val Gly Ala Ala Gly Leu Leu  
   50              55              60
```

```
<210> 1925
<211> 53
<212> PRT
<213> Homo sapiens
```

```

<220>
<221> variant
<222> (1)...(53)
<223> Xaa = Any amino acid
      ,
<400> 1925
Xaa Ser Xaa Arg Ser Cys His Arg Phe Xaa Asn Ser Ser Ser Val Pro
      5                      10                      15
Gly Thr Thr Ala Gln Asn Arg Arg Met Ile Pro Ser Ala Val Met Ile
      20                      25                      30
Arg Phe Leu Val Pro Ser Pro Met Ser Arg Lys Gly Leu Gly Gly Gly
      35                      40                      45
Trp Arg Thr Arg Arg
      50

```

```
<210> 1926
<211> 71
<212> PRT
<213> Homo sapiens
```

```

<400> 1926
Arg Gly Glu Lys Ala Glu Arg Val Pro Val Ile Phe Lys Arg Gln Asn
          5                      10                      15

Ile Ser Pro Leu Pro Arg Lys Leu Phe Ser Pro Arg Glu Lys Met Glu
          20                      25                      30

Val Ile Leu Thr Val His Cys Arg Gly Ile Ser Ser Cys Pro Ile Phe
          35                      40                      45

Cys Met Thr Cys His Gly Thr Ala Leu Phe Gln Thr Val His Cys Asp
          50                      55                      60

Leu Trp Val Phe Glu Phe Gln
          65                      70

```

```
<210> 1927
<211> 73
<212> PRT
<213> Homo sapiens
```

```

<400> 1927
Thr Lys Ile Ser Leu Asn Ile Glu Val Trp Asn Tyr Phe Phe Asp Ile
      5                      10                      15

Ser Ala Asn Ser Leu Lys Leu Lys Asp Pro Gln Ile Thr Val Asn Ser
      20                      25                      30

Leu Lys Gln Gly Cys Thr Met Ala Ser His Ala Lys Asp Gly Thr Arg
      35                      40                      45

Arg Asn Thr Thr Ala Val Asn Cys Glu Asp Asn Phe His Phe Phe Pro
      50                      55                      60

Arg Arg Glu Gln Phe Thr Gly Gln Arg
      65                      70

```

```
<210> 1928
<211> 63
<212> PRT
<213> Homo sapiens
```

```

<400> 1928
Leu Leu Pro Leu Tyr Pro Glu Ile Leu Glu Met Gln Glu Trp Trp Leu
      5              10              15

Gly Trp Lys Ile Met Ile Asp Ser Val Glu Gly Gln Ala Val Gly Val
      20              25              30

Phe Trp Gly Gln Ser Arg Val Asn Thr Val Pro His Tyr Leu Asp Leu
      35              40              45

Leu Ala Pro Ile Pro Gly Gln Met Leu Lys Lys Lys Asn Val Asn
      50              55              60

```

```
<210> 1929
<211> 181
<212> PRT
<213> Homo sapiens
```

```

<400> 1929
Ser Arg Ala Glu Met Leu Gly Ala Ile Asn Gln Glu Ser Arg Val Ser
          5                      10                      15

Lys Ala Val Glu Val Met Ile Gln His Val Glu Asn Leu Lys Arg Met
          20                      25                      30

Tyr Ala Lys Glu His Ala Glu Leu Glu Glu Leu Lys Gln Val Leu Leu
          35                      40                      45

Gln Asn Glu Arg Ser Phe Asn Pro Leu Glu Asp Asp Asp Asp Cys Gln
          50                      55                      60

Ile Lys Lys Arg Ser Ala Ser Leu Asn Ser Lys Pro Ser Ser Leu Arg
          65                      70                      75                      80

```


<400> 1931
Ala Ala Arg Glu Pro Val Trp Ala Gly Ser Val Cys Arg Arg Val Tyr
 5 10 15

Gly Gln Ala Ala Phe Ala Gly Val Phe Thr Gly Arg Gln Arg Leu Gln
 20 25 30

Ala Cys Leu His Ala Gly Val Ala Pro Cys Glu Thr Thr Gly Pro Gly
35 40 45

Phe Gln Arg Ser Cys Ser Gly Glu Ser Ala Val Phe Ser Gln Val His
50 55 60

Gly Ala Glu Trp Val Cys Asn Met Lys Tyr
65 70

<210> 1932

<211> 66

<212> PRT

<213> Homo sapiens

<400> 1932

Leu Asp Asp Gly Leu Gln Pro Leu Ser Val Pro Ser Val Pro His Ser
5 10 15

Thr Ser Ile Ser Cys Cys Thr Pro Thr Gln Leu Arg Glu Leu Val Arg
20 25 30

Thr Gln Pro Ile His Leu Ser Arg Thr Ser Glu Thr Leu Asp Gln Trp
35 40 45

Ser His Met Val Leu Arg Leu His Val Asn Thr Pro Ala Asn Ala Ala
50 55 60

Cys Arg
65

<210> 1933

<211> 63

<212> PRT

<213> Homo sapiens

<400> 1933

Leu Leu Pro Leu Tyr Pro Glu Ile Leu Glu Met Gln Glu Trp Trp Leu
5 10 15

Gly Trp Lys Ile Met Ile Asp Ser Val Glu Gly Gln Ala Val Gly Val
20 25 30

Phe Trp Gly Gln Ser Arg Val Asn Thr Val Pro His Tyr Leu Asp Leu
35 40 45

Leu Ala Pro Ile Pro Gly Gln Met Leu Lys Lys Lys Asn Val Asn
50 55 60

<210> 1934

<211> 169

<212> PRT

<213> Homo sapiens

<400> 1934

Ser Arg Ala Glu Met Leu Gly Ala Ile Asn Gln Glu Ser Arg Val Ser
5 10 15

Lys Ala Val Glu Val Met Ile Gln His Val Glu Asn Leu Lys Arg Met
20 25 30

684

Tyr Ala Lys Glu His Ala Glu Leu Glu Glu Leu Lys Gln Val Leu Leu
 35 40 45
 Gln Asn Glu Arg Ser Phe Asn Pro Leu Glu Asp Asp Asp Asp Cys Gln
 50 55 60
 Ile Lys Lys Arg Ser Ala Ser Leu Asn Ser Lys Pro Ser Ser Leu Arg
 65 70 75 80
 Arg Val Thr Ile Ala Ser Leu Pro Arg Asn Ile Gly Asn Ala Gly Met
 85 90 95
 Val Ala Gly Met Glu Asn Asn Asp Arg Phe Ser Arg Arg Ser Ser Ser
 100 105 110
 Trp Arg Ile Leu Gly Ser Lys Gln Ser Glu His Arg Pro Ser Leu Pro
 115 120 125
 Arg Phe Ile Ser Thr Tyr Ser Trp Ala Asp Ala Glu Glu Glu Lys Cys
 130 135 140
 Glu Leu Lys Thr Lys Asp Asp Ser Glu Pro Ser Gly Glu Glu Thr Val
 145 150 155 160
 Glu Arg Thr Arg Lys Pro Ser Leu Ser
 165

<210> 1935
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 1935
 Val Leu Ile Asn Arg Gly Asn Glu Gly Arg Cys Ser Leu Cys Phe Asp
 5 10 15
 Pro Lys Ile Arg Gln Leu Leu Asp Leu Leu Leu Asn Arg Ser Leu Phe
 20 25 30
 Ser Ile Pro Ala Thr Ile Pro Ala Phe Pro Ile Phe Leu Gly Lys Glu
 35 40 45
 Ala Ile Val Thr Leu Arg Arg Glu Asp Gly Leu Glu Phe Arg Glu Ala
 50 55 60
 Glu Arg Phe Leu Ile Trp Gln Ser Ser Ser Ser Ser Arg Gly Leu Lys
 65 70 75 80
 Asp Leu Ser Phe Cys Arg Arg Thr Cys Phe Ser Ser Ser Asn Ser Ala
 85 90 95
 Cys Ser Leu Ala Tyr Ile Leu Phe Lys Phe Ser Thr Cys
 100 105

<210> 1936
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 1936
 Asp Lys Ser Arg Pro Lys Ser Phe His Arg Asp Gly Met Met Leu Pro

685

5 10 15
 Val His Cys Gln His Gly Trp Glu Glu Ile Thr Asp Lys Thr Asp Gln
 20 25 30
 Ser Val Gly Leu Ala Lys Leu Gln Gly Leu Gln Arg Glu His Phe Ser
 35 40 45
 Asp Arg Lys Pro Trp Trp Gly Asp
 50 55

<210> 1937
 <211> 79
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(79)
 <223> Xaa = Any amino acid

<400> 1937
 Phe Arg Trp Tyr Leu Cys Val Trp Arg Gly His Gly Ile Trp Arg Gly
 5 10 15
 Gly Gln Arg Arg Thr Gln Trp Val Arg Leu Trp Glu Thr Glu Met Ser
 20 25 30
 Glu Glu Leu Gly Ser Glu Gly Arg Ser Ser Ser Arg Gln Gly Leu Xaa
 35 40 45
 Leu Asp Val Glu Ala Glu Pro Asp Pro Gly Tyr Ser Gly Pro Leu His
 50 55 60
 His Asp Phe Leu Gln His Phe Leu Ser Arg Ala His Ile Asp Val
 65 70 75

<210> 1938
 <211> 114
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(114)
 <223> Xaa = Any amino acid

<400> 1938
 Xaa Gln Ser Leu Pro Gly Arg Arg Pro Pro Phe Arg Ala Gln Leu Leu
 5 10 15
 Ala His Leu Cys Leu Pro Lys Pro Asp Pro Leu Cys Ser Ser Leu Pro
 20 25 30
 Ser Pro Pro Tyr Ala Met Ala Pro Pro Asn Thr Glu Ile Pro Ser Lys
 35 40 45
 Leu Val Ser Phe Ser Pro Tyr Thr Ser Ile Pro Pro Pro Gly Phe Pro
 50 55 60
 Ile Ala Glu Val Phe Thr Leu Lys Pro Leu Glu Phe Gly Lys Pro Asn

65						70						75						80
Thr	Leu	Val	Cys	Phe	Val	Ser	Asn	Leu	Phe	Pro	Pro	Met	Leu	Thr	Val			
				85					90					95				
Asn	Trp	Gln	His	His	Ser	Ile	Pro	Val	Glu	Gly	Phe	Gly	Pro	Thr	Phe			
			100					105					110					
Val	Ser																	

```
<210> 1939
<211> 58
<212> PRT
<213> Homo sapiens
```

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<220>  
<221> variant  
<222> (1)...(58)  
<223> Xaa = Any amino acid
```

```

<400> 1939
Pro Gly Ser Gly Ser Ala Ser Thr Ser Xaa Cys Ser Pro Cys Leu Glu
      5                      10                      15

Glu Asp Leu Pro Ser Glu Pro Ser Ser Ser Leu Ile Ser Val Ser Gln
      20                      25                      30

Ser Leu Thr His Cys Val Leu Leu Cys Pro Pro Leu His Met Pro Trp
      35                      40                      45

Pro Leu Gln Thr Gln Arg Tyr His Leu Asn
      50                      55

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```
<210> 1940
<211> 150
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> variant  
<222> (1)...(150)  
<223> Xaa = Any amino acid
```

```

<400> 1940
Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro Tyr Ile Asn
      5                      10                      15

Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser
      20                      25                      30

Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly Ile Leu Ser
      35                      40                      45

Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile Ala Gly Ile
      50                      55                      60

Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys Ser Asn Ile
      65                      70                      75                      80

Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln Thr Ile Glu Ile Lys

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687

85 90 95

Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser Gln Pro Lys Asn Glu
100 105 110

Glu Asp Ile Glu Ile Ile Pro Ile Gln Glu Glu Glu Glu Glu Thr
115 120 125

Glu Thr Asn Phe Pro Glu Pro Pro Gln Asp Gln Glu Ser Ser Xaa Ile
130 135 140

Glu Asn Asp Ser Ser Pro
145 150

<210> 1941
<211> 101
<212> PRT
<213> Homo sapiens

<400> 1941

Ser Trp Gly Gly Ser Gly Lys Phe Val Ser Val Ser Ser Ser Ser Ser
5 10 15

Ser Trp Ile Gly Ile Ile Ser Met Ser Ser Ser Phe Phe Gly Trp Glu
20 25 30

Asp Val Ser Val Ser Pro Thr Thr Ser Ser Phe Ile Ser Ile Val Cys
35 40 45

Ser Phe Phe Ser Ser Ala Asp Arg Arg Thr Met Leu Asp Leu Gly Leu
50 55 60

Glu His Val Leu Phe His Ser Phe Ser Thr Met Pro Ala Ile Thr Ser
65 70 75 80

Ser Trp Lys Lys Ala Lys Ile Ser Ile Thr Asp Lys Met Pro Lys Asn
85 90 95

Arg Asp Cys Met Leu
100

<210> 1942
<211> 87
<212> PRT
<213> Homo sapiens

<400> 1942

Leu Gly Gly Pro Gly Lys Gly Leu Gly His Glu Pro Gly Ser Ser Glu
5 10 15

Ala Val Thr Glu Ala Arg Glu Pro Ala Pro Arg Ser Trp Gly Asp Leu
20 25 30

Ala Leu Thr Pro Gly Leu Gly Ala His Leu Gln Thr Thr Ser Leu Pro
35 40 45

Leu Ser Ala Ala Ser Leu Cys Pro His Arg Trp Leu Ser Gly Gln Cys
50 55 60

Pro Gly Pro Arg Arg Cys Asp Leu Pro Pro Cys Gln Pro Cys Cys His
65 70 75 80

Pro Cys Pro Ala Ala Gly Arg
85

<210> 1943
<211> 113
<212> PRT
<213> Homo sapiens

<400> 1943
Trp Gly Val Arg Glu Arg Gly Trp Ala Met Ser Gln Ala Ala Pro Lys
5 10 15
Gln Ser Leu Arg Pro Gly Ser Leu His Pro Gly His Gly Ala Thr Trp
20 25 30
Leu Ser Leu Leu Ala Trp Val Leu Thr Tyr Arg Pro Leu His Phe Pro
35 40 45
Cys Pro Gln Arg His Tyr Val Leu Ile Gly Gly Cys Leu Val Asn Val
50 55 60
Gln Ala Leu Val Gly Val Ile Phe Leu His Ala Ser Leu Ala Val Ile
65 70 75 80
Leu Val Gln Gln Gln Glu Asp Arg His Asp Asp Glu Glu Asp Asp Gln
85 90 95
Gln Arg Leu Asp His Asp Asp Thr Ile Leu Gln Arg Val Pro Leu Leu
100 105 110
Gln

<210> 1944
<211> 79
<212> PRT
<213> Homo sapiens

<400> 1944
Leu Lys Gln Arg Asn Thr Leu Lys Asp Gly Ile Ile Met Ile Gln Thr
5 10 15
Leu Leu Ile Ile Leu Phe Ile Ile Val Pro Ile Phe Leu Leu Leu Asp
20 25 30
Lys Asp Asp Ser Lys Ala Gly Met Glu Glu Asp His Thr Tyr Glu Gly
35 40 45
Leu Asp Ile Asp Gln Thr Ala Thr Tyr Glu Asp Ile Val Thr Leu Arg
50 55 60
Thr Gly Glu Val Lys Trp Ser Val Gly Glu His Pro Gly Gln Glu
65 70 75

<210> 1945
<211> 54
<212> PRT
<213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(54)
 <223> Xaa = Any amino acid

 <400> 1945
 Thr Val Ile Cys Trp Phe Ser Leu Lys Asn Asp Leu Trp Cys Glu Ala
 5 10 15

 Gln Ile Ser Gly Asn Ile Arg Lys Thr Trp Ser Gly Gly Gly Ser Ser
 20 25 30

 Gly Ala Cys Ile Thr Xaa Pro Ala Pro Gln Leu Phe Pro Ala Ser Ser
 35 40 45

 Ala Ser Cys Arg Thr Tyr
 50

<210> 1946
 <211> 55
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(55)
 <223> Xaa = Any amino acid

 <400> 1946
 Leu Tyr Val Arg Gln Leu Ala Glu Glu Ala Gly Lys Ser Cys Gly Ala
 5 10 15

 Xaa Ser Val Met Gln Ala Pro Glu Glu Pro Pro Pro Asp Gln Val Phe
 20 25 30

 Arg Met Phe Pro Asp Ile Cys Ala Ser His Gln Arg Ser Phe Phe Arg
 35 40 45

 Glu Asn Gln Gln Ile Thr Val
 50 55

<210> 1947
 <211> 61
 <212> PRT
 <213> Homo sapiens

<400> 1947
 Cys Arg Pro Pro Arg Ser Arg Arg Gln Thr Arg Ser Ser Gly Cys Phe
 5 10 15

 Gln Ile Phe Val Pro His Thr Arg Asp His Phe Ser Glu Lys Thr Asn
 20 25 30

 Arg Ser Pro Ser Lys Cys Val Ala Trp Ala Pro His Pro Val Cys Val
 35 40 45

 Leu His Pro Ser Pro Cys Tyr Ser Gly Pro His His Asp
 50 55 60

<210> 1948

690

```
<211> 96
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> variant
<222> (1)...(96)
<223> Xaa = Any amino acid
```

```

<400> 1948
Val Cys Pro Ala Thr Gly Arg Arg Gly Trp Glu Glu Leu Trp Ser Arg
                    5                      10                      15

Xaa Cys Asp Ala Gly Pro Arg Gly Ala Ala Ala Arg Pro Gly Leu Pro
                    20                      25                      30

Asp Val Ser Arg Tyr Leu Cys Leu Thr Pro Glu Ile Ile Phe Gln Arg
                    35                      40                      45

Lys Pro Thr Asp His Arg Leu Ser Ala Ser Leu Gly Arg Pro Thr Pro
                    50                      55                      60

Ser Ala Ser Cys Ile His Leu Pro Val Thr Val Ala Arg Ile Met Ile
                    65                      70                      75                      80

Lys Glu Cys Gly Ser Leu Cys Leu Gly Trp Asp Ala Leu Leu Cys Thr
                    85                      90                      95

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```
<210> 1949
<211> 65
<212> PRT
<213> Homo sapiens
```

```

<400> 1949
Lys Ser Gly Val Gly Ile Pro Phe His Met His Ile Asp Tyr Phe Leu
          5                      10                      15

Ser Phe Phe Lys Thr Cys Phe Ser Gly Phe Leu Asn Val Pro Asp Asp
          20                      25                      30

Ser Leu Ser Cys Arg Thr Val Asn Val Asn Leu Ser Arg Gly Leu Trp
          35                      40                      45

Leu Asp Val Asn Leu Ile Lys Leu Leu Cys Pro Arg Asn Ser Ala Pro
          50                      55                      60

Pro
65

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```
<210> 1950
<211> 107
<212> PRT
<213> Homo sapiens
```

<400> 1950
Lys Met Glu His Ser Asp Glu Asn Ile Gln Phe Trp Met Ala Cys Glu
 5 10 15

Thr Tyr Lys Lys Ile Ala Ser Arg Trp Ser Arg Ile Ser Arg Ala Lys
 20 25 30

Lys Leu Tyr Lys Ile Tyr Ile Gln Pro Gln Ser Pro Arg Glu Ile Asn
 35 40 45
 Ile Asp Ser Ser Thr Arg Glu Thr Ile Ile Arg Asn Ile Gln Glu Pro
 50 55 60
 Thr Glu Thr Cys Phe Glu Glu Ala Gln Lys Ile Val Tyr Met His Met
 65 70 75 80
 Glu Arg Asp Ser Tyr Pro Arg Phe Leu Lys Ser Glu Met Tyr Gln Lys
 85 90 95
 Leu Leu Lys Thr Met Gln Ser Asn Asn Ser Phe
 100 105

<210> 1951
 <211> 74
 <212> PRT
 <213> Homo sapiens

<400> 1951
 Lys Trp Ser Thr Val Thr Arg Ile Phe Asn Ser Gly Trp His Val Lys
 5 10 15
 Pro Ile Arg Lys Leu Pro His Gly Gly Ala Glu Phe Leu Gly Gln Arg
 20 25 30
 Ser Phe Ile Arg Phe Thr Ser Ser His Ser Pro Leu Glu Arg Leu Thr
 35 40 45
 Leu Thr Val Arg Gln Glu Arg Leu Ser Ser Gly Thr Phe Arg Asn Pro
 50 55 60
 Leu Lys His Val Leu Lys Lys Leu Arg Lys
 65 70

<210> 1952
 <211> 94
 <212> PRT
 <213> Homo sapiens

<400> 1952
 Pro Ile Ile Glu Ile Ser Ala Pro Ala Cys Lys Ala Ser Met Asn Ala
 5 10 15
 Leu Val Pro Asp Leu Ala Ile Val Pro Arg Leu Leu Ile Lys Ser Ala
 20 25 30
 Leu Val Ile Pro Ile Pro Val Ser Thr Ile Val Arg Val Arg Ser Cys
 35 40 45
 Leu Phe Gly Ile Arg Leu Ile Cys Ser Ser Phe Ser Glu Ser Asn Leu
 50 55 60
 Leu Gly Ser Val Lys Leu Ser Tyr Arg Ile Leu Ser Asn Ala Ser Asp
 65 70 75 80
 Glu Phe Glu Met Ser Ser Leu Arg Lys Ile Ser Leu Phe Glu
 85 90

<210> 1953
<211> 61
<212> PRT
<213> Homo sapiens

<400> 1953
Asn His Arg Asp Ile Cys Thr Ser Leu Gln Ser Phe His Glu Arg Phe
 5 10 15

Gly Pro Arg Leu Gly Asp Ser Thr Lys Val Ile Asp Gln Val Ser Leu
 20 25 30

Gly His Ser Asn Ser Ser Ile His Asn Ser Glu Ser Ser Ile Leu Phe
 35 40 45

Val Arg Tyr Lys Val Asn Met Gln Leu Phe Leu Arg Val
 50 55 60

<210> 1954
<211> 58
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(58)
<223> Xaa = Any amino acid

<400> 1954
Gly Asn Pro Asp Pro Arg Pro Thr Asp Gly Gly Xaa Gly Gly Xaa Xaa
 5 10 15

Val Arg Leu Ser Gly Arg Asn Cys Pro Val Asp Val Ile Asp His Gln
 20 25 30

Tyr Phe Leu Leu Glu Gln Arg Asp Leu Ser Glu Arg Ala His Phe Lys
 35 40 45

Phe Ile Arg Cys Ile Gly Gln Asn Pro Val
 50 55

<210> 1955
<211> 139
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(139)
<223> Xaa = Any amino acid

<400> 1955
Xaa Thr Gly Ala Val Ser Phe Xaa Met Xaa Glu Glu Thr Gln Thr Gln
 5 10 15

Asp Gln Pro Met Glu Glu Xaa Glu Val Xaa Thr Phe Ala Phe Gln Ala
 20 25 30

Glu Ile Ala Gln Leu Met Ser Leu Ile Ile Asn Thr Phe Tyr Ser Asn
 35 40 45

Lys Glu Ile Phe Leu Arg Glu Leu Ile Ser Asn Ser Ser Asp Ala Leu
 50 55 60
 Asp Lys Ile Arg Tyr Glu Ser Leu Thr Asp Pro Ser Lys Leu Asp Ser
 65 70 75 80
 Glu Lys Glu Leu His Ile Asn Leu Ile Pro Asn Lys Gln Asp Arg Thr
 85 90 95
 Leu Thr Ile Val Asp Thr Gly Ile Gly Met Thr Lys Ala Asp Leu Ile
 100 105 110
 Asn Asn Leu Gly Thr Ile Ala Lys Ser Gly Thr Lys Ala Phe Met Glu
 115 120 125
 Ala Leu Gln Ala Gly Ala Asp Ile Ser Met Ile
 130 135

<210> 1956
 <211> 62
 <212> PRT
 <213> Homo sapiens

<400> 1956
 Val Phe Leu Ser Pro Trp Val Lys Ser Glu Ser Gly Ser Leu Cys Leu
 5 10 15
 Ser Val Leu Val Tyr Cys Trp Ser Glu Ser Lys Phe Leu Ile Lys Ala
 20 25 30
 Val Asp Leu Ala Leu Thr Val Tyr Ala Asp Ile Gly Glu Thr Ile Trp
 35 40 45
 Leu Phe Gln Thr Ser Gln Asp Leu Ser Lys Lys Thr Trp Leu
 50 55 60

<210> 1957
 <211> 86
 <212> PRT
 <213> Homo sapiens

<400> 1957
 Glu Pro Ser Gln Gln Leu Leu Ser Arg Ile Tyr Ser Leu Thr Ser Asn
 5 10 15
 Lys Gln Ala Leu Arg Asp Thr Glu Ser Gln Ile Gln Ile Leu Pro Met
 20 25 30
 Gly Ile Lys Arg Leu Arg Leu Ser Pro His Leu Glu Asn Tyr Leu His
 35 40 45
 His Lys Tyr Ile Ile Thr Gly Ser Leu Tyr Glu Ala Asp Thr Lys Cys
 50 55 60
 Tyr Arg His Ser Gln Asn Ile Ile Leu Gly Asn Asn Val Ile Lys Met
 65 70 75 80
 Pro Asn Leu Ser Gln Gln
 85

<210> 1958
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 1958
 Thr Lys Pro Leu Tyr Val Ala Leu Ala Gln Arg Lys Glu Glu Arg Gln
 5 10 15
 Ala His Leu Thr Asn Gln Tyr Met Gln Arg Met Ala Ser Val Arg Ala
 20 25 30
 Val Pro Asn Pro Val Ile Asn Pro Tyr Gln Pro Ala Pro Pro Ser Gly
 35 40 45
 Tyr Phe Met Ala Ala Ile Pro Gln Thr Gln Asn Arg Ala Ala Tyr Tyr
 50 55 60
 Pro Pro Ser Gln Ile Ala Gln Leu Arg Pro Ser Pro Arg Trp Thr Ala
 65 70 75 80
 Gln Gly Ala Arg Pro His Pro Phe Gln Asn Met Pro Gly Ala Ile Arg
 85 90 95
 Pro

<210> 1959
 <211> 57
 <212> PRT
 <213> Homo sapiens

<400> 1959
 Ser Ile Pro Gly Gly Tyr Asn Thr Asp Ile Ser Arg Val Phe Asn Gly
 5 10 15
 Asn Asn Cys Thr Ser Cys Gln Gln Lys Leu Leu Pro Gly Pro Leu Glu
 20 25 30
 Ile Tyr Asp Ile Asp Ala Ile Thr Phe Pro Phe Ile Asp Val Leu Phe
 35 40 45
 His Leu Glu Val Lys Ile Gly Ala Thr
 50 55

<210> 1960
 <211> 78
 <212> PRT
 <213> Homo sapiens

<400> 1960
 Leu Asp Val Leu Gln Met Lys Glu Glu Asp Val Leu Lys Phe Leu Ala
 5 10 15
 Ala Gly Thr His Leu Gly Gly Thr Asn Leu Asp Phe Gln Met Glu Gln
 20 25 30
 Tyr Ile Tyr Lys Arg Lys Ser Asp Gly Ile Tyr Ile Ile Asn Leu Lys
 35 40 45
 Arg Thr Trp Glu Lys Leu Leu Leu Ala Ala Arg Ala Ile Val Ala Ile

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<210> 1961
<211> 65
<212> PRT
<213> Homo sapiens
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Leu
65

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<210> 1962
<211> 64
<212> PRT
<213> Homo sapiens
```

Ile Phe Gln Thr Ser Ile Asn Ser Ala Ile Lys Arg Cys Ser Phe Phe
50 55 60

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<210> 1963
<211> 79
<212> PRT
<213> Homo sapiens
```

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<220>  
<221> variant  
<222> (1)...(79)  
<223> Xaa = Any amino acid
```

Leu Leu Ile Ile Xaa Xaa Xaa Ile Val Pro Ile Phe Leu Leu Leu Asp
20 25 30

Lys Asp Asp Ser Lys Ala Gly Met Glu Glu Asp His Thr Tyr Glu Gly
 35 40 45
 Leu Asp Ile Asp Gln Thr Ala Thr Tyr Glu Asp Ile Val Thr Leu Arg
 50 55 60
 Thr Gly Glu Val Lys Trp Ser Val Gly Glu His Pro Gly Gln Glu
 65 70 75

<210> 1964
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 1964
 Leu Gly Gly Pro Gly Lys Gly Leu Gly His Glu Pro Gly Ser Ser Glu
 5 10 15
 Ala Val Thr Glu Ala Arg Glu Pro Ala Pro Arg Ser Trp Gly Asp Leu
 20 25 30
 Ala Leu Thr Pro Gly Leu Gly Ala His Leu Gln Thr Thr Ser Leu Pro
 35 40 45
 Leu Ser Ala Ala Ser Leu Cys Pro His Arg Trp Leu Ser Gly Gln Cys
 50 55 60
 Pro Gly Pro Arg Arg Cys Asp Leu Pro Pro Cys Gln Pro Cys Cys His
 65 70 75 80
 Pro Cys Pro Ala Ala Gly Arg
 85

<210> 1965
 <211> 113
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(113)
 <223> Xaa = Any amino acid

<400> 1965
 Trp Gly Val Arg Glu Arg Gly Trp Ala Met Ser Gln Ala Ala Pro Lys
 5 10 15
 Gln Ser Leu Arg Pro Gly Ser Leu His Pro Gly His Gly Ala Thr Trp
 20 25 30
 Leu Ser Leu Leu Ala Trp Val Leu Thr Tyr Arg Pro Leu His Phe Pro
 35 40 45
 Cys Pro Gln Arg His Tyr Val Leu Ile Gly Gly Cys Leu Val Asn Val
 50 55 60
 Gln Ala Leu Val Gly Val Ile Phe Leu His Ala Ser Leu Ala Val Ile
 65 70 75 80
 Leu Val Gln Gln Gln Glu Asp Arg His Asp Xaa Xaa Xaa Asp Asp Gln

His Pro Met Leu Trp Ser Cys His Pro Leu Gln Met Leu Leu Gly Thr
 100 105 110

Thr Ser His Gly Cys
 115

<210> 1968
 <211> 83
 <212> PRT
 <213> Homo sapiens

<400> 1968
 Val Ile Ser Val Arg Thr Leu Pro Ser Ile Leu Met Asn Arg Cys Met
 5 10 15

Gln Ile Phe Phe Thr Ser Ser Pro Val Arg Ala Tyr Leu Ser Leu Phe
 20 25 30

Leu Arg Lys Met Met Arg Gly Arg His Ser Leu Asn Leu Trp Gly Pro
 35 40 45

Val Asp Gly Arg Gly Ala Asn Thr Pro Val Asn Leu Ser Ser Ile Gln
 50 55 60

Cys Phe Gly Ala Ala Thr Arg Phe Arg Cys Phe Leu Gly Pro Arg Ala
 65 70 75 80

Met Ala Ala

<210> 1969
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(67)
 <223> Xaa = Any amino acid

<400> 1969
 Leu Lys Gln Arg Asn Thr Leu Lys Asp Gly Ile Ile Met Ile Xaa Thr
 5 10 15

Leu Leu Ile Ile Leu Phe Ile Ile Val Pro Ile Phe Leu Leu Leu Asp
 20 25 30

Lys Asp Asp Ser Lys Ala Gly Met Glu Glu Asp His Xaa Tyr Glu Gly
 35 40 45

Leu Asp Ile Asp Gln Thr Ala Thr Tyr Glu Asp Ile Val Thr Leu Arg
 50 55 60

Thr Gly Glu
 65

<210> 1970
 <211> 74
 <212> PRT

<213> Homo sapiens

<400> 1970

Ile Tyr Asp Ser Leu Ala Tyr Trp Asn Trp Ser Ala Ser Lys Thr Gly
 5 10 15

Trp Leu His Arg Arg Thr Arg Gln Ser Arg Leu Phe Leu Cys Thr Asp
 20 25 30

Ser Glu Thr Val Leu Ser Gly Arg Ser Ser Gly Leu Pro Gly Pro Asp
 35 40 45

Thr Cys Pro Arg Glu Ser Pro Glu Ala Trp Thr Val Leu Leu Cys Phe
 50 55 60

His Arg Ser Gly Arg Gly Glu Ser Pro Trp
 65 70

<210> 1971

<211> 101

<212> PRT

<213> Homo sapiens

<400> 1971

Lys Thr Ile Tyr Arg Gln Phe Phe Thr Ser Leu Ile Phe Thr Asp Ser
 5 10 15

Thr Ser Tyr Gly Met Ala Tyr Gly Leu Pro Pro Lys Tyr Thr Ile Leu
 20 25 30

Trp His Ile Gly Ile Gly Gln Pro Gln Arg Pro Ala Gly Tyr Ile Val
 35 40 45

Ala Arg Asp Ser Pro Ala Tyr Ser Ser Ala Arg Thr Arg Arg Arg Ser
 50 55 60

Ser Ala Gly Gly Ala Gln Val Ser Leu Gly Gln Thr Arg Ala Pro Glu
 65 70 75 80

Ser Pro Gln Lys His Gly Gln Phe Cys Ser Val Ser Ile Ala Gln Ala
 85 90 95

Gly Glu Arg Val Arg
 100

<210> 1972

<211> 101

<212> PRT

<213> Homo sapiens

<400> 1972

Lys Gln Ser Thr Gly Ser Ser Leu Gln Val Ser Tyr Leu Gln Ile Ala
 5 10 15

Gln Ala Met Ala Trp Arg Met Ala Ser Leu Leu Asn Ile Arg Phe Phe
 20 25 30

Gly Ile Leu Glu Leu Val Ser Leu Lys Asp Arg Leu Ala Thr Ser Ser
 35 40 45

His Glu Thr Val Pro Leu Ile Pro Leu His Gly Leu Gly Asp Gly Pro

50 55 60
 Gln Arg Glu Glu Leu Arg Ser Pro Trp Ala Arg His Val Pro Gln Arg
 65 70 75 80
 Val Pro Arg Ser Met Asp Ser Ser Ala Leu Phe Pro Ser Leu Arg Gln
 85 90 95
 Gly Arg Glu Ser Val
 100

<210> 1973
 <211> 74
 <212> PRT
 <213> Homo sapiens

<400> 1973
 His Gly Leu Ser Pro Leu Pro Glu Arg Trp Lys Gln Ser Arg Thr Val
 5 10 15
 His Ala Ser Gly Asp Ser Leu Gly His Val Ser Gly Pro Gly Arg Pro
 20 25 30
 Glu Leu Leu Pro Leu Arg Thr Val Ser Glu Ser Val Gln Arg Asn Lys
 35 40 45
 Arg Asp Cys Leu Val Arg Arg Cys Ser Gln Pro Val Phe Glu Ala Asp
 50 55 60
 Gln Phe Gln Tyr Ala Lys Glu Ser Tyr Ile
 65 70

<210> 1974
 <211> 64
 <212> PRT
 <213> Homo sapiens

<400> 1974
 Gly Pro Ser Pro Ser Pro Cys Arg Gly Ile Ser Gly Thr Val Ser Cys
 5 10 15
 Asp Asp Val Ala Ser Arg Ser Leu Arg Leu Thr Asn Ser Asn Met Pro
 20 25 30
 Lys Asn Arg Ile Phe Arg Arg Glu Ala Ile Arg His Ala Ile Ala Cys
 35 40 45
 Ala Ile Cys Lys Tyr Glu Thr Cys Lys Glu Leu Pro Val Asp Cys Phe
 50 55 60

<210> 1975
 <211> 98
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(98)
 <223> Xaa = Any amino acid

<400> 1975

Pro Asn Cys Leu Ser Asn Val Cys Ile Asn Cys Glu Ser Gln Xaa Xaa
 5 10 15

Gln Leu Leu Ser Arg Ile Tyr Ser Leu Thr Ser Asn Lys Gln Ala Leu
 20 25 30

Arg Asp Thr Glu Ser Gln Ile Gln Ile Leu Pro Met Gly Ile Lys Arg
 35 40 45

Leu Arg Leu Ser Pro His Leu Glu Asn Tyr Leu His His Lys Tyr Ile
 50 55 60

Ile Thr Gly Ser Leu Tyr Glu Ala Asp Thr Lys Cys Tyr Arg His Ser
 65 70 75 80

Gln Asn Ile Ile Leu Gly Asn Asn Val Ile Lys Met Pro Asn Leu Ser
 85 90 95

Gln Gln

<210> 1976

<211> 66

<212> PRT

<213> Homo sapiens

<400> 1976

Lys Asp Gly Ile Ile Met Ile Gln Thr Leu Leu Ile Ile Leu Phe Ile
 5 10 15

Ile Val Pro Ile Phe Leu Leu Leu Asp Lys Asp Asp Ser Lys Ala Gly
 20 25 30

Met Glu Glu Asp His Thr Tyr Glu Gly Leu Asp Ile Asp Gln Thr Ala
 35 40 45

Thr Tyr Glu Asp Ile Val Thr Leu Arg Thr Gly Glu Val Lys Trp Phe
 50 55 60

Cys Arg
65

<210> 1977

<211> 84

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(84)

<223> Xaa = Any amino acid

<400> 1977

Pro Ala Pro Arg Ser Trp Gly Asp Leu Ala Leu Thr Pro Gly Leu Gly
 5 10 15

Xaa Ser Pro Thr Glu Pro Leu His Phe Pro Cys Pro Gln Arg His Tyr
 20 25 30

Val Leu Ile Gly Gly Cys Leu Val Asn Val Gln Ala Leu Val Gly Val

35 40 45
 Ile Phe Leu His Ala Ser Leu Ala Val Ile Leu Val Gln Gln Gln Glu
 50 55 60
 Asp Arg His Asp Asp Glu Glu Asp Asp Gln Gln Arg Leu Asp His Asp
 65 70 75 80
 Asp Thr Ile Leu

<210> 1978
 <211> 64
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(64)
 <223> Xaa = Any amino acid

<400> 1978
 Cys Thr Gln Val Met Gly Arg Pro Gly Ser His Ser Trp Pro Gly Cys
 5 10 15
 Xaa Thr Tyr Arg Thr Thr Ser Leu Pro Leu Ser Ala Ala Ser Leu Cys
 20 25 30
 Pro His Arg Trp Leu Ser Gly Gln Cys Pro Gly Pro Arg Arg Cys Asp
 35 40 45
 Leu Pro Pro Cys Gln Pro Cys Cys His Pro Cys Pro Ala Ala Gly Arg
 50 55 60

<210> 1979
 <211> 69
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(69)
 <223> Xaa = Any amino acid

<400> 1979
 Leu Leu Leu Pro Asp Thr Leu His Arg Leu Val Asp Phe Gly Met Ser
 5 10 15
 Gly Leu Arg Leu His Ala Arg Gly Cys Asn Thr Met Tyr Ser Lys Ala
 20 25 30
 Thr Leu Gly Val Ile Asp Gln Thr Glu Ile Leu Ser Arg Leu Xaa Asn
 35 40 45
 Ala Asp Asp Ile His Glu Ser Ser Xaa Gly Arg Xaa Tyr Gln Phe Gly
 50 55 60
 Pro Cys His Xaa Phe
 65

<210> 1980
<211> 57
<212> PRT
<213> Homo sapiens

<400> 1980
Ala Thr Cys Phe Ser Phe Gly Arg Asn Ser Leu Pro Thr Gly Ile Thr
 5 10 15

Thr Gly Ser Tyr Ser Phe Cys Phe Gln Thr His Ser Ile Ala Leu Ser
 20 25 30

Ile Leu Glu Cys Leu Gly Ser Asp Phe Met Leu Val Gly Val Ile Arg
 35 40 45

Cys Thr Ala Lys Arg Pro Leu Val Ser
 50 55

<210> 1981
<211> 66
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(66)
<223> Xaa = Any amino acid

<400> 1981
Ile Arg Arg Lys Phe Ser Pro Val Leu Xaa Met Leu Met Thr Ser Met
 5 10 15

Asn Pro Ala Xaa Val Gly Xaa Ile Ser Ser Asp Leu Ala Ile Xaa Phe
 20 25 30

Asn Glu Pro Leu His Ala Asn Leu Leu Tyr Phe Ile Xaa Xaa Gln Gly
 35 40 45

Ile Leu Lys Ser Val Pro Gln Glu Asn Asp Glu Gly Glu Thr Leu Ser
 50 55 60

Xaa Leu
 65

<210> 1982
<211> 67
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(67)
<223> Xaa = Any amino acid

<400> 1982
Lys Xaa Arg Glu Cys Leu Pro Leu Ile Ile Phe Leu Arg Asn Arg Leu
 5 10 15

Lys Tyr Ala Leu Xaa Xaa Asp Glu Val Lys Lys Ile Cys Met Gln Arg
 20 25 30

Phe Ile Lys Xaa Asp Gly Lys Val Arg Thr Asp Xaa Thr Tyr Xaa Cys
 35 40 45

Trp Ile His Gly Cys His Gln His Xaa Gln Asp Gly Arg Glu Phe Pro
 50 55 60

Ser Asp Leu
 65

<210> 1983
 <211> 99
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(99)
 <223> Xaa = Any amino acid

<400> 1983
 Arg Arg Phe Ala Cys Ser Gly Ser Leu Lys Xaa Met Ala Arg Ser Glu
 5 10 15

Leu Ile Xaa Pro Thr Xaa Ala Gly Phe Met Asp Val Ile Ser Ile Xaa
 20 25 30

Lys Thr Gly Glu Asn Phe Arg Leu Ile Tyr Asp Thr Lys Gly Arg Phe
 35 40 45

Ala Val His Arg Ile Thr Pro Thr Ser Met Lys Ser Glu Pro Arg His
 50 55 60

Ser Lys Ile Asp Lys Ala Met Glu Cys Val Trp Lys Gln Lys Leu Tyr
 65 70 75 80

Glu Pro Val Val Ile Pro Val Gly Arg Leu Phe Arg Pro Asn Glu Lys
 85 90 95

Gln Val Ala

<210> 1984
 <211> 50
 <212> PRT
 <213> Homo sapiens

<400> 1984
 Arg Ile Gly Phe Ser His Gln Gly Tyr Asn Cys Trp Trp Trp Cys His
 5 10 15

Ser Thr His Pro Gln Ile Ser Asp Trp Glu Glu Arg Thr Thr Glu Asp
 20 25 30

Cys Leu Lys Asp Ala Trp Ile Pro Cys Tyr Leu Arg Thr Leu Asn Thr
 35 40 45

Leu Thr
 50

<210> 1985

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<211> 134
<212> PRT
<213> Homo sapiens
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<400> 1985
Ala Ser Ala Glu Phe Glu Met Ala Gly Gly Lys Ala Gly Lys Asp Ser
      5                      10                      15

Gly Lys Ala Lys Thr Lys Ala Val Ser Arg Ser Gln Arg Ala Gly Leu
      20                      25                      30

Gln Phe Pro Val Gly Arg Ile His Arg His Leu Lys Ser Arg Thr Thr
      35                      40                      45

Ser His Gly Arg Val Gly Ala Thr Ala Ala Val Tyr Ser Ala Ala Ile
      50                      55                      60

Leu Glu Tyr Leu Thr Ala Glu Val Leu Glu Leu Ala Gly Asn Ala Ser
      65                      70                      75                      80

Lys Asp Leu Lys Val Lys Arg Ile Thr Pro Arg His Leu Gln Leu Ala
      85                      90                      95

Ile Arg Gly Asp Glu Glu Leu Asp Ser Leu Ile Lys Ala Thr Ile Ala
      100                     105                     110

Gly Gly Gly Val Ile Pro His Ile His Lys Ser Leu Ile Gly Lys Lys
      115                     120                     125

Gly Gln Gln Lys Thr Val
      130
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<210> 1986
<211> 67
<212> PRT
<213> Homo sapiens
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<400> 1986
Arg Cys Asp Glu Gly Val Gly Gly Gly Ile Ser Pro Trp Val Arg Leu
          5                                10                    15

Ala Phe Ser Leu Pro Cys Leu Leu Glu Leu Gln Arg Asn Ser Lys Trp
          20                                25                    30

Leu Ala Val Arg Leu Glu Arg Thr Pro Glu Arg Pro Arg Gln Arg Arg
          35                                40                    45

Phe Pro Ala Arg Arg Glu Pro Ala Cys Ser Ser Gln Trp Ala Val Phe
          50                                55                    60

Ile Asp Thr
          65

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<210> 1987
<211> 60
<212> PRT
<213> Homo sapiens
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<400> 1987
Asp Asn Lys Glu Ser Arg His Pro Leu Asp Ser Leu Leu Leu Ser Phe
5 10 15

Leu Pro Asn Gln Arg Phe Val Asp Val Trp Asn Asp Thr Thr Thr Ser
 20 25 30

Asn Cys Ser Leu Asp Glu Arg Ile Gln Phe Phe Ile Ser Thr Asn Ser
 35 40 45

Lys Leu Gln Val Thr Arg Gly Asn Thr Leu Tyr Leu
 50 55 60

<210> 1988
 <211> 64
 <212> PRT
 <213> Homo sapiens

<400> 1988
 Ile Arg Pro Thr Gly Asn Cys Lys Pro Ala Leu Cys Glu Arg Glu Thr
 5 10 15

Ala Phe Val Leu Ala Phe Pro Glu Ser Phe Pro Ala Leu Pro Pro Ala
 20 25 30

Ile Ser Asn Ser Ala Glu Ala Gln Ala Ser Lys Ala Glu Lys Arg Leu
 35 40 45

Ile Gly Pro Thr Val Arg Ser His His Leu Leu Leu Arg Arg Thr Ala
 50 55 60

<210> 1989
 <211> 53
 <212> PRT
 <213> Homo sapiens

<400> 1989
 Ile Leu Gly Val Asp Glu Tyr Gly Pro Leu Gly Thr Ala Ser Arg Leu
 5 10 15

Ser Ala Ser Gly Lys Pro Pro Leu Ser Trp Pro Phe Arg Ser Pro Phe
 20 25 30

Gln Pro Tyr Arg Gln Pro Phe Arg Ile Pro Leu Lys Leu Lys Gln Ala
 35 40 45

Arg Gln Arg Lys Gly
 50

<210> 1990
 <211> 62
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(62)
 <223> Xaa = Any amino acid

<400> 1990
 Val Phe Leu Ser Pro Trp Val Lys Ser Glu Ser Gly Ser Leu Cys Leu
 5 10 15

Ser Val Leu Val Tyr Cys Trp Ser Glu Ser Lys Phe Leu Ile Lys Xaa
20 25 30

Val Asp Leu Ala Leu Thr Val Tyr Ala Asp Ile Gly Glu Thr Ile Trp
35 40 45

Leu Phe Gln Thr Ser Gln Asp Leu Ser Lys Lys Thr Trp Leu
50 55 60

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<210> 1991
<211> 86
<212> PRT
<213> Homo sapiens
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<220>  
<221> variant  
<222> (1)...(86)  
<223> Xaa = Any amino acid
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<400> 1991
Glu Pro Ser Gln Gln Xaa Leu Ser Arg Ile Tyr Ser Leu Thr Ser Asn
 5 10 15

Lys Gln Ala Leu Arg Asp Thr Glu Ser Gln Ile Gln Ile Leu Pro Met
20 25 30

Gly Ile Lys Arg Leu Arg Leu Xaa Pro His Leu Glu Xaa Tyr Leu His
35 40 45

His Lys Tyr Ile Ile Thr Gly Ser Leu Tyr Glu Ala Asp Thr Lys Cys
50 55 60

Tyr Arg His Ser Gln Asn Ile Ile Leu Gly Asn Asn Val Ile Lys Met
65 70 75 80

Pro Asn Xaa Ser Gln Gln
85

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<210> 1992
<211> 185
<212> PRT
<213> Homo sapiens
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<400> 1992
Phe Asp Asp Arg Arg Gly Arg Pro Val Gly Phe Pro Met Arg Gly Arg
 5 10 15

Gly Gly Phe Asp Arg Met Pro Pro Gly Arg Gly Gly Arg Pro Met Pro
20 25 30

Pro Ser Arg Arg Asp Tyr Asp Asp Met Ser Pro Arg Arg Gly Pro Pro
35 40 45

Pro Pro Pro Pro Gly Arg Gly Gly Arg Gly Gly Ser Arg Ala Arg Asn
50 55 60

Leu Pro Leu Pro Pro Pro Pro Pro Arg Gly Gly Asp Leu Met Ala
65 70 75 80

Tyr Asp Arg Arg Gly Arg Pro Gly Asp Arg Tyr Asp Gly Met Val Gly
85 90 95

Phe Ser Ala Asp Glu Thr Trp Asp Ser Ala Ile Asp Thr Trp Ser Pro
 100 105 110
 Ser Glu Trp Gln Met Ala Tyr Glu Pro Gln Gly Gly Ser Gly Tyr Asp
 115 120 125
 Tyr Ser Tyr Ala Gly Gly Arg Gly Ser Tyr Gly Asp Leu Gly Gly Pro
 130 135 140
 Ile Ile Thr Thr Gln Val Thr Ile Pro Lys Asp Leu Ala Gly Ser Ile
 145 150 155 160
 Ile Gly Lys Gly Gly Gln Arg Ile Lys Gln Ile Arg His Glu Ser Gly
 165 170 175
 Ala Ser Ile Lys Ile Asp Glu Pro Leu
 180 185

<210> 1993
 <211> 65
 <212> PRT
 <213> Homo sapiens

<400> 1993
 Ala Leu Val Glu Asp His Leu Pro Leu Leu Pro Asp Glu Ala Ala Gly
 5 10 15
 Val Val Ala Glu Leu Gly Ile Phe Leu Phe Leu His His His His Leu
 20 25 30
 Glu Gly Glu Thr Ser Trp Pro Met Thr Glu Glu Gly Asp Leu Glu Thr
 35 40 45
 Val Thr Thr Ala Trp Leu Val Ser Val Leu Met Lys Leu Gly Thr Leu
 50 55 60
 Gln
 65

<210> 1994
 <211> 112
 <212> PRT
 <213> Homo sapiens

<400> 1994
 Trp Ala Pro Cys Ile Tyr Cys Arg Val Pro Ser Phe Ile Ser Thr Glu
 5 10 15
 Thr Asn His Ala Val Val Thr Val Ser Arg Ser Pro Ser Ser Val Ile
 20 25 30
 Gly His Glu Val Ser Pro Ser Arg Trp Trp Trp Trp Arg Lys Arg Lys
 35 40 45
 Ile Pro Ser Ser Ala Thr Thr Pro Ala Ala Ser Ser Gly Arg Arg Gly
 50 55 60
 Arg Trp Ser Ser Thr Arg Ala His Ile Ile Ile Ile Ser Ser Arg Trp
 65 70 75 80

Arg His Gly Thr Pro Thr Pro Thr Arg Arg His Ser Val Lys Thr Thr
85 90 95

Ser Ser Pro His Gly Lys Ser His Trp Ala Ser Ala Thr Val Ile Lys
100 105 110

<210> 1995
<211> 87
<212> PRT
<213> Homo sapiens

<400> 1995
Ile Leu Thr Leu Tyr Ser Glu Pro Ser Phe Asn Thr Met Val Ser Phe
5 10 15

Leu Arg Ala Ser Arg Ser Pro Val Arg Ser Met Val Ile Gly Pro Gly
20 25 30

Ala Leu Ser Gln Thr Arg Val Ser Arg Val Thr Thr Thr Leu Gly Ala
35 40 45

Phe Gly Ser Val Thr Thr Gly Pro Ser Pro Ser Ser Val Phe Leu Tyr
50 55 60

Leu Ile Arg Leu Ser Ser Ser Leu Ser Ile Ser Cys Ser Ser Phe Arg
65 70 75 80

Asp Phe Cys Gly Gly Gly Leu
85

<210> 1996
<211> 55
<212> PRT
<213> Homo sapiens

<400> 1996
His Asn Gly Phe Leu Phe Glu Gly Phe Gln Ile Ser Ser Lys Val His
5 10 15

Gly Asp Trp Ser Arg Gly Thr Leu Thr Asn Gln Gly Glu Pro Gly Asp
20 25 30

Asn Asp Ile Gly Gly Phe Arg Ile Cys His His Arg Thr Ile Ser Gln
35 40 45

Gln Arg Phe Leu Val Leu Asn
50 55

<210> 1997
<211> 123
<212> PRT
<213> Homo sapiens

<400> 1997
Ile Arg Met Thr Glu Lys Ala Pro Glu Pro His Val Glu Glu Asp Asp
5 10 15

Asp Asp Glu Leu Asp Ser Lys Leu Asn Tyr Lys Pro Pro Pro Gln Lys
20 25 30

Ser Leu Lys Glu Leu Gln Glu Met Asp Lys Asp Asp Glu Ser Leu Ile
 35 40 45
 Lys Tyr Lys Lys Thr Leu Leu Gly Asp Gly Pro Val Val Thr Asp Pro
 50 55 60
 Lys Ala Pro Asn Val Val Thr Arg Leu Thr Leu Val Cys Glu Ser
 65 70 75 80
 Ala Pro Gly Pro Ile Thr Met Asp Leu Thr Gly Asp Leu Glu Ala Leu
 85 90 95
 Lys Lys Glu Thr Ile Val Leu Lys Glu Gly Ser Glu Tyr Arg Val Lys
 100 105 110
 Ile His Phe Lys Val Asn Arg Asp Ile Val Ser
 115 120

<210> 1998
 <211> 191
 <212> PRT
 <213> Homo sapiens

<400> 1998
 Pro Lys Glu Val Arg Gln Leu Ala Glu Asp Phe Leu Lys Asp Tyr Ile
 5 10 15
 His Ile Asn Ile Gly Ala Leu Glu Leu Ser Ala Asn His Asn Ile Leu
 20 25 30
 Gln Ile Val Asp Val Cys His Asp Val Glu Lys Asp Glu Lys Leu Ile
 35 40 45
 Arg Leu Met Glu Glu Ile Met Ser Glu Lys Glu Asn Lys Thr Ile Val
 50 55 60
 Phe Val Glu Thr Lys Arg Arg Cys Asp Glu Leu Thr Arg Lys Met Arg
 65 70 75 80
 Arg Asp Gly Trp Pro Ala Met Gly Ile His Gly Asp Lys Ser Gln Gln
 85 90 95
 Glu Arg Asp Trp Val Leu Asn Glu Phe Lys His Gly Lys Ala Pro Ile
 100 105 110
 Leu Ile Ala Thr Asp Val Ala Ser Arg Gly Leu Asp Val Glu Asp Val
 115 120 125
 Lys Phe Val Ile Asn Tyr Asp Tyr Pro Asn Ser Ser Glu Asp Tyr Ile
 130 135 140
 His Arg Ile Gly Arg Thr Ala Arg Ser Thr Lys Thr Gly Thr Ala Tyr
 145 150 155 160
 Thr Phe Phe Thr Pro Asn Asn Ile Lys Gln Val Ser Asp Leu Ile Ser
 165 170 175
 Val Leu Arg Glu Ala Asn Gln Ala Ile Asn Pro Lys Leu Leu Gln
 180 185 190

<210> 1999

<211> 51
<212> PRT
<213> Homo sapiens

<400> 1999
Leu Lys Gln Leu Gly Ile Asn Cys Leu Ile Ser Phe Thr Lys His Arg
5 10 15
Asp Lys Val Ala His Leu Leu Tyr Val Ile Arg Cys Lys Glu Ser Val
20 25 30
Cys Cys Ala Cys Phe Gly Thr Ala Ser Ser Ser Ser Asn Ser Met Asn
35 40 45
Ile Ile Leu
50

<210> 2000
<211> 51
<212> PRT
<213> Homo sapiens

<400> 2000
Asn Pro Val Thr Leu Leu Leu Thr Leu Val Thr Met Asp Thr His Gly
5 10 15
Arg Pro Pro Ile Ser Pro His Phe Ser Gly Lys Leu Ile Thr Ser Ser
20 25 30
Phe Gly Phe His Lys Asn Asn Gly Phe Ile Leu Leu Leu Thr His Asp
35 40 45
Leu Phe His
50

<210> 2001
<211> 55
<212> PRT
<213> Homo sapiens

<400> 2001
Leu Leu Ser Pro Trp Ile Pro Met Ala Gly His Pro Ser Leu Leu Ile
5 10 15
Phe Leu Val Ser Ser Ser His Leu Leu Leu Val Ser Thr Lys Thr Met
20 25 30
Val Leu Phe Ser Phe Ser Leu Met Ile Ser Ser Ile Arg Arg Ile Ser
35 40 45
Phe Ser Ser Phe Ser Thr Ser
50 55

<210> 2002
<211> 95
<212> PRT
<213> Homo sapiens

<220>
<221> variant

<222> (1)...(95)

<223> Xaa = Any amino acid

<400> 2002

Pro Leu Xaa Val Ala Leu Ala Gln Arg Lys Glu Glu Arg Gln Ala His
 5 10 15

Leu Thr Asn Gln Tyr Met Gln Arg Met Ala Ser Val Arg Ala Val Pro
 20 25 30

Asn Pro Val Ile Asn Pro Tyr Gln Pro Ala Pro Pro Ser Gly Tyr Phe
 35 40 45

Met Ala Ala Ile Pro Gln Thr Gln Asn Xaa Ala Ala Tyr Tyr Pro Pro
 50 55 60

Ser Gln Ile Ala Gln Leu Arg Pro Ser Pro Arg Trp Thr Ala Gln Gly
 65 70 75 80

Ala Arg Pro His Pro Phe Gln Asn Met Pro Gly Ala Ile Arg Pro
 85 90 95

<210> 2003

<211> 60

<212> PRT

<213> Homo sapiens

<400> 2003

Pro Gly Phe Pro Leu Trp Glu Val Leu Phe Leu Ala Gly Gln Leu Gly
 5 10 15

Arg Glu Trp Arg Thr Glu Lys Arg Val Glu Ile Thr Cys Ser Leu Glu
 20 25 30

Leu Ser Trp Gly Thr Ser Pro His Ser Val His Lys Ser Leu Pro Leu
 35 40 45

Glu Met Glu Cys Ser Phe Tyr His Gly Lys Arg Ile
 50 55 60

<210> 2004

<211> 57

<212> PRT

<213> Homo sapiens

<400> 2004

Val Gly His Asp Ser Glu Gln Asp Arg Pro Lys Glu Val Gln Gly Leu
 5 10 15

Trp Ser Gly Met Glu Thr Ser Ser Glu Arg Thr His Gly Arg Ser Arg
 20 25 30

Cys Arg Arg Tyr Thr Ser Ser Arg Ile Thr His Arg Met Asp Pro Leu
 35 40 45

Glu Val Lys Thr Cys Gly Lys Thr Val
 50 55

<210> 2005

<211> 50

<212> PRT

<213> Homo sapiens

<400> 2005

Cys Cys Asn Gln Val Ser Pro Cys Gly Lys Cys Cys Phe Leu Leu Gly
5 10 15

Ser Trp Glu Gly Asn Gly Glu Gln Arg Arg Glu Trp Lys Ser His Ala
20 25 30

His Leu Asn Phe Pro Gly Glu Arg Leu Leu Thr Ala Tyr Thr Arg Ala
35 40 45

Ser Leu
50

<210> 2006

<211> 53

<212> PRT

<213> Homo sapiens

<400> 2006

Lys Trp Ser Val His Phe Ile Met Gly Lys Glu Ser Glu Trp Asp Met
5 10 15

Ile Gln Asn Arg Thr Gly Pro Arg Lys Cys Arg Gly Cys Gly Val Gly
20 25 30

Trp Arg Gln Ala Leu Lys Gly His Met Gly Asp Leu Asp Val Glu Gly
35 40 45

Thr Gln Val Val Gly
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<210> 2007

<211> 65

<212> PRT

<213> Homo sapiens

<400> 2007

His Pro Gly Phe Gln Val Leu Ser Asn Thr Val Gly Pro Leu Lys Ala
5 10 15

Ser Ser Phe Leu Pro Leu Pro Gln Ser His Pro Tyr Gln Asp Lys Gly
20 25 30

Leu Leu Thr Val Leu Ser Ile Ala Pro Thr Val Thr Met Phe Ala Ser
35 40 45

Leu Leu Ser Pro Thr Glu Gln Leu Pro Ile Thr Leu Ser Tyr His Met
50 55 60

Ser
65

<210> 2008

<211> 64

<212> PRT

<213> Homo sapiens

<400> 2008

Ile Ser His Val Ser Phe Gln Ser Leu Ser Pro Ser His Ser Thr Ala
5 10 15

Pro Ala Leu Pro Trp Ala Gly Pro Val Leu Asn His Val Pro Leu Arg
20 25 30

Phe Phe Ser His Asp Lys Met Asn Thr Pro Phe Leu Lys Gly Gly Ser
35 40 45

Cys Val Arg Cys Glu Glu Thr Phe Pro Arg Lys Val Gln Val Ser Met
50 55 60

<210> 2009

<211> 52

<212> PRT

<213> Homo sapiens

<400> 2009

Ala Trp Gly Ile His Leu Pro Arg Ile Ser Ile Leu Ala Ser Arg Ser
5 10 15

Ser Leu Ile Gln Trp Gly Leu Ser Arg His Pro Leu Ser Phe Leu Tyr
20 25 30

Leu Lys Ala Thr Leu Ile Arg Ile Lys Gly Ser Ser Leu Ser Ser Pro
35 40 45

Leu Pro Pro Arg
50

<210> 2010

<211> 67

<212> PRT

<213> Homo sapiens

<400> 2010

Gln Cys Leu Leu Pro Tyr Phe Leu Gln Leu Ser Ser Phe Leu Leu His
5 10 15

Cys Leu Thr Thr Cys Leu Asn Leu Gln Trp Ile His Pro Val Ser Tyr
20 25 30

Pro Thr Thr Cys Val Pro Ser Thr Ser Arg Ser Pro Met Cys Pro Phe
35 40 45

Arg Ala Cys Leu His Pro Thr Pro Gln Pro Leu His Phe Leu Gly Pro
50 55 60

Val. Leu Phe
65

<210> 2011

<211> 58

<212> PRT

<213> Homo sapiens

<400> 2011

Leu Thr Arg Gly Leu Thr Pro Arg Glu Phe Ile Gln Phe Leu Asn Val
5 10 15

Arg Ser Ser Leu Val Ser Pro Ser Arg Ala Pro Gln Ser Met Ser Trp
 20 25 30
 Phe Ser Gly Leu Cys Arg Ala Gly Tyr Leu Leu Lys Arg Leu Ala Ile
 35 40 45
 Lys Ala Lys Phe Asn Leu Gly Phe Pro Arg
 50 55

<210> 2012
 <211> 76
 <212> PRT
 <213> Homo sapiens

<400> 2012
 Leu Pro Asn Gln Gly Gln Cys Glu Ser Ala Val Ser Phe Ile Glu Ile
 5 10 15
 Leu Ser Thr Asp Ala Asn Gln Gly Glu Leu Arg Leu Ile Leu Pro Gln
 20 25 30
 Phe Tyr Arg Val Val Thr Ile Leu Lys Leu Leu His Ile Ala Ser Gln
 35 40 45
 Phe Gly Val Trp Arg Phe Val Tyr Ser Val Pro Val Asn Arg Asn Phe
 50 55 60
 Asp Leu Phe Ile Glu Leu Glu Asp Asp Gln Gly Ile
 65 70 75

<210> 2013
 <211> 63
 <212> PRT
 <213> Homo sapiens

<400> 2013
 Val Thr Val Gln Met Ile Asp Ser Arg Val Asn Thr Gln Gly Val His
 5 10 15
 Pro Val Pro Lys Cys Pro Leu Phe Ser Arg Leu Thr Phe Lys Ser Pro
 20 25 30
 Pro Val Asn Val Leu Val Leu Trp Phe Val Gln Gly Arg Val Ser Val
 35 40 45
 Lys Glu Val Gly Asn Lys Ser Gln Val Gln Leu Gly Val Pro Ser
 50 55 60

<210> 2014
 <211> 156
 <212> PRT
 <213> Homo sapiens

<400> 2014
 Arg Gly Asn Pro Lys Leu Asn Leu Ala Phe Ile Ala Asn Leu Phe Asn
 5 10 15
 Arg Tyr Pro Ala Leu His Lys Pro Glu Asn Gln Asp Ile Asp Trp Gly
 20 25 30

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<210> 2015
<211> 62
<212> PRT
<213> Homo sapiens
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<220>
<221> variant
<222> (1)...(62)
<223> Xaa = Any amino acid
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<400> 2015
Val Phe Leu Ser Pro Trp Val Lys Ser Glu Ser Gly Ser Leu Cys Xaa
          5                      10                      15

Ser Val Leu Val Tyr Cys Trp Ser Glu Ser Lys Phe Leu Ile Lys Ala
          20                      25                      30

Val Asp Leu Ala Leu Thr Val Tyr Ala Xaa Ile Gly Glu Thr Ile Trp
          35                      40                      45

Leu Phe Gln Thr Ser Gln Asp Xaa Ser Lys Xaa Thr Trp Leu
          50                      55                      60

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<210> 2016
<211> 86
<212> PRT
<213> Homo sapiens
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<220>
<221> variant
<222> (1)...(86)
<223> Xaa = Any amino acid
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<400> 2016
Glu Pro Ser Gln Gln Leu Leu Ser Arg Ile Tyr Ser Leu Thr Ser Asn
5 10 15

Lys Gln Ala Leu Xaa Asp Thr Glu Ser Gln Ile Gln Ile Leu Pro Met
 20 25 30
 Gly Ile Lys Arg Leu Arg Leu Ser Pro His Leu Glu Asn Tyr Leu His
 35 40 45
 His Lys Tyr Ile Ile Thr Gly Ser Leu Tyr Glu Ala Asp Thr Lys Cys
 50 55 60
 Tyr Arg His Ser Gln Asn Ile Ile Leu Gly Asn Asn Val Ile Lys Met
 65 70 75 80
 Pro Asn Leu Ser Gln Gln
 85

<210> 2017
 <211> 69
 <212> PRT
 <213> Homo sapiens

<400> 2017
 Leu Cys Leu Arg Ala Leu Ala Gly Gln Glu Gln Asp Ser Trp Asp Gly
 5 10 15
 Ala Ala Gln Ala Trp Phe Leu Leu Pro Val Ala Ala Asp Asn Leu Gly
 20 25 30
 Gly Asn Leu Pro Leu Ala Val Leu Glu Ala Thr Val Leu Ser Pro Ser
 35 40 45
 Ile Thr Ala Leu Gly Pro Gly Asp Ala Lys Gly Gln Asn Gln Asp Lys
 50 55 60
 Glu Ala Gln Ser Gln
 65

<210> 2018
 <211> 102
 <212> PRT
 <213> Homo sapiens

<400> 2018
 Leu Pro Thr Ser Pro Ser Ala Leu Ala Ser Tyr Ser Pro Ser Thr Thr
 5 10 15
 Asp Met Ala Gln Ser Leu Ala Leu Ser Leu Leu Ile Leu Val Leu Ala
 20 25 30
 Phe Gly Ile Pro Arg Thr Gln Gly Ser Asp Gly Gly Ala Gln Asp Cys
 35 40 45
 Cys Leu Lys Tyr Ser Gln Arg Lys Ile Pro Ala Lys Val Val Arg Ser
 50 55 60
 Tyr Arg Lys Gln Glu Pro Ser Leu Gly Cys Ser Ile Pro Ala Ile Leu
 65 70 75 80
 Phe Leu Pro Arg Lys Arg Ser Gln Ala Glu Leu Cys Ala Asp Pro Lys
 85 90 95

Glu Leu Trp Val Gln Gln
100

<210> 2019
<211> 77
<212> PRT
<213> Homo sapiens

<400> 2019
Ala Ser Leu Ser Trp Phe Trp Pro Leu Ala Ser Pro Gly Pro Lys Ala
5 10 15

Val Met Glu Gly Leu Arg Thr Val Ala Ser Ser Thr Ala Lys Gly Arg
20 25 30

Phe Pro Pro Arg Leu Ser Ala Ala Thr Gly Ser Arg Asn Gln Ala Trp
35 40 45

Ala Ala Pro Ser Gln Leu Ser Cys Ser Cys Pro Ala Ser Ala Leu Arg
50 55 60

Gln Ser Tyr Val Gln Thr Gln Arg Ser Ser Gly Cys Ser
65 70 75

<210> 2020
<211> 60
<212> PRT
<213> Homo sapiens

<400> 2020
Trp Arg Gly Ser Gly Leu Leu Pro Gln Val Gln Pro Lys Glu Asp Ser
5 10 15

Arg Gln Gly Cys Pro Gln Leu Pro Glu Ala Gly Thr Lys Leu Gly Leu
20 25 30

Leu His Pro Ser Tyr Pro Val Leu Ala Pro Gln Ala Leu Ser Gly Arg
35 40 45

Ala Met Cys Arg Pro Lys Gly Ala Leu Gly Ala Ala
50 55 60

<210> 2021
<211> 115
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(115)
<223> Xaa = Any amino acid

<400> 2021
Pro Met Trp Leu Val Phe Ser Leu Gln Leu Ala Arg Phe His Thr Leu
5 10 15

Thr Ser Leu Ser Gln Pro Gln Glu Thr Met Ile Gly Leu Leu Leu
20 25 30

Gly Glu Lys Arg Thr Gln Asp Thr His Ser Glu Trp Leu Ser Ser Trp

35 40 45
 Thr Val Tyr Leu His Thr Pro Arg Val Phe His Ser Leu Met Val Leu
 50 55 60
 Ser Arg Asp Pro Xaa Thr Ile Cys Arg Leu Ser Glu Glu Lys Ala Thr
 65 70 75 80
 Leu Xaa Thr Ser Leu Ala Trp Pro Thr Asn Xaa Xaa Val Val Val Pro
 85 90 95
 Val Val Arg Ser Gln Arg Arg Arg Val Pro Ser Gln Glu Pro Glu Arg
 100 105 110
 Ala Asn Trp
 115

<210> 2022
 <211> 50
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(50)
 <223> Xaa = Any amino acid

<400> 2022
 Leu Asp Gly Phe Ile Ser Arg Ser Xaa Asp Asn Leu Pro Val Val Arg
 5 10 15
 Gly Glu Gly His Thr Xaa His Ile Leu Gly Met Ala His Lys Ser Xaa
 20 25 30
 Xaa Gly Gly Ala Arg Cys Glu Ile Pro Glu Ala Gln Gly Ser Ile Pro
 35 40 45
 Gly Ala
 50

<210> 2023
 <211> 114
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(114)
 <223> Xaa = Any amino acid

<400> 2023
 Gln Phe Ala Leu Ser Gly Ser Trp Asp Gly Thr Leu Arg Leu Trp Asp
 5 10 15
 Leu Thr Thr Gly Thr Thr Xaa Xaa Arg Phe Val Gly His Ala Lys Asp
 20 25 30
 Val Xaa Ser Val Ala Phe Ser Ser Asp Asn Arg Gln Ile Val Xaa Gly
 35 40 45
 Ser Arg Asp Lys Thr Ile Lys Leu Trp Asn Thr Leu Gly Val Cys Lys

720

50 55 60
 Tyr Thr Val Gln Asp Glu Ser His Ser Glu Trp Val Ser Cys Val Arg
 65 70 75 80
 Phe Ser Pro Asn Ser Ser Asn Pro Ile Ile Val Ser Cys Gly Trp Asp
 85 90 95
 Lys Leu Val Lys Val Trp Asn Leu Ala Asn Cys Lys Leu Lys Thr Asn
 100 105 110
 His Ile

<210> 2024
 <211> 74
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(74)
 <223> Xaa = Any amino acid

<400> 2024
 Val Trp Pro Ser Pro Leu Thr Thr Gly Arg Leu Ser Xaa Asp Leu Glu
 5 10 15
 Ile Lys Pro Ser Ser Tyr Gly Ile Pro Trp Val Cys Ala Asn Thr Leu
 20 25 30
 Ser Arg Met Arg Ala Thr Gln Ser Gly Cys Leu Val Ser Ala Ser Arg
 35 40 45
 Pro Thr Ala Ala Thr Leu Ser Ser Ser Pro Val Ala Gly Thr Ser Trp
 50 55 60
 Ser Arg Tyr Gly Thr Trp Leu Thr Ala Ser
 65 70

<210> 2025
 <211> 62
 <212> PRT
 <213> Homo sapiens

<400> 2025
 Val Phe Leu Ser Pro Trp Val Lys Ser Glu Ser Gly Ser Leu Cys Leu
 5 10 15
 Ser Val Leu Val Tyr Cys Trp Ser Glu Ser Lys Phe Leu Ile Lys Ala
 20 25 30
 Val Asp Leu Ala Pro Thr Val Tyr Ala Asp Ile Gly Glu Thr Ile Trp
 35 40 45
 Leu Phe Gln Thr Ser Gln Asp Leu Ser Lys Lys Thr Trp Leu
 50 55 60

<210> 2026
 <211> 116

<212> PRT

<213> Homo sapiens

<400> 2026

Glu Pro Cys Phe Ile Thr Arg Ser Ser Tyr Ser Asn Pro Val Met Phe
 5 10 15

 Glu Ile Thr Lys Leu Ser Leu Gln Cys Leu His Lys Leu Trp Glu Pro
 20 25 30

 Ser Gln Gln Leu Leu Ser Arg Ile Tyr Ser Leu Thr Ser Asn Lys Gln
 35 40 45

 Ala Leu Arg Asp Thr Glu Ser Gln Ile Gln Ile Leu Pro Met Gly Ile
 50 55 60

 Lys Arg Leu Arg Leu Ser Pro His Leu Glu Asn Tyr Leu His His Lys
 65 70 75 80

 Tyr Ile Ile Thr Gly Ser Leu Tyr Glu Ala Asp Thr Lys Cys Tyr Arg
 85 90 95

 His Ser Gln Asn Ile Ile Leu Gly Asn Asn Val Ile Lys Met Pro Asn
 100 105 110

 Leu Ser Gln Gln
 115

<210> 2027

<211> 87

<212> PRT

<213> Homo sapiens

<400> 2027

Leu Gly Gly Pro Gly Lys Gly Leu Gly His Glu Pro Gly Ser Ser Glu
 5 10 15

 Ala Val Thr Glu Ala Arg Glu Pro Ala Pro Arg Ser Trp Gly Asp Leu
 20 25 30

 Ala Leu Thr Pro Gly Leu Gly Ala His Leu Gln Thr Thr Ser Leu Pro
 35 40 45

 Leu Ser Ala Ala Ser Leu Cys Pro His Arg Trp Leu Ser Gly Gln Cys
 50 55 60

 Pro Gly Pro Arg Arg Cys Asp Leu Pro Pro Cys Gln Pro Cys Cys His
 65 70 75 80

 Pro Cys Pro Ala Ala Gly Arg
 85

<210> 2028

<211> 113

<212> PRT

<213> Homo sapiens

<400> 2028

Trp Gly Val Arg Glu Arg Gly Trp Ala Met Ser Gln Ala Ala Pro Lys
 5 10 15

Gln Ser Leu Arg Pro Gly Ser Leu His Pro Gly His Gly Ala Thr Trp
 20 25 30
 Leu Ser Leu Leu Ala Trp Val Leu Thr Tyr Arg Pro Leu His Phe Pro
 35 40 45
 Cys Pro Gln Arg His Tyr Val Leu Ile Gly Gly Cys Leu Val Asn Val
 50 55 60
 Gln Ala Leu Val Gly Val Ile Phe Leu His Ala Ser Leu Ala Val Ile
 65 70 75 80
 Leu Val Gln Gln Gln Glu Asp Arg His Asp Asp Glu Glu Asp Asp Gln
 85 90 95
 Gln Arg Leu Asp His Asp Asp Thr Ile Leu Gln Arg Val Pro Leu Leu
 100 105 110
 Gln

<210> 2029
 <211> 79
 <212> PRT
 <213> Homo sapiens

<400> 2029
 Leu Lys Gln Arg Asn Thr Leu Lys Asp Gly Ile Ile Met Ile Gln Thr
 5 10 15
 Leu Leu Ile Ile Leu Phe Ile Ile Val Pro Ile Phe Leu Leu Leu Asp
 20 25 30
 Lys Asp Asp Ser Lys Ala Gly Met Glu Glu Asp His Thr Tyr Glu Gly
 35 40 45
 Leu Asp Ile Asp Gln Thr Ala Thr Tyr Glu Asp Ile Val Thr Leu Arg
 50 55 60
 Thr Gly Glu Val Lys Trp Ser Val Gly Glu His Pro Gly Gln Glu
 65 70 75

<210> 2030
 <211> 52
 <212> PRT
 <213> Homo sapiens

<400> 2030
 Arg Thr Ile Gly Gly Cys Arg His Val Leu Leu Glu Gln Leu Pro Arg
 5 10 15
 Thr Thr Leu Leu Arg Ser Gly Phe Gln Arg Pro Pro Asn Phe Val Ser
 20 25 30
 Phe Asn Ser Phe Arg Pro Asp Leu Leu Phe Gly Ser Val Thr Gly Arg
 35 40 45
 Gln Val Ser Thr
 50

<210> 2031
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 2031
 His Met Pro Asp Trp Leu Phe Ala Thr His Leu Lys Asp Thr Thr Gln
 5 10 15
 Ser Met Glu Ala Phe Asn Arg Thr Ala Leu Pro Ile Ser Gly Leu Leu
 20 25 30
 Ala Asp Ala Asp Met Phe Tyr Ser Ser Ser Tyr Gln Gly Pro Leu Tyr
 35 40 45
 Cys Asp Gln Asp Ser Asn Asp His Leu Ile Ser Tyr Leu Ser Thr Leu
 50 55 60
 Phe Asp Arg Thr Ser Tyr Ser Glu Ala Leu Gln Glu Asp Arg Ser Gln
 65 70 75 80
 Leu Arg Asp Gln Ile Thr Leu Ser Thr Leu Trp Asp Arg Cys Asn Leu
 85 90 95
 Ala Leu Gln Gly Ser Ala Pro Ile Thr Ser Arg Pro Ala Asn Thr Asp
 100 105 110
 Leu Glu Val
 115

<210> 2032
 <211> 52
 <212> PRT
 <213> Homo sapiens

<400> 2032
 Val Glu Thr Cys Leu Pro Val Thr Leu Pro Asn Lys Arg Ser Gly Arg
 5 10 15
 Lys Glu Leu Lys Asp Thr Lys Leu Gly Gly Arg Trp Asn Pro Asp Arg
 20 25 30
 Ser Lys Val Val Leu Gly Asn Cys Ser Ser Arg Thr Cys Leu His Pro
 35 40 45
 Pro Ile Val Arg
 50

<210> 2033
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 2033
 Asn Met Ser Ala Ser Ala Asn Ser Pro Leu Ile Gly Arg Ala Val Arg
 5 10 15
 Leu Lys Ala Ser Ile Asp Trp Val Val Ser Phe Lys Trp Val Ala Lys
 20 25 30
 Ser Gln Ser Gly Ile Cys His Glu Gly Phe Ser Asp Arg Leu Met Val

35 40 45

Cys Cys Leu Thr Ser Leu Gly Lys
50 55

<210> 2034
<211> 86
<212> PRT
<213> Homo sapiens

<400> 2034
Glu Pro Ser Gln Gln Leu Leu Ser Arg Ile Tyr Ser Leu Thr Ser Asn
5 10 15
Lys Gln Ala Leu Arg Asp Thr Glu Ser Gln Ile Gln Ile Leu Pro Met
20 25 30
Gly Ile Lys Arg Leu Arg Leu Ser Pro His Leu Glu Asn Tyr Leu His
35 40 45
His Lys Tyr Ile Ile Thr Gly Ser Leu Tyr Glu Ala Asp Thr Lys Cys
50 55 60
Tyr Arg His Ser Gln Asn Ile Ile Leu Gly Asn Asn Val Ile Lys Met
65 70 75 80
Pro Asn Leu Ser Gln Gln
85

<210> 2035
<211> 62
<212> PRT
<213> Homo sapiens

<400> 2035
Val Phe Leu Ser Pro Trp Val Lys Ser Glu Ser Gly Ser Leu Cys Leu
5 10 15
Ser Val Leu Val Tyr Cys Trp Ser Glu Ser Lys Phe Leu Ile Lys Ala
20 25 30
Val Asp Leu Ala Leu Thr Val Tyr Ala Asp Ile Gly Glu Thr Ile Trp
35 40 45
Leu Phe Gln Thr Ser Gln Asp Leu Ser Lys Lys Thr Trp Leu
50 55 60

<210> 2036
<211> 191
<212> PRT
<213> Homo sapiens

<400> 2036
Pro Lys Glu Val Arg Gln Leu Ala Glu Asp Phe Leu Lys Asp Tyr Ile
5 10 15
His Ile Asn Ile Gly Ala Leu Glu Leu Ser Ala Asn His Asn Ile Leu
20 25 30
Gln Ile Val Asp Val Cys His Asp Val Glu Lys Asp Glu Lys Leu Ile

35	40	45
Arg Leu Met Glu Glu Ile Met Ser Glu Lys Glu Asn Lys Thr Ile Val		
50	55	60
Phe Val Glu Thr Lys Arg Arg Cys Asp Glu Leu Thr Arg Lys Met Arg		
65	70	75
Arg Asp Gly Trp Pro Ala Met Gly Ile His Gly Asp Lys Ser Gln Gln		
	85	90
Glu Arg Asp Trp Val Leu Asn Glu Phe Lys His Gly Lys Ala Pro Ile		
	100	105
Leu Ile Ala Thr Asp Val Ala Ser Arg Gly Leu Asp Val Glu Asp Val		
	115	120
Lys Phe Val Ile Asn Tyr Asp Tyr Pro Asn Ser Ser Glu Asp Tyr Ile		
	130	135
His Arg Ile Gly Arg Thr Ala Arg Ser Thr Lys Thr Gly Thr Ala Tyr		
	145	150
Thr Phe Phe Thr Pro Asn Asn Ile Lys Gln Val Ser Asp Leu Ile Ser		
	165	170
Val Leu Arg Glu Ala Asn Gln Ala Ile Asn Pro Lys Leu Leu Gln		
	180	185
		190

<210> 2037

<211> 51

<212> PRT

<213> Homo sapiens

<400> 2037

Leu Lys Gln Leu Gly Ile Asn Cys Leu Ile Ser Phe Thr Lys His Arg		
	5	10
Asp Lys Val Ala His Leu Leu Tyr Val Ile Arg Cys Lys Glu Ser Val		
	20	25
Cys Cys Ala Cys Phe Gly Thr Ala Ser Ser Ser Ser Asn Ser Met Asn		
	35	40
Ile Ile Leu		
	50	

<210> 2038

<211> 51

<212> PRT

<213> Homo sapiens

<400> 2038

Asn Pro Val Thr Leu Leu Leu Thr Leu Val Thr Met Asp Thr His Gly		
	5	10
Arg Pro Pro Ile Ser Pro His Phe Ser Gly Lys Leu Ile Thr Ser Ser		
	20	25
Phe Gly Phe His Lys Asn Asn Gly Phe Ile Leu Leu Leu Thr His Asp		
	35	40
		45

Leu Phe His
50

<210> 2039
<211> 55
<212> PRT
<213> Homo sapiens

<400> 2039
Leu Leu Ser Pro Trp Ile Pro Met Ala Gly His Pro Ser Leu Leu Ile
5 10 15

Phe Leu Val Ser Ser Ser His Leu Leu Leu Val Ser Thr Lys Thr Met
20 25 30

Val Leu Phe Ser Phe Ser Leu Met Ile Ser Ser Ile Arg Arg Ile Ser
35 40 45

Phe Ser Ser Phe Ser Thr Ser
50 55

<210> 2040
<211> 87
<212> PRT
<213> Homo sapiens

<400> 2040
Leu Gly Gly Pro Gly Lys Gly Leu Gly His Glu Pro Gly Ser Ser Glu
5 10 15

Ala Val Thr Glu Ala Arg Glu Pro Ala Pro Arg Ser Trp Gly Asp Leu
20 25 30

Ala Leu Thr Pro Gly Leu Gly Ala His Leu Gln Thr Thr Ser Leu Pro
35 40 45

Leu Ser Ala Ala Ser Leu Cys Pro His Arg Trp Leu Ser Gly Gln Cys
50 55 60

Pro Gly Pro Arg Arg Cys Asp Leu Pro Pro Cys Gln Pro Cys Cys His
65 70 75 80

Pro Cys Pro Ala Ala Gly Arg
85

<210> 2041
<211> 113
<212> PRT
<213> Homo sapiens

<400> 2041
Trp Gly Val Arg Glu Arg Gly Trp Ala Met Ser Gln Ala Ala Pro Lys
5 10 15

Gln Ser Leu Arg Pro Gly Ser Leu His Pro Gly His Gly Ala Thr Trp
20 25 30

Leu Ser Leu Leu Ala Trp Val Leu Thr Tyr Arg Pro Leu His Phe Pro
35 40 45

Cys Pro Gln Arg His Tyr Val Leu Ile Gly Gly Cys Leu Val Asn Val
 50 55 60
 Gln Ala Leu Val Gly Val Ile Phe Leu His Ala Ser Leu Ala Val Ile
 65 70 75 80
 Leu Val Gln Gln Gln Glu Asp Arg His Asp Asp Glu Glu Asp Asp Gln
 85 90 95
 Gln Arg Leu Asp His Asp Asp Thr Ile Leu Gln Arg Val Pro Leu Leu
 100 105 110
 Gln

<210> 2042
 <211> 79
 <212> PRT
 <213> Homo sapiens

<400> 2042
 Leu Lys Gln Arg Asn Thr Leu Lys Asp Gly Ile Ile Met Ile Gln Thr
 5 10 15
 Leu Leu Ile Ile Leu Phe Ile Ile Val Pro Ile Phe Leu Leu Leu Asp
 20 25 30
 Lys Asp Asp Ser Lys Ala Gly Met Glu Glu Asp His Thr Tyr Glu Gly
 35 40 45
 Leu Asp Ile Asp Gln Thr Ala Thr Tyr Glu Asp Ile Val Thr Leu Arg
 50 55 60
 Thr Gly Glu Val Lys Trp Ser Val Gly Glu His Pro Gly Gln Glu
 65 70 75

<210> 2043
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 2043
 Ile Ser Thr Ser Leu Leu Leu Met Leu Leu Val Ser Ser Leu Ser Pro
 5 10 15
 Val Gln Gly Val Leu Glu Val Tyr Tyr Thr Ser Leu Arg Cys Arg Cys
 20 25 30
 Val Gln Glu Ser Ser Val Phe Ile Pro Arg Arg Phe Ile Asp Arg Ile
 35 40 45
 Gln Ile Leu Pro Arg Gly Asn Gly Cys Pro Arg Lys Glu Ile Ile Val
 50 55 60
 Trp Lys Lys Asn Lys Ser Ile Val Cys Val Asp Pro Gln Ala Glu Trp
 65 70 75 80
 Ile Gln Arg Met Met Glu Val Leu Arg Lys Arg Ser Ser Ser Thr Leu
 85 90 95

Pro Val Pro Val Phe Lys Arg Lys Ile Pro
100 105

<210> 2044
<211> 53
<212> PRT
<213> Homo sapiens

<400> 2044
Ile Phe Ser Arg Lys Lys Asn Phe Pro Ile Gln Ile Ser Met Arg Leu
5 10 15

Cys Lys Asn Asn Leu Ala Glu Ala Asp Gly Ala Asn Ser Ser Phe Phe
20 25 30

Thr His Ser Thr Leu Tyr Thr Leu Gly Val Cys Ile Leu Ile His Arg
35 40 45

Gly Gly Lys Phe Leu
50

<210> 2045
<211> 55
<212> PRT
<213> Homo sapiens

<400> 2045
Glu Lys Glu Val Leu Gln Leu Tyr Gln Phe Gln Cys Leu Arg Glu Arg
5 10 15

Phe Pro Asp Ala Asp Ile Ser Thr Lys Asn Thr Cys Ile Leu Pro Leu
20 25 30

Ser Leu Leu Trp Ile Leu Val Leu Cys Leu Val Lys Ser Phe Pro Gly
35 40 45

Lys Arg Thr Ser Pro Tyr Lys
50 55

<210> 2046
<211> 51
<212> PRT
<213> Homo sapiens

<400> 2046
Asp Tyr Val Lys Ile Thr Leu Gln Lys Leu Met Gly Gln Thr Gln Ala
5 10 15

Ser Ser Leu Thr Ala Pro Tyr Ile His Leu Glu Phe Ala Phe Leu Phe
20 25 30

Ile Gly Glu Glu Ser Phe Phe Glu Asn Ser Tyr Ser Val Ile Ser Asn
35 40 45

Thr Gly Leu
50

<210> 2047
<211> 51

<212> PRT

<213> Homo sapiens

<400> 2047

Ser His Ala Tyr Leu Tyr Gly Glu Val Leu Phe Pro Gly Lys Asp Leu
5 10 15

Thr Lys His Lys Thr Lys Ile Gln Ser Arg Asp Lys Gly Arg Met Gln
20 25 30

Val Phe Leu Val Glu Ile Ser Ala Ser Gly Asn Leu Ser Leu Lys His
35 40 45

Trp Asn Trp
50

<210> 2048

<211> 78

<212> PRT

<213> Homo sapiens

<400> 2048

Cys Pro Arg Trp Gly Thr Pro Arg Tyr Trp Leu Gly Ala Leu Tyr Arg
5 10 15

Asn Gln Gln Ser Ser Pro Thr Ala Pro Pro Gly Leu Leu Pro Leu Glu
20 25 30

Tyr Phe Pro Ala Ala Pro His Cys Ser His Ser Arg Gln Trp Arg Cys
35 40 45

Ser Gln Thr His Arg Ile His His His Pro Gln Met Leu Gly Pro Cys
50 55 60

Arg Gln Glu Ile Cys Gly Glu Ile Gln Gly Cys Gly Trp Phe
65 70 75

<210> 2049

<211> 134

<212> PRT

<213> Homo sapiens

<400> 2049

Asn Leu Leu Ile Glu Pro Gln Gln Gly Ala Asp Asn Cys Asp Val Asn
5 10 15

Gln Cys His Ser Phe Ala His Gln Lys Ser Pro Arg Leu Gln Val Ser
20 25 30

Ile Gln Gln Pro Gln Asn Ser Pro His Phe Leu Leu Cys Ile Leu Ser
35 40 45

Gly Leu Phe Val Val Val His Asp Ala Gln Gly Gly Glu His Pro Gly
50 55 60

Thr Gly Trp Gly His Tyr Ile Gly Ile Ser Lys Ala His Pro Leu His
65 70 75 80

His Leu Gly Cys Cys Leu Trp Ser Thr Ser Pro Gln Leu Leu Ile Ala
85 90 95

His Ile Val Gly Asn Gly Val Ala Leu Lys His Thr Glu Ser Ile Ile
 100 105 110
 Thr Leu Lys Cys Trp Asp Leu Ala Gly Arg Lys Phe Ala Glu Lys Phe
 115 120 125
 Arg Gly Ala Val Gly Leu
 130

<210> 2050
 <211> 66
 <212> PRT
 <213> Homo sapiens

<400> 2050
 Ala Ser Ser Ser Pro Arg Ile Arg Leu Thr Ser Ser Phe Ala Phe Ser
 5 10 15
 Val Ala Cys Leu Leu Trp Cys Met Met Pro Lys Val Gly Asn Thr Gln
 20 25 30
 Val Leu Ala Gly Gly Thr Ile Ser Glu Ser Ala Lys Leu Thr His Cys
 35 40 45
 Thr Thr Trp Ala Ala Ala Ser Gly Val Leu Pro Arg Ser Ser Ser Leu
 50 55 60
 Leu Thr
 65

<210> 2051
 <211> 141
 <212> PRT
 <213> Homo sapiens

<400> 2051
 Gln Thr Asn Arg Thr Pro Glu Phe Leu Arg Lys Phe Pro Ala Gly Lys
 5 10 15
 Val Pro Ala Phe Glu Gly Asp Asp Gly Phe Cys Val Phe Glu Ser Asn
 20 25 30
 Ala Ile Ala Tyr Tyr Val Ser Asn Glu Glu Leu Arg Gly Ser Thr Pro
 35 40 45
 Glu Ala Ala Ala Gln Val Val Gln Trp Val Ser Phe Ala Asp Ser Asp
 50 55 60
 Ile Val Pro Pro Ala Ser Thr Trp Val Phe Pro Thr Leu Gly Ile Met
 65 70 75 80
 His His Asn Lys Gln Ala Thr Glu Asn Ala Lys Glu Glu Val Arg Arg
 85 90 95
 Ile Leu Gly Leu Leu Asp Ala Tyr Leu Lys Thr Arg Thr Phe Leu Val
 100 105 110
 Gly Glu Arg Val Thr Leu Val Asp Ile Thr Val Val Cys Thr Leu Leu
 115 120 125
 Trp Leu Tyr Lys Gln Val Leu Glu Pro Ser Phe His Gln

130 135 140

<210> 2052
 <211> 61
 <212> PRT
 <213> Homo sapiens

<400> 2052
 Cys His Lys Arg Ser Leu Pro Ile Cys Thr Tyr Ser Gln Glu Glu His
 5 10 15
 Leu Tyr Gly Lys Asp Gly Ser Pro Val Ser Leu Pro Tyr Thr Leu Gln
 20 25 30
 Gly Leu Ser Glu Ala Ser Leu Met Arg Cys Leu Lys Pro Gly His Gly
 35 40 45
 Tyr Lys Gln Leu His Gly Ser Lys Lys Phe Cys Pro Phe
 50 55 60

<210> 2053
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 2053
 Ser Ile Phe Trp Gly Tyr Asp Gly Leu Thr Phe Ile Arg Lys Tyr Gly
 5 10 15
 Phe Ile Leu Ile Val Ala Ser Ser Ser Gly Gly Val Asn His Phe Ile
 20 25 30
 Phe Thr Leu Thr Trp Phe Glu Phe Leu Ser His Tyr Cys Ile Tyr Phe
 35 40 45
 Ala Phe Pro
 50

<210> 2054
 <211> 192
 <212> PRT
 <213> Homo sapiens

<400> 2054
 Leu Leu Trp Lys Gly Ser Phe Lys Pro Ser Glu His Val Lys Pro Arg
 5 10 15
 Ala Pro Gly Asn Leu Thr Val His Thr Asn Val Ser Asp Thr Leu Leu
 20 25 30
 Leu Thr Trp Ser Asn Pro Tyr Pro Pro Asp Asn Tyr Leu Tyr Asn His
 35 40 45
 Leu Thr Tyr Ala Val Asn Ile Trp Ser Glu Asn Asp Pro Ala Asp Phe
 50 55 60
 Arg Ile Tyr Asn Val Thr Tyr Leu Glu Pro Ser Leu Arg Ile Ala Ala
 65 70 75 80
 Ser Thr Leu Lys Ser Gly Ile Ser Tyr Arg Ala Arg Val Arg Ala Trp

				85					90					95			
Ala	Gln	Cys	Tyr	Asn	Thr	Thr	Trp	Ser	Glu	Trp	Ser	Pro	Ser	Thr	Lys		
			100					105						110			
Trp	His	Asn	Ser	Tyr	Arg	Glu	Pro	Phe	Glu	Gln	His	Leu	Leu	Leu	Gly		
		115					120					125					
Val	Ser	Ala	Ser	Cys	Ile	Val	Ile	Leu	Ala	Val	Cys	Leu	Leu	Cys	Tyr		
	130				135						140						
Val	Ser	Ile	Thr	Lys	Ile	Lys	Lys	Glu	Trp	Trp	Asp	Gln	Ile	Pro	Asn		
145					150					155					160		
Pro	Ala	Arg	Ser	Arg	Leu	Val	Ala	Ile	Ile	Ile	Gln	Asp	Ala	Gln	Gly		
				165					170					175			
Ser	Gln	Trp	Glu	Lys	Arg	Ser	Arg	Gly	Gln	Glu	Pro	Ala	Lys	Cys	Pro		
			180					185					190				

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<210> 2055
<211> 75
<212> PRT
<213> Homo sapiens
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```
<400> 2055  
Gly Pro Gly Leu Ser Ala Ile Thr Pro Pro Gly Val Ser Gly Ala Pro  
                    5                      10                  15  
  
Ala Pro Ser Gly Thr Thr Pro Thr Gly Ser Pro Ser Ser Ser Thr Ser  
                20              25          30  
  
Cys Trp Ala Ser Ala Leu Pro Ala Leu Ser Ser Trp Pro Ser Ala Cys  
        35              40              45  
  
Cys Ala Met Ser Ala Ser Pro Arg Leu Arg Lys Asn Gly Gly Ile Arg  
      50              55              60  
  
Phe Pro Thr Gln Pro Ala Ala Ala Ser Trp Leu  
    65              70              75
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<210> 2056
<211> 64
<212> PRT
<213> Homo sapiens
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<400> 2056
Arg Pro Ala Gly Gly Ala Ala Arg Arg Ala Pro Cys Arg Ser Cys Ala
          5                      10                      15

Thr Trp Cys Trp Gly Ser Thr His Ser Arg Trp Cys Tyr Ser Thr Glu
          20                      25                      30

Pro Arg Pro Ser Pro Val Pro Cys Arg Lys Ser Gln Thr Ser Gly Cys
          35                      40                      45

Trp Leu Arg Cys Gly Gly Arg Val Leu Gly Arg Ser Arg Tyr Arg Phe
          50                      55                      60

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<210> 2057

<211> 104
 <212> PRT
 <213> Homo sapiens

<400> 2057
 Pro Leu Ser Ile Leu Asp Tyr Tyr Ser His Glu Ala Ala Ala Gly Trp
 5 10 15
 Val Gly Asn Leu Ile Pro Pro Phe Phe Leu Asn Leu Gly Asp Ala Asp
 20 25 30
 Ile Ala Gln Gln Ala Asp Gly Gln Asp Asp Asn Ala Gly Ser Ala Asp
 35 40 45
 Ala Gln Gln Glu Val Leu Leu Glu Gly Leu Pro Val Gly Val Val Pro
 50 55 60
 Leu Gly Ala Gly Ala Pro Leu Thr Pro Gly Gly Val Ile Ala Leu Ser
 65 70 75 80
 Pro Gly Pro His Pro Cys Pro Val Gly Asn Pro Arg Leu Gln Gly Ala
 85 90 95
 Gly Cys Asp Ala Glu Gly Gly Phe
 100

<210> 2058
 <211> 71
 <212> PRT
 <213> Homo sapiens

<400> 2058
 Val Gly His Val Ile Asp Ser Glu Ile Cys Arg Val Val Phe Thr Pro
 5 10 15
 Asn Val Asp Cys Ile Gly Glu Met Ile Ile Gln Val Ile Val Arg Gly
 20 25 30
 Ile Arg Val Ala Pro Gly Gln Gln Gln Ser Val Gly Asp Ile Gly Val
 35 40 45
 Asn Cys Gln Val Ser Trp Gly Pro Gly Phe His Met Leu Ala Gly Leu
 50 55 60
 Glu Gly Ala Leu Pro Gln Gln
 65 70

<210> 2059
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 2059
 Thr Leu Pro Pro Asp Arg Met Lys Phe Ile Ser Thr Ser Leu Leu Leu
 5 10 15
 Met Leu Leu Val Ser Ser Leu Ser Pro Val Gln Gly Val Leu Glu Val
 20 25 30
 Tyr Tyr Thr Ser Leu Arg Cys Arg Cys Val Gln Glu Ser Ser Val Phe
 35 40 45

Ile Pro Arg Arg Phe Ile Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn
 50 55 60
 Gly Cys Pro Arg Lys Glu Ile Ile Val Trp Lys Lys Asn Lys Ser Ile
 65 70 75 80
 Val Cys Val Asp Pro Gln Ala Glu Trp Ile Gln Arg Met Met Glu Val
 85 90 95
 Leu Arg Lys Arg Ser Ser Ser Thr Leu Pro Val Pro Val Phe Lys Arg
 100 105 110
 Lys Ile Pro
 115

<210> 2060
 <211> 55
 <212> PRT
 <213> Homo sapiens

<400> 2060
 Glu Lys Glu Val Leu Gln Leu Tyr Gln Phe Gln Cys Leu Arg Glu Arg
 5 10 15
 Phe Pro Asp Ala Asp Ile Ser Thr Lys Asn Thr Cys Ile Leu Pro Leu
 20 25 30
 Ser Leu Leu Trp Ile Leu Val Leu Cys Leu Val Lys Ser Phe Pro Gly
 35 40 45
 Lys Arg Thr Ser Pro Tyr Lys
 50 55

<210> 2061
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 2061
 Ser His Ala Tyr Leu Tyr Gly Glu Val Leu Phe Pro Gly Lys Asp Leu
 5 10 15
 Thr Lys His Lys Thr Lys Ile Gln Ser Arg Asp Lys Gly Arg Met Gln
 20 25 30
 Val Phe Leu Val Glu Ile Ser Ala Ser Gly Asn Leu Ser Leu Lys His
 35 40 45
 Trp Asn Trp
 50

<210> 2062
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 2062
 Asn Lys Lys Ala Met Leu Val Glu Cys Thr Val His Ile Gly Gly Ala
 5 10 15

Arg Leu Ile Thr Ile Arg Leu Leu Ala Ser Pro Val Gln Ser Phe Leu
 20 25 30
 Trp Lys Ala Val Asp Phe Ser Leu Ala Ser Leu Ser Ser Ser Val Ser
 35 40 45
 Thr Tyr Arg Ile Ser Arg Ser Gln Pro Tyr Arg
 50 55

<210> 2063
 <211> 64
 <212> PRT
 <213> Homo sapiens

<400> 2063
 Thr Ala Lys Arg Ser Lys Ile Arg Arg Gln Cys Leu Trp Asn Val Gln
 5 10 15
 Cys Ile Leu Ala Ala His Ala Ser Leu Arg Phe Ala Cys Leu Leu Leu
 20 25 30
 Leu Phe Asn Arg Phe Phe Gly Arg Gln Trp Ile Phe Leu Leu Arg Leu
 35 40 45
 Cys Leu Leu Gln Phe Arg Leu Ile Glu Phe Leu Asp Leu Ser His Ile
 50 55 60

<210> 2064
 <211> 57
 <212> PRT
 <213> Homo sapiens

<400> 2064
 Glu Gly Asn Ala Cys Gly Met Tyr Ser Ala Tyr Trp Arg Arg Thr Pro
 5 10 15
 His Tyr Asp Ser Pro Ala Cys Phe Ser Cys Ser Ile Val Ser Leu Glu
 20 25 30
 Gly Ser Gly Phe Phe Ser Cys Val Ser Val Phe Phe Ser Phe Asp Leu
 35 40 45
 Ser Asn Phe Ser Ile Ser Ala Ile Ser
 50 55

<210> 2065
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 2065
 Arg Arg Gln Arg Arg Lys Arg Lys Ile His Cys Leu Pro Lys Lys Arg
 5 10 15
 Leu Asn Arg Arg Ser Lys Gln Ala Asn Arg Asn Glu Ala Cys Ala Ala
 20 25 30
 Asn Met His Cys Thr Phe His Lys His Cys Leu Leu Ile Leu Leu Leu
 35 40 45

Leu Ala Val
50

<210> 2066
<211> 50
<212> PRT
<213> Homo sapiens

<400> 2066
Asp Arg Tyr Trp Tyr Ser Phe Ile Ile Glu Thr Lys Arg Ser Ala Leu
5 10 15
Leu Asp Phe Pro Leu Phe Val Leu Lys Gly Ile Lys Asp Cys Arg Phe
20 25 30
Pro Ala Leu Ser Ser Arg Gly His Tyr Glu Gln Ile Lys Trp Lys Asp
35 40 45

Lys Phe
50

<210> 2067
<211> 51
<212> PRT
<213> Homo sapiens

<400> 2067
Trp Pro Arg Glu Asp Arg Ala Gly Asn Leu Gln Ser Leu Ile Pro Phe
5 10 15
Arg Thr Lys Ser Gly Lys Ser Ser Lys Ala Asp Leu Leu Val Ser Ile
20 25 30
Ile Lys Glu Tyr Gln Tyr Arg Ser Gln Lys Arg Ser Val Ser Leu Gln
35 40 45

Gly Tyr Phe
50

<210> 2068
<211> 66
<212> PRT
<213> Homo sapiens

<400> 2068
Val Thr Pro Phe Pro Phe Pro Glu Ile Gly Thr Ser Tyr Ser Lys Gly
5 10 15
Glu Arg Arg Ala Gln Arg Asp Leu Tyr Arg Thr Ser Leu Ala His Gly
20 25 30
Asp Trp Arg Gln Arg Val Gly Ser Trp Arg Gly Val Gln Ser Leu Gln
35 40 45
Gln Ile Leu Arg Ala Ser Lys Ser Ser Ser Trp Thr Phe Leu Leu Ile
50 55 60
Trp Ile
65

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<210> 2070
<211> 82
<212> PRT
<213> Homo sapiens
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```
<210> 2071
<211> 53
<212> PRT
<213> Homo sapiens
```

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<400> 2071
Ile Gln Ile Lys Arg Asn Val Gln Glu Glu Leu Phe Glu Ala Leu Asn
      5                      10                      15

Ile Cys Trp Arg Asp Trp Thr Pro Leu Gln Leu Pro Thr Leu Cys Leu
      20                      25                      30

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Gln Ser Pro Cys Ala Arg Glu Val Leu Tyr Arg Ser Leu Trp Ala Leu
 35 40 45

Leu Ser Pro Leu Glu
 50

<210> 2072

<211> 63

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(63)

<223> Xaa = Any amino acid

<400> 2072

Gly Gly Lys Met Ala Val Gln Ile Ser Lys Lys Arg Lys Phe Val Ala
 5 10 15

Asp Gly Ile Phe Lys Ala Glu Leu Asn Glu Phe Leu Thr Arg Glu Leu
 20 25 30

Ala Glu Asp Gly Tyr Ser Gly Val Glu Gly Ala Ser Tyr Thr Asn Gln
 35 40 45

Asp Arg Asn His Tyr Leu Xaa His Gln Asn Thr Xaa Cys Ser Trp
 50 55 60

<210> 2073

<211> 70

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(70)

<223> Xaa = Any amino acid

<400> 2073

Met Ser Phe Leu Leu Gly Ser Trp Leu Lys Met Ala Thr Leu Glu Leu
 5 10 15

Arg Val Arg Val Thr Pro Thr Arg Thr Glu Ile Ile Ile Leu Xaa Thr
 20 25 30

Arg Thr Xaa Asn Val Leu Gly Glu Lys Gly Arg Arg Ile Arg Glu Leu
 35 40 45

Thr Ala Val Val Gln Lys Arg Phe Gly Phe Pro Glu Gly Ser Val Glu
 50 55 60

Leu Tyr Ala Xaa Lys Val
 65 70

<210> 2074

<211> 76

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(76)

<223> Xaa = Any amino acid

<400> 2074

Thr Thr Ala Val Ser Ser Arg Ile Arg Arg Pro Phe Ser Pro Arg Thr
 5 10 15

Xaa Cys Val Leu Val Xaa Lys Ile Met Ile Ser Val Leu Val Gly Val
 20 25 30

Thr Arg Thr Leu Asn Ser Arg Val Ala Ile Phe Ser Gln Leu Pro Ser
 35 40 45

Lys Lys Leu Ile Gln Phe Ser Phe Glu Asp Ala Ile Ser Asp Lys Leu
 50 55 60

Pro Leu Leu Gly Tyr Leu His Cys His Leu Ala Ala
 65 70 75

<210> 2075

<211> 67

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(67)

<223> Xaa = Any amino acid

<400> 2075

Glu Xaa Ser Ser Gln Pro Thr Val Pro Ile Val Gly Ile Ile Ala Gly
 5 10 15

Leu Val Leu Leu Gly Ala Val Ile Thr Gly Ala Val Val Ala Ala Val
 20 25 30

Met Trp Arg Arg Asn Ser Ser Asp Arg Lys Gly Gly Ser Tyr Ser Gln
 35 40 45

Ala Ala Ser Ser Asp Ser Ala Gln Gly Ser Asp Val Ser Leu Thr Ala
 50 55 60

Cys Lys Val
 65

<210> 2076

<211> 70

<212> PRT

<213> Homo sapiens

<400> 2076

Pro Met Trp Leu Val Phe Ser Leu Gln Leu Ala Arg Phe His Thr Leu
 5 10 15

Thr Ser Leu Ser Gln Pro Gln Glu Thr Met Ile Gly Leu Leu Leu Leu
 20 25 30

Gly Glu Lys Arg Thr Gln Asp Thr His Ser Glu Trp Leu Ser Ser Trp

35 40 45
 Thr Val Tyr Leu His Thr Pro Arg Val Phe His Ser Leu Met Val Leu
 50 55 60
 Ser Arg Asp Pro Lys Thr
 65 70

<210> 2077
 <211> 70
 <212> PRT
 <213> Homo sapiens

<400> 2077
 Ile Val Phe Gly Ser Arg Asp Lys Thr Ile Lys Leu Trp Asn Thr Leu
 5 10 15
 Gly Val Cys Lys Tyr Thr Val Gln Asp Glu Ser His Ser Glu Trp Val
 20 25 30
 Ser Cys Val Arg Phe Ser Pro Asn Ser Ser Asn Pro Ile Ile Val Ser
 35 40 45
 Cys Gly Trp Asp Lys Leu Val Lys Val Trp Asn Leu Ala Asn Cys Lys
 50 55 60
 Leu Lys Thr Asn His Ile
 65 70

<210> 2078
 <211> 64
 <212> PRT
 <213> Homo sapiens

<400> 2078
 Leu Phe Leu Asp Leu Glu Ile Lys Pro Ser Ser Tyr Gly Ile Pro Trp
 5 10 15
 Val Cys Ala Asn Thr Leu Ser Arg Met Arg Ala Thr Gln Ser Gly Cys
 20 25 30
 Leu Val Ser Ala Ser Arg Pro Thr Ala Ala Thr Leu Ser Ser Ser Pro
 35 40 45
 Val Ala Gly Thr Ser Trp Ser Arg Tyr Gly Thr Trp Leu Thr Ala Ser
 50 55 60

<210> 2079
 <211> 90
 <212> PRT
 <213> Homo sapiens

<400> 2079
 Pro Lys Glu Val Arg Gln Leu Ala Glu Asp Phe Leu Lys Asp Tyr Ile
 5 10 15
 His Ile Asn Ile Gly Ala Leu Glu Leu Ser Ala Asn His Asn Ile Leu
 20 25 30
 Gln Ile Val Asp Val Cys His Asp Val Glu Lys Asp Glu Lys Leu Ile

35 40 45
 Arg Leu Met Glu Glu Ile Met Ser Glu Lys Glu Asn Lys Thr Ile Val
 50 55 60
 Phe Val Glu Thr Lys Arg Arg Cys Asp Glu Leu Thr Arg Lys Met Arg
 65 70 75 80
 Arg Asp Gly Trp Pro Ala Met Gly Ile His
 85 90

<210> 2080
 <211> 52
 <212> PRT
 <213> Homo sapiens

<400> 2080
 Pro Trp Ile Pro Met Ala Gly His Pro Ser Leu Leu Ile Phe Leu Val
 5 10 15
 Ser Ser Ser His Leu Leu Leu Val Ser Thr Lys Thr Met Val Leu Phe
 20 25 30
 Ser Phe Ser Leu Met Ile Ser Ser Ile Arg Arg Ile Ser Phe Ser Ser
 35 40 45
 Phe Ser Thr Ser
 50

<210> 2081
 <211> 74
 <212> PRT
 <213> Homo sapiens

<400> 2081
 Ala Ala Arg Glu Pro Val Trp Ala Gly Ser Val Cys Arg Arg Val Tyr
 5 10 15
 Gly Gln Ala Ala Phe Ala Gly Val Phe Thr Gly Arg Gln Arg Leu Gln
 20 25 30
 Ala Cys Leu His Ala Gly Val Ala Pro Cys Glu Thr Thr Gly Pro Gly
 35 40 45
 Phe Gln Arg Ser Cys Ser Gly Glu Ser Ala Val Phe Ser Gln Val His
 50 55 60
 Gly Ala Glu Trp Val Cys Asn Met Lys Tyr
 65 70

<210> 2082
 <211> 66
 <212> PRT
 <213> Homo sapiens

<400> 2082
 Leu Asp Asp Gly Leu Gln Pro Leu Ser Val Leu Ser Val Pro His Ser
 5 10 15
 Thr Ser Ile Ser Cys Cys Thr Pro Thr Gln Leu Arg Glu Leu Val Arg

20 25 30
 Thr Gln Pro Ile His Leu Ser Arg Thr Ser Glu Thr Leu Asp Gln Trp
 35 40 45
 Ser His Met Val Leu Arg Leu His Val Asn Thr Pro Ala Asn Ala Ala
 50 55 60
 Cys Arg
 65

<210> 2083
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 2083
 Trp Arg Gly Ser Gly Leu Leu Pro Gln Val Gln Pro Lys Glu Asp Ser
 5 10 15
 Arg Gln Gly Cys Pro Gln Leu Pro Glu Ala Gly Thr Lys Leu Arg Leu
 20 25 30
 Leu His Pro Ser Tyr Pro Val Leu Ala Pro Gln Ala Leu Ser Gly Arg
 35 40 45
 Ala Met Cys Arg Pro Lys Gly Ala Leu Gly Ala Ala
 50 55 60

<210> 2084
 <211> 95
 <212> PRT
 <213> Homo sapiens

<400> 2084
 Leu Ala Ser Tyr Ser Pro Ser Thr Thr Asp Met Ala Gln Ser Leu Ala
 5 10 15
 Leu Ser Leu Leu Thr Leu Val Leu Ala Phe Gly Ile Pro Arg Thr Gln
 20 25 30
 Gly Ser Asp Gly Gly Ala Gln Asp Cys Cys Leu Lys Tyr Ser Gln Arg
 35 40 45
 Lys Ile Pro Ala Lys Val Val Arg Ser Tyr Arg Lys Gln Glu Pro Ser
 50 55 60
 Leu Gly Cys Ser Ile Pro Ala Ile Leu Phe Leu Pro Arg Lys Arg Ser
 65 70 75 80
 Gln Ala Glu Leu Cys Ala Asp Pro Lys Glu Leu Trp Val Gln Gln
 85 90 95

<210> 2085
 <211> 50
 <212> PRT
 <213> Homo sapiens

<400> 2085
 Ala Trp Phe Leu Leu Pro Val Ala Ala Asp Asn Leu Gly Gly Asn Leu

743

5 10 15
 Pro Leu Ala Val Leu Glu Ala Thr Val Leu Ser Pro Ser Ile Thr Ala
 20 25 30
 Leu Gly Pro Gly Asp Ala Lys Gly Gln Asn Gln Gly Lys Glu Ala Gln
 35 40 45
 Ser Gln
 50

<210> 2086
 <211> 62
 <212> PRT
 <213> Homo sapiens

<400> 2086
 Val Ala Val Ser Ser Leu Arg His Gly Val Cys Ser Pro Thr Asp Ile
 5 10 15
 Gly Val Leu Arg Lys Gly Gly Val Ile Trp Gln Lys Cys His Phe Ala
 20 25 30
 Cys Cys Ile Gln Gly Ser Tyr Ser Thr Arg Tyr Cys Glu Leu Cys Ser
 35 40 45
 His Gln Leu Ala Gln Lys Gln Gln Thr Ala Leu Cys Cys Gln
 50 55 60

<210> 2087
 <211> 94
 <212> PRT
 <213> Homo sapiens

<400> 2087
 Trp Leu Ser Pro Leu Ser Ala Met Ala Cys Ala Arg Pro Leu Ile Ser
 5 10 15
 Val Tyr Ser Glu Lys Gly Glu Ser Ser Gly Lys Asn Val Thr Leu Pro
 20 25 30
 Ala Val Phe Lys Ala Pro Ile Arg Pro Asp Ile Val Asn Phe Val His
 35 40 45
 Thr Asn Leu Arg Lys Asn Asn Arg Gln Pro Tyr Ala Val Ser Glu Leu
 50 55 60
 Ala Gly His Gln Thr Ser Ala Glu Ser Trp Gly Thr Gly Arg Ala Val
 65 70 75 80
 Ala Arg Ile Pro Arg Val Arg Gly Gly Gly Thr His Arg Ser
 85 90

<210> 2088
 <211> 76
 <212> PRT
 <213> Homo sapiens

<400> 2088
 Thr Lys Leu Val Met Met Gln Lys Leu Leu Lys Cys Ser Arg Leu Val

5 10 15
 Leu Ala Leu Ala Leu Ile Leu Val Leu Glu Ser Ser Val Gln Gly Tyr
 20 25 30
 Pro Thr Gln Arg Ala Arg Tyr Gln Trp Val Arg Cys Asn Pro Asp Ser
 35 40 45
 Asn Ser Ala Asn Cys Leu Glu Glu Lys Gly Pro Met Phe Glu Leu Leu
 50 55 60
 Pro Gly Glu Ser Asn Lys Ile Pro Arg Leu Arg Thr
 65 70 75

<210> 2089
 <211> 68
 <212> PRT
 <213> Homo sapiens

<400> 2089
 Cys Arg Ser Tyr Ser Asn Ala Val Gly Leu Ser Trp Leu Leu Pro Ser
 5 10 15
 Ser Trp Phe Trp Asn Pro Gln Phe Lys Val Ile Leu Arg Arg Glu Pro
 20 25 30
 Gly Thr Asn Gly Cys Ala Ala Ile Gln Thr Val Ile Leu Gln Thr Ala
 35 40 45
 Leu Lys Lys Lys Asp Gln Cys Ser Asn Tyr Phe Gln Val Asn Pro Thr
 50 55 60
 Arg Ser Pro Val
 65

<210> 2090
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 2090
 Ile Leu Thr Leu Tyr Ser Glu Pro Ser Phe Asn Thr Met Val Ser Phe
 5 10 15
 Leu Arg Ala Ser Arg Ser Pro Val Arg Ser Met Val Ile Gly Pro Gly
 20 25 30
 Ala Leu Ser Gln Thr Arg Val Ser Arg Val Thr Thr Thr Leu Gly Ala
 35 40 45
 Phe Gly Ser Val Thr Thr Gly Pro Ser Pro Ser Ser Val Phe Leu Tyr
 50 55 60
 Leu Ile Arg Leu Ser Ser Ser Leu Ser Ile Ser Cys Ser Ser Phe Arg
 65 70 75 80
 Asp Phe Cys Gly Gly Gly Leu
 85

<210> 2091

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<211> 55
<212> PRT
<213> Homo sapiens
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<400> 2091
His Asn Gly Phe Leu Phe Glu Gly Phe Gln Ile Ser Ser Lys Val His
      5                                10                                15

Gly Asp Trp Ser Arg Gly Thr Leu Thr Asn Gln Gly Glu Pro Gly Asp
      20                                25                                30

Asn Asp Ile Gly Gly Phe Arg Ile Cys His His Arg Thr Ile Ser Gln
      35                                40                                45

Gln Arg Phe Leu Val Leu Asn
      50                                55

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<210> 2092
<211> 120
<212> PRT
<213> Homo sapiens
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<400> 2092
Leu Lys Lys Pro Gln Ser Pro His Val Glu Glu Asp Asp Asp Asp Glu
      5                      10                      15

Leu Asp Ser Lys Leu Asn Tyr Lys Pro Pro Pro Gln Lys Ser Leu Lys
      20                      25                      30

Glu Leu Gln Glu Met Asp Lys Asp Asp Glu Ser Leu Ile Lys Tyr Lys
      35                      40                      45

Lys Thr Leu Leu Gly Asp Gly Pro Val Val Thr Asp Pro Lys Ala Pro
      50                      55                      60

Asn Val Val Val Thr Arg Leu Thr Leu Val Cys Glu Ser Ala Pro Gly
      65                      70                      75                      80

Pro Ile Thr Met Asp Leu Thr Gly Asp Leu Glu Ala Leu Lys Lys Glu
      85                      90                      95

Thr Ile Val Leu Lys Glu Gly Ser Glu Tyr Arg Val Lys Ile His Phe
      100                     105                     110

Lys Val Asn Arg Asp Ile Val Ser
      115                     120

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<210> 2093
<211> 50
<212> PRT
<213> Homo sapiens
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<400> 2093
Leu Thr Leu Pro Gly Gly Ile Arg Val Arg Arg Arg Gly Arg Gly Trp
           5                      10                      15

Arg Ser Gly Gly Asp His Gly Val Ser Arg Pro His Cys Ala Ser His
           20                      25                      30

Cys Asp Glu Arg Val Leu Gly Leu Arg Arg Leu Leu Gly Ala Leu Val
           35                      40                      45

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His Pro
50

<210> 2094
<211> 93
<212> PRT
<213> Homo sapiens

<400> 2094
Gly Asp Gly Val Gly Val Gly Ala Gln Ala Ala Thr Met Ala Tyr His
5 10 15
Gly Leu Thr Val Pro Leu Ile Val Met Ser Val Phe Trp Gly Phe Val
20 25 30
Gly Phe Leu Val Pro Trp Phe Ile Pro Lys Gly Pro Asn Arg Gly Val
35 40 45
Ile Ile Thr Met Leu Val Thr Cys Ser Val Cys Cys Tyr Leu Phe Trp
50 55 60
Leu Ile Ala Ile Leu Ala Gln Leu Asn Pro Leu Phe Gly Pro Gln Leu
65 70 75 80
Lys Asn Glu Thr Ile Trp Tyr Leu Lys Tyr His Trp Pro
85 90

<210> 2095
<211> 65
<212> PRT
<213> Homo sapiens

<400> 2095
Thr Gly His Gln His Gly Asn Asp Asn Ser Pro Val Arg Thr Leu Arg
5 10 15
Asp Glu Pro Arg His Gln Glu Ala Asp Glu Ala Pro Glu His Ala His
20 25 30
His Asn Glu Arg His Ser Glu Ala Val Ile Arg His Gly Arg Arg Leu
35 40 45
Ser Ala Asn Pro Tyr Pro Val Ala Ser Leu Gly Ser His Gln Glu Val
50 55 60
Ser
65

<210> 2096
<211> 73
<212> PRT
<213> Homo sapiens

<400> 2096
Arg Met Leu Ser Tyr Ser Ser Met Leu Pro Pro Ser Gly Leu Met Leu
5 10 15
His Tyr Thr Leu Leu Gly Ser Asn Leu Pro Leu Arg Leu Lys Ala Leu
20 25 30

Glu Gly Arg Val Phe Lys Met Leu Asp Leu Val Gln Ala Gln Ile Leu
 35 40 45

Glu Leu Lys Ala Glu Gly Phe Leu Val Ala Glu Lys Lys Gln Asn Leu
 50 55 60

Met Thr Phe Gly Thr Pro Val Leu Arg
 65 70

<210> 2097
 <211> 52
 <212> PRT
 <213> Homo sapiens

<400> 2097
 Leu His Ala Ala Ala Glu Trp Leu Asp Ala Pro Leu His Pro Pro Trp
 5 10 15

Ile Gln Pro Ser Ile Lys Ala Glu Gly Ser Arg Gly Gln Ser Ile Gln
 20 25 30

Asp Val Arg Ser Gly Pro Ser Pro Asn Ser Arg Val Lys Ser Arg Gly
 35 40 45

Val Leu Ser Gly
 50

<210> 2098
 <211> 64
 <212> PRT
 <213> Homo sapiens

<400> 2098
 Trp Lys Val Gly Ser Lys Glu Gly Val Met Glu His Gln Ala Thr Arg
 5 10 15

Arg Gln His Gly Ala Ile Thr Lys His Pro Leu Gly Phe Cys Leu Ser
 20 25 30

Arg His Leu Ala Leu Thr Leu Asp Leu Val Thr Val Val Trp Leu Ile
 35 40 45

Pro Val Asn Ile Trp Arg Gln Ser Tyr Leu Ala Phe Ala Ser Arg Ala
 50 55 60

<210> 2099
 <211> 55
 <212> PRT
 <213> Homo sapiens

<400> 2099
 Leu Lys Thr Gly Val Pro Asn Val Ile Arg Phe Cys Phe Phe Ser Ala
 5 10 15

Thr Lys Asn Pro Ser Ala Phe Asn Ser Arg Ile Trp Ala Trp Thr Arg
 20 25 30

Ser Asn Ile Leu Asn Thr Leu Pro Ser Arg Ala Phe Ser Leu Asn Gly
 35 40 45

Arg Leu Asp Pro Arg Arg Val
50 55

<210> 2100
<211> 87
<212> PRT
<213> Homo sapiens

<400> 2100
Ile Leu Thr Leu Tyr Ser Glu Pro Ser Phe Asn Thr Met Val Ser Phe
5 10 15
Leu Arg Ala Ser Arg Ser Pro Val Arg Ser Met Val Ile Gly Pro Gly
20 25 30
Ala Leu Ser Gln Thr Arg Val Ser Arg Val Thr Thr Thr Leu Gly Ala
35 40 45
Phe Gly Ser Val Thr Thr Gly Pro Ser Pro Ser Ser Val Phe Leu Tyr
50 55 60
Leu Ile Arg Leu Ser Ser Ser Leu Ser Ile Ser Cys Ser Ser Phe Arg
65 70 75 80
Asp Phe Cys Gly Gly Gly Leu
85

<210> 2101
<211> 55
<212> PRT
<213> Homo sapiens

<400> 2101
His Asn Gly Phe Leu Phe Glu Gly Phe Gln Ile Ser Ser Lys Val His
5 10 15
Gly Asp Trp Ser Arg Gly Thr Leu Thr Asn Gln Gly Glu Pro Gly Asp
20 25 30
Asn Asp Ile Gly Gly Phe Arg Ile Cys His His Arg Thr Ile Ser Gln
35 40 45
Gln Arg Phe Leu Val Leu Asn
50 55

<210> 2102
<211> 50
<212> PRT
<213> Homo sapiens

<400> 2102
Thr Leu Ile Ile Phe Val His Phe Leu Gln Leu Phe Gln Gly Leu Leu
5 10 15
Trp Trp Arg Leu Ile Ile Glu Leu Ala Val Gln Leu Ile Ile Val Ile
20 25 30
Leu Leu His Met Trp Leu Trp Gly Phe Phe Ser His Ser Asp Leu Phe
35 40 45

Ile Gln
50

<210> 2103
<211> 123
<212> PRT
<213> Homo sapiens

<400> 2103
Ile Arg Met Thr Glu Lys Ala Pro Glu Pro His Val Glu Glu Asp Asp
5 10 15
Asp Asp Glu Leu Asp Ser Lys Leu Asn Tyr Lys Pro Pro Pro Gln Lys
20 25 30
Ser Leu Lys Glu Leu Gln Glu Met Asp Lys Asp Asp Glu Ser Leu Ile
35 40 45
Lys Tyr Lys Lys Thr Leu Leu Gly Asp Gly Pro Val Val Thr Asp Pro
50 55 60
Lys Ala Pro Asn Val Val Val Thr Arg Leu Thr Leu Val Cys Glu Ser
65 70 75 80
Ala Pro Gly Pro Ile Thr Met Asp Leu Thr Gly Asp Leu Glu Ala Leu
85 90 95
Lys Lys Glu Thr Ile Val Leu Lys Glu Gly Ser Glu Tyr Arg Val Lys
100 105 110
Ile His Phe Lys Val Asn Arg Asp Ile Val Ser
115 120

<210> 2104
<211> 69
<212> PRT
<213> Homo sapiens

<400> 2104
Lys Leu Leu Lys Cys Ser Arg Leu Val Leu Ala Leu Ala Leu Ile Leu
5 10 15
Val Leu Glu Ser Ser Val Gln Gly Tyr Pro Thr Gln Arg Ala Arg Tyr
20 25 30
Gln Trp Val Arg Cys Asn Pro Asp Ser Asn Ser Ala Asn Cys Leu Glu
35 40 45
Glu Lys Gly Pro Met Phe Glu Leu Leu Pro Gly Glu Ser Asn Lys Ile
50 55 60
Pro Arg Leu Arg Thr
65

<210> 2105
<211> 66
<212> PRT
<213> Homo sapiens

<400> 2105

Ser Tyr Ser Asn Ala Val Gly Leu Ser Trp Leu Leu Pro Ser Ser Trp
 5 10 15

Phe Trp Asn Pro Gln Phe Lys Val Ile Leu Arg Arg Glu Pro Gly Thr
 20 25 30

Asn Gly Cys Ala Ala Ile Gln Thr Val Ile Leu Gln Thr Ala Leu Lys
 35 40 45

Lys Lys Asp Gln Cys Ser Asn Tyr Phe Gln Val Asn Pro Thr Arg Ser
 50 55 60

Pro Val
 65

<210> 2106

<211> 58

<212> PRT

<213> Homo sapiens

<400> 2106

Gln Arg His Cys Gln Trp Leu Arg Gly Leu His Ser His Gly Val Gly
 5 10 15

Asp Pro Gly Trp Gly Pro Asp Ala Ala Pro Ala Gly Ala Arg Arg His
 20 25 30

Pro Gly Gly Pro His Gln Ala Cys Gly His Cys Gly Leu Ala His His
 35 40 45

Ser Pro Glu Arg Ala Ala Gln Cys Arg Leu
 50 55

<210> 2107

<211> 109

<212> PRT

<213> Homo sapiens

<400> 2107

His Thr Ala Pro Val Leu Asp Ile Ala Trp Cys Pro His Asn Asp Asn
 5 10 15

Val Ile Ala Ser Gly Ser Glu Asp Cys Thr Val Met Val Trp Glu Ile
 20 25 30

Pro Asp Gly Gly Leu Met Leu Pro Leu Arg Glu Pro Val Val Thr Leu
 35 40 45

Glu Gly His Thr Lys Arg Val Gly Ile Val Ala Trp His Thr Thr Ala
 50 55 60

Gln Asn Val Leu Leu Ser Ala Gly Cys Asp Asn Val Ile Met Val Trp
 65 70 75 80

Asp Val Gly Thr Gly Ala Ala Met Leu Thr Leu Gly Pro Glu Val His
 85 90 95

Pro Asp Thr Ile Tyr Ser Val Asp Trp Ser Arg Asp Gly
 100 105

<210> 2108
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 2108
 Ile Val Ser Gly Cys Thr Ser Gly Pro Ser Val Ser Met Ala Ala Pro
 5 10 15
 Val Pro Thr Ser His Thr Met Ile Thr Leu Ser Gln Pro Ala Leu Ser
 20 25 30
 Ser Thr Phe Trp Ala Val Val Cys Gln Ala Thr Met Pro Thr Arg Leu
 35 40 45
 Val Trp Pro Ser Arg Val Thr Thr Gly Ser Arg Arg Gly Ser Ile Arg
 50 55 60
 Pro Pro Ser Gly Ile Ser His Thr Met Thr Val Gln Ser Ser Glu Pro
 65 70 75 80
 Leu Ala Met Thr Leu Ser Leu Cys Gly His Gln Ala Met Ser Ser Thr
 85 90 95
 Gly Ala Val Trp
 100

<210> 2109
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 2109
 Ser Ile Ser Ala Pro Val His Thr Val Asp Arg Val Trp Val His Leu
 5 10 15
 Trp Ala Gln Cys Gln His Gly Arg Pro Ser Ala His Val Pro His His
 20 25 30
 Asp His Val Val Thr Thr Cys Thr Glu Gln His Val Leu Gly Cys Gly
 35 40 45
 Val Pro Gly His Asn Ala His Thr Leu Gly Val Ala Leu Gln Gly Asp
 50 55 60
 Asp Gly Leu Pro Gln Gly Gln His Gln Ala Pro Ile Arg Asp Leu Pro
 65 70 75 80
 His His Asp Cys Ala Val Leu Gly Ala Thr Gly Asn Asp Val Val Ile
 85 90 95
 Val Arg Ala Pro Gly Asp Val
 100

<210> 2110
 <211> 55
 <212> PRT
 <213> Homo sapiens

<400> 2110
 His Met Val Arg Leu Asp Gly Pro Ser Ser Ser Glu Thr Gln Gln Glu

5 10 15
 Ser Gln Gly Glu Gly Ser Gln Asp His Ser Ser Asp Met Glu His Ser
 20 25 30
 Val Phe Arg Ala His Val Val Gly Ser Ile Ile Asp Asp Cys Glu His
 35 40 45
 Arg Asn Ser Asp Glu Glu Leu
 50 55

<210> 2111
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 2111
 Gln Phe Leu Ile Thr Val Pro Val Leu Thr Val Ile Asn Tyr Arg Pro
 5 10 15
 His Asn Met Arg Pro Glu Asp Arg Met Phe His Ile Arg Ala Val Ile
 20 25 30
 Leu Arg Ala Leu Ser Leu Ala Phe Leu Leu Ser Leu Arg Gly Ala Gly
 35 40 45
 Ala Ile Lys Ala Asp His Val Ser Thr Tyr Ala Ala Phe Val Gln Thr
 50 55 60
 His Arg Pro Thr Gly Glu Phe Met Phe Glu Phe Asp Glu Asp Glu Met
 65 70 75 80
 Phe Tyr Val Asp Leu Asp Lys Lys Glu Thr Val Trp His Leu Glu Glu
 85 90 95
 Phe

<210> 2112
 <211> 55
 <212> PRT
 <213> Homo sapiens

<400> 2112
 Val Ser Glu Glu Leu Gly Pro Ser Arg Arg Thr Met Cys Gln Leu Met
 5 10 15
 Pro Arg Leu Tyr Arg Arg Ile Asp Gln Gln Gly Ser Leu Cys Leu Asn
 20 25 30
 Leu Met Lys Met Arg Cys Ser Met Trp Ile Trp Thr Arg Arg Arg Pro
 35 40 45
 Ser Gly Ile Trp Arg Ser Leu
 50 55

<210> 2113
 <211> 89
 <212> PRT
 <213> Homo sapiens

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<400> 2113
Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly
      5                      10                      15
Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro Leu Lys Glu
      20                      25                      30
Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg
      35                      40                      45
Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys Gln
      50                      55                      60
Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg
      65                      70                      75                      80
Ala Lys Pro Val Thr Gln Ile Val Ser
      85

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<210> 2114
<211> 89
<212> PRT
<213> Homo sapiens
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<400> 2114
Ala Asp Asp Leu Gly Asp Arg Phe Gly Pro Ile Leu Gly Pro Leu Val
      5                                10                                15

Ile Leu Arg Glu Pro Val Glu Leu Asp Leu Thr Ala Glu Val Val Ala
      20                                25                                30

Gly Val Leu Pro Glu Gly Gly Arg Asp Pro Gln Ala Ala Ala Gln Ala
      35                                40                                45

Val Ser Gly Val Ile Glu Gly Gly Leu Leu Leu Glu Gly Leu Arg Val
      50                                55                                60

Cys Ala Asp Pro Thr Val His Leu Leu Pro Ile His Pro Pro Ala Gln
      65                                70                                75                                80

Leu His Val Val Gly Val Glu Ala Cys
      85

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<210> 2115
<211> 59
<212> PRT
<213> Homo sapiens
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<400> 2115
Gln Arg Lys Trp Leu Arg Gly Phe Cys Gln Lys Val Ala Glu Thr Leu
      5                                10                        15

Arg Arg Leu Leu Arg Gln Tyr Leu Glu Ser Leu Arg Ala Gly Cys Ser
      20                                25                        30

Leu Arg Gly Cys Gly Ser Val Leu Thr Pro Leu Cys Thr Ser Phe Pro
      35                                40                        45

Phe Thr His Gln Leu Ser Ser Thr Trp Ser Gly
      50                                55

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<210> 2116
 <211> 71
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(71)
 <223> Xaa = Any amino acid

<400> 2116
 Ile Arg Ser Lys Ser His Pro Gly Leu Gly Pro Ser Thr His Ser Arg
 5 10 15
 Ile Gly Ser Ala Asp Thr Glu Gly Gly His Gly Thr Arg Arg Leu His
 20 25 30
 Gly Arg Leu Leu Ser Arg Leu Tyr Pro Gly His Gln Arg Xaa Val Leu
 35 40 45
 Thr Cys Ile Asn Cys Xaa Trp Asn Ser Pro His His Arg Gly Tyr Pro
 50 55 60
 Trp Pro Xaa Xaa Leu Lys Cys
 65 70

<210> 2117
 <211> 97
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(97)
 <223> Xaa = Any amino acid

<400> 2117
 Ala Ser Tyr Ser Tyr Xaa Xaa Glu Lys Pro Ser Ala Ile Gln Gln Arg
 5 10 15
 Ala Ile Leu Pro Cys Ile Lys Gly Tyr Asp Val Ile Ala Gln Ala Gln
 20 25 30
 Ser Gly Thr Gly Lys Thr Ala Thr Phe Ala Ile Ser Ile Leu Xaa Gln
 35 40 45
 Ile Glu Leu Asp Leu Lys Ala Thr Gln Ala Leu Val Leu Ala Pro Thr
 50 55 60
 Arg Glu Leu Ala Gln Gln Ile Gln Lys Val Val Met Ala Leu Gly Asp
 65 70 75 80
 Tyr Met Gly Ala Ser Cys His Ala Cys Ile Arg Gly Thr Asn Val Xaa
 85 90 95
 Cys

<210> 2118

<211> 52
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(52)
 <223> Xaa = Any amino acid

<400> 2118
 Pro Pro Ser Val Ser Ala Glu Pro Ile Leu Glu Trp Val Leu Gly Pro
 5 10 15
 Arg Pro Gly Trp Leu Leu Asp Leu Ile Gln Ser Xaa Ala Glu Ser Ile
 20 25 30
 Trp Gln Met Trp Pro Phe Ser Gln Ser Gln Ile Gly Leu Glu Gln Ser
 35 40 45
 His His Asn Pro
 50

<210> 2119
 <211> 70
 <212> PRT
 <213> Homo sapiens

<400> 2119
 Ser Gly His Ser Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu
 5 10 15
 Leu Leu Leu Trp Leu Pro Gly Ala Lys Cys Asp Ile Gln Met Thr Gln
 20 25 30
 Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Thr Ser Tyr Asn Lys
 35 40 45
 Leu Ser Gly Leu Ser Glu Tyr Arg Ser Val Val Gly Leu Ala Ser Thr
 50 55 60
 Glu Thr Arg Gln Ser Pro
 65 70

<210> 2120
 <211> 97
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(97)
 <223> Xaa = Any amino acid

<400> 2120
 Pro Asn Leu Leu Pro Pro Cys Leu His Leu Ser Glu Ile Gln Val Thr
 5 10 15
 Ile Ser Cys Arg Ala Ser Gln Asn Ile Asp Arg Trp Leu Ala Trp His
 20 25 30
 Gln Gln Lys Pro Gly Lys Ala Pro Asn Val Leu Ile Tyr Ala Thr Ser

35 40 45
 Ser Leu Glu Glu Gly Val Ser Leu Arg Phe Thr Gly Ser Gly Ser Gly
 50 55 60
 Thr Gln Phe Asn Leu Thr Ile Thr Ser Leu Gln Pro Asp Asp Ser Ala
 65 70 75 80
 Thr Tyr Tyr Xaa Gln His Tyr Ser Ala Ser Leu Arg Ser Phe Trp Thr
 85 90 95

Ser

<210> 2121
 <211> 72
 <212> PRT
 <213> Homo sapiens

<400> 2121
 Asp Ile Arg Gly Phe Ala Trp Phe Leu Leu Met Pro Gly Gln Pro Pro
 5 10 15
 Ile Tyr Ile Leu Arg Gly Pro Thr Thr Tyr Cys Asn Leu Tyr Leu Arg
 20 25 30
 Gln Met Gln Thr Gly Trp Lys Glu Ile Gly Ser Ser Gly Cys His Ile
 35 40 45
 Trp His Leu Gly Ala Arg Ala Ala Gly Ala Pro Gly Ala Glu Arg Gly
 50 55 60
 Pro Ser Cys Pro Cys Cys Val Leu
 65 70

<210> 2122
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 2122
 Glu Ala Arg Gln Leu Ile Val Thr Cys Ile Ser Asp Arg Cys Arg Gln
 5 10 15
 Gly Gly Arg Arg Leu Gly His Leu Asp Val Thr Phe Gly Thr Trp Glu
 20 25 30
 Pro Glu Gln Gln Glu Pro Gln Glu Leu Ser Gly Asp Pro His Val His
 35 40 45
 Ala Val Ser
 50

<210> 2123
 <211> 53
 <212> PRT
 <213> Homo sapiens

<400> 2123
 Ala Asn Thr Leu Ile Asn Gln Ser Pro Gly Lys Gln Leu Glu Cys Ile

757

5 10 15
 Ile Leu Trp Ser Ser Ile Leu Cys Ser Cys Ala Asp Ile Ser Leu Ser
 20 25 30
 His Cys Val Ser Leu Ser Val Asp Thr Leu Lys Val Ala Leu Trp Lys
 35 40 45
 Met Ser Lys Phe Phe
 50

<210> 2124
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(67)
 <223> Xaa = Any amino acid

<400> 2124
 Lys Pro Pro Phe Phe Xaa Leu Leu Lys Arg Lys Gly Pro Gln Asp Thr
 5 10 15
 Ile Phe Glu Trp Leu Met Val Phe Lys Xaa Phe Arg Glu Leu Pro Ala
 20 25 30
 Phe Tyr Leu Glu Thr Glu Lys Ala Arg Lys Ile Leu Ser Phe Leu Ala
 35 40 45
 Cys Ile Ser Arg Val Gly Ala Asn Asp Ser Lys Leu Val Ser Lys Pro
 50 55 60
 Ile Pro Leu
 65

<210> 2125
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 2125
 Pro Pro Arg Val Arg Ala Pro Ser Val Pro Gly Pro Arg Pro Ser Arg
 5 10 15
 Gln Arg Ser Phe His Ser Ala Trp Asp Asp Gly Glu Glu Lys Asn Pro
 20 25 30
 Asp Leu Pro His Pro Gly Pro Lys Glu Ser Ala Gly Asp Val His Gln
 35 40 45
 Ala Glu Val Arg Ala Asp Glu Glu
 50 55

<210> 2126
 <211> 56
 <212> PRT
 <213> Homo sapiens

```

<400> 2126
Arg Arg Gly Ser Val Arg Pro Ala Ser Gln Gly Pro Gly Arg Ala Asp
          5                      10                      15

Lys Asp His Ser Thr Gln Pro Gly Thr Met Gly Arg Lys Lys Ile Gln
          20                      25                      30

Ile Ser Arg Ile Leu Asp Gln Arg Asn Arg Gln Val Thr Phe Thr Lys
          35                      40                      45

Arg Lys Phe Gly Leu Met Lys Lys
          50                      55

```

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<210> 2127
<211> 56
<212> PRT
<213> Homo sapiens
```

```

<400> 2127
Leu Leu His Gln Pro Glu Leu Pro Leu Gly Glu Arg His Leu Pro Ile
      5              10              15

Pro Leu Val Gln Asp Ala Gly Asp Leu Asp Phe Phe Pro Pro His Arg
      20              25              30

Pro Arg Leu Ser Gly Met Ile Phe Val Cys Ser Ala Trp Ala Leu Gly
      35              40              45

Arg Trp Ala His Gly Pro Ala Ala
      50              55

```

```
<210> 2128
<211> 56
<212> PRT
<213> Homo sapiens
```

```

<400> 2128
Gly Val Phe Leu His Thr Phe Thr Ser Ser Ala Leu Ser Ile Tyr Thr
      5                      10                      15

His Thr Gln His Pro Gln Tyr Leu Thr Ser Asn Arg Leu Tyr His Leu
      20                      25                      30

Tyr Leu Thr Met Thr Pro Gly Arg Arg Ser Lys Phe Phe Phe Thr Ile
      35                      40                      45

Ser Asn Ser Ser Leu Ser Leu Phe
      50                      55

```

```
<210> 2129
<211> 50
<212> PRT
<213> Homo sapiens
```

```

<400> 2129
Ile Ser Gln Ile Thr Lys Ser Ser Leu Arg Gln Gln Phe Lys Thr Val
          5                      10                      15

Pro Gly Ile Lys Ile Tyr Ser His Leu Arg Ser Leu Pro Ser His Leu
          20                      25                      30

```

His Leu Leu Ser Leu Lys Tyr Ile His Thr His Pro Thr Pro Ser Ile
 35 40 45

Leu Asp
 50

<210> 2130
 <211> 70
 <212> PRT
 <213> Homo sapiens

<400> 2130
 Arg Ser Ala Tyr Ala Ala Arg Trp Val Ala Lys Ser Leu Val Lys Gly
 5 10 15

Gly Leu Cys Arg Arg Val Leu Val Gln Val Ser Tyr Ala Ile Gly Val
 20 25 30

Ser His Pro Leu Ser Ile Ser Ile Phe His Tyr Gly Thr Ser Gln Lys
 35 40 45

Ser Glu Arg Glu Leu Leu Glu Ile Val Lys Lys Asn Phe Asp Leu Arg
 50 55 60

Pro Gly Val Ile Val Arg
 65 70

<210> 2131
 <211> 53
 <212> PRT
 <213> Homo sapiens

<400> 2131
 Gly Leu Leu Met Leu Leu Val Gly Trp Gln Asn Pro Leu Leu Lys Glu
 5 10 15

Val Cys Ala Gly Gly Phe Leu Phe Arg Ser Leu Met Leu Leu Glu Phe
 20 25 30

Leu Ile His Tyr Leu Ser Pro Phe Ser Ile Met Val Pro Leu Arg Arg
 35 40 45

Val Arg Glu Ser Tyr
 50

<210> 2132
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 2132
 Leu Ala Cys Cys Ser Gly Pro Trp Ser Cys Pro Val Leu Gln His Gly
 5 10 15

Val Ser Glu Ala Pro Trp Arg Leu Leu His Gly Ser Ser Asp Ser Asp
 20 25 30

Thr Asp Gly Ala Glu Leu Pro Thr Gly Phe Gly Trp Gly His Gln Thr
 35 40 45

Thr Phe Leu Gly Val Leu Tyr Val
50 55

<210> 2133
<211> 177
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(177)
<223> Xaa = Any amino acid

<400> 2133
Leu Pro Ala Ala Leu Ala Pro Gly Pro Val Leu Phe Ser Ser Met Val
5 10 15

Cys Leu Arg Leu Pro Gly Gly Ser Cys Met Ala Val Leu Thr Val Thr
20 25 30

Leu Met Val Leu Ser Ser Pro Leu Ala Leu Ala Gly Asp Thr Arg Pro
35 40 45

Arg Phe Leu Glu Tyr Ser Thr Ser Glu Cys His Phe Phe Asn Gly Thr
50 55 60

Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu Tyr
65 70 75 80

Val Arg Phe Asp Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu Leu
85 90 95

Gly Arg Pro Asp Glu Glu Tyr Trp Asn Ser Gln Lys Asp Phe Leu Glu
100 105 110

Asp Arg Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly Val
115 120 125

Gly Glu Ser Phe Thr Val Gln Arg Arg Val His Pro Lys Val Thr Val
130 135 140

Tyr Pro Ser Lys Thr His Pro Cys Ser Thr Thr Thr Ser Trp Ser Val
145 150 155 160

Leu Xaa Val Val Ser Ile Gln Ala Ala Leu Asn Xaa Val Val Pro Glu
165 170 175

Trp

<210> 2134
<211> 56
<212> PRT
<213> Homo sapiens

<400> 2134
Ala Pro His Trp Leu Trp Leu Gly Thr Pro Asp His Val Ser Trp Ser
5 10 15

Thr Leu Arg Leu Ser Val Ile Ser Ser Met Gly Arg Ser Gly Cys Gly

761

20 25 30

Ser Trp Thr Asp Thr Ser Ile Thr Lys Arg Ser Thr Cys Ala Ser Thr
 35 40 45

Ala Thr Trp Gly Ser Ser Gly Arg
 50 55

<210> 2135

<211> 70

<212> PRT

<213> Homo sapiens

<400> 2135

Ser Ser His Gln Pro Arg Ser Cys Val Cys Ser Arg Cys Pro Pro Arg
 5 10 15

Pro Ala Cys Leu Pro Gly Ser Pro Ser Gly Cys Ser Ser Thr Pro His
 20 25 30

Gln Ala Ala Pro Ala Pro Ser Pro Pro Gly Thr Pro Pro Arg Arg Cys
 35 40 45

Arg Ser Ala Arg Thr Pro Leu Gly Tyr Arg Ser Ile Cys Pro Gly Thr
 50 55 60

Ala Pro Ala Pro Ser His
 65 70

<210> 2136

<211> 53

<212> PRT

<213> Homo sapiens

<400> 2136

Ser Thr Pro Arg Asn Val Val Trp Cys Pro Gln Pro Lys Pro Val Gly
 5 10 15

Ser Ser Ala Pro Ser Val Ser Leu Ser Glu Leu Pro Cys Arg Ser Leu
 20 25 30

Gln Gly Ala Ser Asp Thr Pro Cys Trp Arg Thr Gly Gln Asp Gln Gly
 35 40 45

Pro Glu Gln Gln Ala
 50

<210> 2137

<211> 146

<212> PRT

<213> Homo sapiens

<400> 2137

Arg Ile His Ser His Leu Arg Met Asp Ser Pro Leu His Cys Glu Ala
 5 10 15

Leu Thr Asn Pro Val Val Val Ser Ala Val Gly Val His Arg Gly Pro
 20 25 30

Pro Val Phe Gln Glu Val Leu Leu Ala Val Pro Val Leu Leu Ile Arg

35 40 45
 Pro Pro Gln Leu Arg His Arg Pro Glu Leu Pro His Val Ala Val Glu
 50 55 60
 Ala His Val Leu Leu Leu Val Ile Glu Val Ser Val Gln Glu Pro His
 65 70 75 80
 Pro Leu Arg Pro Ile Glu Glu Met Thr Leu Arg Arg Arg Val Leu Gln
 85 90 95
 Glu Thr Trp Ser Gly Val Pro Ser Gln Ser Gln Trp Gly Ala Gln His
 100 105 110
 His Gln Cys His Cys Gln Asn Cys His Ala Gly Ala Ser Arg Glu Pro
 115 120 125
 Gln Thr His His Ala Gly Glu Gln Asp Arg Thr Arg Gly Gln Ser Ser
 130 135 140
 Arg Gln
 145

<210> 2138
 <211> 58
 <212> PRT
 <213> Homo sapiens

<400> 2138
 His Ser Asp Val Glu Tyr Ser Lys Lys Arg Gly Leu Val Ser Pro Ala
 5 10 15
 Lys Ala Ser Gly Glu Leu Ser Thr Ile Ser Val Thr Val Arg Thr Ala
 20 25 30
 Met Gln Glu Pro Pro Gly Ser Leu Arg His Thr Met Leu Glu Asn Arg
 35 40 45
 Thr Gly Pro Gly Ala Arg Ala Ala Gly Lys
 50 55

<210> 2139
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 2139
 Ala Leu Asn Glu Asp Leu Arg Ser Trp Thr Ala Ala Asp Met Ala Ala
 5 10 15
 Gln Ile Thr Lys Arg Lys Trp Glu Ala Ala His Glu Ala Glu Gln Leu
 20 25 30
 Arg Ala Tyr Leu Asp Gly Thr Cys Val Glu Trp Leu Arg Arg Tyr Leu
 35 40 45
 Glu Asn Gly Lys Glu Thr Leu Gln Arg Thr Asp Pro Pro Lys Thr His
 50 55 60
 Met Thr His His Pro Ile Ser Asp His Glu Ala Thr Leu Arg Cys Trp
 65 70 75 80

Ala Leu Gly Phe Tyr Pro Ala Glu Ile Thr Leu Thr Trp Gln Arg Asp
85 90 95

Gly Glu Asp Gln Thr Gln Asp Thr Glu Leu Val Glu Thr Arg
100 105 110

<210> 2140
<211> 110
<212> PRT
<213> Homo sapiens

<400> 2140
Pro Gly Leu His Glu Leu Arg Val Leu Gly Leu Val Leu Pro Ile Pro
5 10 15

Leu Pro Gly Gln Cys Asp Leu Arg Arg Val Glu Ala Gln Gly Pro Ala
20 25 30

Pro Gln Gly Gly Leu Met Val Arg Asp Gly Val Val Gly His Met Cys
35 40 45

Leu Gly Gly Val Arg Ala Leu Gln Arg Leu Leu Pro Val Leu Gln Val
50 55 60

Ser Ala Glu Pro Leu His Ala Arg Ala Ile Gln Val Gly Ser Gln Leu
65 70 75 80

Leu Arg Leu Met Gly Arg Leu Pro Leu Ala Leu Gly Asp Leu Ser Arg
85 90 95

His Val Arg Arg Gly Pro Arg Ala Gln Val Leu Val Gln Gly
100 105 110

<210> 2141
<211> 70
<212> PRT
<213> Homo sapiens

<400> 2141
Ser Pro Gln Gly Arg Ser Pro Gly Pro Ser Thr Ser Gly Trp Pro His
5 10 15

Gly Gln Arg Trp Gly Gly Gly Ser Tyr Val Ser Trp Gly Gly Pro Cys
20 25 30

Ala Ala Ala Ser Pro Ser Arg Ser Pro Gly Ile Cys Gly Ala Thr Pro
35 40 45

Arg Thr Cys His Pro Gly Arg Leu Ser Thr Ala Pro Pro His Gly Pro
50 55 60

Pro Pro Thr Cys Ala Trp
65 70

<210> 2142
<211> 71
<212> PRT
<213> Homo sapiens

<210> 2143

<211> 124

<212> PRT

<213> Homo sapiens

<400> 2143

<210> 2144

<211> 51

<212> PRT

<213> Homo sapiens

<400> 2144

His	Leu	Thr	Asn	Gln	Ser	Tyr	Lys	Phe	His	Ile	Ser	Val	Thr	Gln	Met
				5					10					15	
Ser	Ile	Tyr	Gln	Val	Arg	Gly	Asn	Lys	Thr	Cys	Thr	Tyr	Thr	Lys	Val
			20					25					30		
Glu	Arg	Glu	Asn	Thr	His	Ala	Phe	Arg	Ser	Ser	Gln	Ile	Lys	Ser	Pro
		35					40					45			

Leu Ile Ile
50

<210> 2145
<211> 51
<212> PRT
<213> Homo sapiens

<400> 2145
Pro Arg Leu Ile Ala Ser Arg Gly Ser Pro Ser Ala Asp Gln Leu Asn
5 10 15
Thr Asn Phe Phe Leu Leu Phe Ser Thr Trp Phe Gly Lys Ser His Ser
20 25 30
Phe Gln Ala Pro Ser Val Trp Arg Lys Tyr Ile Leu Lys His Pro Gln
35 40 45
Phe Thr Phe
50

<210> 2146
<211> 66
<212> PRT
<213> Homo sapiens

<400> 2146
Asp His Leu Lys Ser Cys Tyr Gln Asp Ser His Glu Asp Pro Thr Lys
5 10 15
Met Lys Arg Phe Leu Phe Leu Leu Leu Thr Ile Ser Leu Leu Val Met
20 25 30
Val Gln Ile Gln Thr Gly Leu Ser Gly Gln Asn Asp Thr Ser Gln Thr
35 40 45
Ser Ser Pro Ser Ala Ser Ser Ser Met Ser Gly Gly Ile Phe Leu Phe
50 55 60
Phe Val
65

<210> 2147
<211> 75
<212> PRT
<213> Homo sapiens

<400> 2147
Thr Lys Arg Ser Leu Gln Thr Ala Leu Arg Ser Pro Lys Lys Leu Leu
5 10 15
Pro Arg Gln Pro Arg Arg Ser Tyr Gln Asn Glu Ala Leu Pro Leu Pro
20 25 30
Pro Thr His His Gln Pro Pro Gly Tyr Gly Thr Asp Thr Asn Trp Thr
35 40 45
Leu Arg Thr Lys Arg His Gln Pro Asn Gln Gln Pro Leu Ser Ile Gln
50 55 60

766

Gln His Glu Arg Arg His Phe Pro Phe Leu Arg
 65 70 75

<210> 2148
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 2148
 Thr Lys Lys Arg Lys Met Pro Pro Leu Met Leu Leu Asp Ala Glu Gly
 5 10 15
 Leu Leu Val Trp Leu Val Ser Phe Cys Pro Glu Ser Pro Val Cys Ile
 20 25 30
 Cys Thr Ile Thr Arg Arg Leu Met Val Ser Arg Arg Lys Arg Lys Arg
 35 40 45
 Phe Ile Leu Val Gly Ser Ser Trp Leu Ser Trp
 50 55

<210> 2149
 <211> 94
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(94)
 <223> Xaa = Any amino acid

<400> 2149
 Xaa Leu Ala Cys Cys Ser Gly Pro Trp Ser Cys Pro Val Leu Gln His
 5 10 15
 Gly Val Ser Glu Ala Pro Trp Arg Leu Leu His Gly Ser Ser Asp Ser
 20 25 30
 Asp Thr Asp Gly Ala Glu Leu Pro Thr Cys Phe Gly Leu Gly Thr Pro
 35 40 45
 Asp His Val Ser Trp Ser Thr Leu Arg Leu Ser Val Ile Ser Ser Met
 50 55 60
 Gly Arg Ser Gly Cys Gly Ser Trp Thr Asp Thr Ser Ile Thr Lys Arg
 65 70 75 80
 Ser Thr Cys Ala Ser Thr Ala Thr Trp Gly Ser Ser Gly Arg
 85 90

<210> 2150
 <211> 57
 <212> PRT
 <213> Homo sapiens

<400> 2150
 Val Leu Pro Ala Ala Leu Ala Pro Gly Pro Val Leu Phe Ser Ser Met
 5 10 15
 Val Cys Leu Arg Leu Pro Gly Gly Ser Cys Met Ala Val Leu Thr Val

20 25 30
 Thr Leu Met Val Leu Ser Ser Pro Leu Ala Leu Gly Trp Gly His Gln
 35 40 45

Thr Thr Phe Leu Gly Val Leu Tyr Val
 50 55

<210> 2151
 <211> 93
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(93)
 <223> Xaa = Any amino acid

<400> 2151
 Ala Pro His Leu Leu Trp Ala Gly Asp Thr Arg Pro Arg Phe Leu Glu
 5 10 15
 Tyr Ser Thr Ser Glu Cys His Phe Phe Asn Gly Thr Glu Arg Val Arg
 20 25 30
 Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu Tyr Val Arg Phe Asp
 35 40 45
 Ser Asp Val Gly Glu Phe Arg Ala Val Xaa Glu Leu Gly Arg Ala Asp
 50 55 60
 Glu Glu Tyr Trp Asn Ser Xaa Xaa Gly Leu Pro Gly Xaa Gln Ala Xaa
 65 70 75 80
 Arg Gly Gly His Leu Leu Xaa Thr Gln Leu Arg Gly Trp
 85 90

<210> 2152
 <211> 121
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(121)
 <223> Xaa = Any amino acid

<400> 2152
 Val Ser Thr Ala Xaa Arg Leu Xaa Ser Arg Lys Ser Xaa Xaa Ala Val
 5 10 15
 Pro Val Leu Leu Ile Ser Pro Pro Gln Leu Xaa His Arg Pro Glu Leu
 20 25 30
 Pro His Val Ala Val Glu Ala His Val Leu Leu Leu Val Ile Glu Val
 35 40 45
 Ser Val Gln Glu Pro His Pro Leu Arg Pro Ile Glu Glu Met Thr Leu
 50 55 60
 Arg Arg Arg Val Leu Gln Glu Thr Trp Ser Gly Val Pro Ser Pro Lys

65 70 75 80
Gln Val Gly Ser Ser Ala Pro Ser Val Ser Leu Ser Glu Leu Pro Cys
 85 90 95
Arg Ser Leu Gln Gly Ala Ser Asp Thr Pro Cys Trp Arg Thr Gly Gln
 100 105 110
Asp Gln Gly Pro Glu Gln Gln Ala Arg
 115 120

<210> 2153
<211> 54
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(54)
<223> Xaa = Any amino acid

<400> 2153
Gln Pro Arg Ser Cys Xaa Cys Ser Arg Cys Pro Pro Xaa Pro Ala Cys
 5 10 15
Xaa Pro Gly Ser Pro Xaa Trp Leu Phe Gln Tyr Ser Ser Ser Ala Arg
 20 25 30
Pro Ser Xaa Val Thr Ala Arg Asn Ser Pro Thr Ser Leu Ser Lys Arg
 35 40 45
Thr Tyr Ser Ser Trp Leu
 50

<210> 2154
<211> 59
<212> PRT
<213> Homo sapiens

<400> 2154
His Ser Asp Val Glu Tyr Ser Lys Lys Arg Gly Leu Val Ser Pro Ala
 5 10 15
Gln Ser Lys Trp Gly Ala Gln His His Gln Cys His Cys Gln Asn Cys
 20 25 30
His Ala Gly Ala Ser Arg Glu Pro Gln Thr His His Ala Gly Glu Gln
 35 40 45
Asp Arg Thr Arg Gly Gln Ser Ser Arg Gln Asp
 50 55

<210> 2155
<211> 67
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(67)

<223> Xaa = Any amino acid

<400> 2155

```

Asn Pro Val Val Val Xaa Ala Val Gly Val His Arg Xaa Pro Pro Xaa
      5                      10                      15

Phe Gln Glu Val Leu Xaa Gly Cys Ser Ser Thr Pro His Gln Pro Ala
      20                      25                      30

Pro Ala Xaa Ser Pro Pro Gly Thr Pro Pro Arg Arg Cys Arg Ser Ala
      35                      40                      45

Arg Thr Pro Leu Gly Tyr Arg Ser Ile Cys Pro Gly Thr Ala Pro Ala
      50                      55                      60

Pro Ser His
      65

```

<210> 2156

<211> 55

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(55)

<223> Xaa = Any amino acid

<400> 2156

```

Ser Thr Pro Arg Asn Val Val Trp Cys Pro Gln Pro Lys Ala Ser Gly
      5                      10                      15

Glu Leu Ser Thr Ile Ser Val Thr Val Arg Thr Ala Met Gln Glu Pro
      20                      25                      30

Pro Gly Ser Leu Arg His Thr Met Leu Glu Asn Arg Thr Gly Pro Gly
      35                      40                      45

Ala Arg Ala Ala Gly Lys Xaa
      50                      55

```

<210> 2157

<211> 123

<212> PRT

<213> Homo sapiens

<400> 2157

```

Gly His Ser Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu
      5                      10                      15

Leu Leu Trp Leu Pro Gly Ala Lys Cys Asp Ile Gln Met Thr Gln Ser
      20                      25                      30

Pro Ser Thr Leu Ser Ala Ser Ala Gly Asn Thr Val Thr Ile Ser Cys
      35                      40                      45

Arg Ala Ser Gln Asn Ile Asp Arg Trp Leu Ala Trp His Gln Gln Lys
      50                      55                      60

Pro Gly Lys Ala Pro Asn Val Leu Ile Tyr Ala Thr Ser Ser Leu Glu
      65                      70                      75                      80

```


Glu Gly Val Ser Leu Arg Phe Thr Gly Ser Gly Ser Gly Thr Gln Phe
 85 90 95

Asn Leu Thr Ile Thr Ser Leu Gln Pro Asp Asp Ser Ala Thr Tyr Tyr
 100 105 110

Cys Gln His Tyr Ser Ala Ser Leu Arg Ser Phe
 115 120

<210> 2158
 <211> 71
 <212> PRT
 <213> Homo sapiens

<400> 2158
 Asp Ile Arg Gly Phe Ala Trp Phe Leu Leu Met Pro Gly Gln Pro Pro
 5 10 15

Ile Tyr Ile Leu Arg Gly Pro Thr Thr Tyr Cys Asn Cys Ile Ser Gly
 20 25 30

Arg Cys Arg Gln Gly Gly Arg Arg Leu Gly His Leu Asp Val Thr Phe
 35 40 45

Gly Thr Trp Glu Pro Glu Gln Gln Glu Pro Gln Glu Leu Ser Gly Asp
 50 55 60

Pro His Val His Ala Val Ser
 65 70

<210> 2159
 <211> 62
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(62)
 <223> Xaa = Any amino acid

<400> 2159
 Asp Leu Leu Gly Gly Met Ala Pro Pro Gly Ser Ser Thr Val Phe Leu
 5 10 15

Leu Ala Leu Thr Ile Ile Ala Ser Thr Trp Ala Leu Thr Pro Thr His
 20 25 30

Tyr Leu Thr Lys His Asp Xaa Glu Arg Leu Lys Ala Ser Leu Asp Pro
 35 40 45

Pro Phe His Lys Val Gly Ser Xaa Val Phe Tyr Ser Ile Xaa
 50 55 60

<210> 2160
 <211> 53
 <212> PRT
 <213> Homo sapiens

<400> 2160

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<210> 2161
<211> 83
<212> PRT
<213> Homo sapiens
```

```
<400> 2161  
Gly Ser Lys Asp Gln Ala Lys Gly Ala Gly Pro Pro Leu Glu Gly Leu  
          5                      10                15  
  
Arg Gly Thr Ser Ser Ala Gly Val Cys Ile Gln Gly Ser Ser Arg Ile  
      20                        25               30  
  
Ser Ser Ser Glu Gly Arg Glu Glu Gly Leu Gly Ala Arg His Arg Arg  
    35                  40              45  
  
Ile Arg Ala Gln Gln Ser Trp Gly Lys His Gly Leu Gly Lys Trp Ser  
   50                    55             60  
  
Ser Ala Ser Arg Ile Ser Trp Ser Leu Ser Lys Gly Met Ser Pro His  
  65                   70                 75            80  
  
Thr Met Ser
```

```
<210> 2162
<211> 115
<212> PRT
<213> Homo sapiens
```

```

<400> 2162
Gly Val His Pro Arg Leu Val Phe Ala Ser Arg Gly Pro Ala Gly Ser
      5                                10                                15
Leu Pro Val Arg Val Gly Lys Lys Val Trp Gly Pro Gly Thr Gly Gly
      20                                25                                30
Leu Gly His Ser Asn Leu Gly Glu Asn Met Gly Leu Gly Ser Gly Ala
      35                                40                                45
Gln Leu Pro Glu Ser Pro Gly Pro Ser Gln Arg Glu Cys Pro His Thr
      50                                55                                60
Pro Cys His Arg Gly Gly Cys Pro Val Thr Arg Gln Trp Pro Gly Val
      65                                70                                75                                80
His Gly Thr Gly Val Glu Arg Ser Thr Leu Gly Gly Cys Thr Pro Leu
      85                                90                                95
Ser His Gln Ser Gln Cys Arg Val His His Glu Ala Gly His Gln Asn

```

Gln Asn Gln
115

<210> 2163
<211> 165
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(165)
<223> Xaa = Any amino acid

<400> 2163
Trp Gln Pro Ser Ser Thr Ala Ile Ser Arg Xaa Val Val His Arg Asp
 5 10 15

Ile Lys Asp Glu Xaa Ile Leu Ile Asp Leu Arg Arg Gly Cys Ala Lys
 20 25 30

Leu Ile Asp Phe Gly Ser Gly Ala Leu Leu His Asp Glu Pro Tyr Thr
 35 40 45

Asp Phe Asp Gly Thr Arg Val Tyr Ser Pro Pro Glu Trp Ile Ser Arg
 50 55 60

His Gln Tyr His Ala Leu Pro Ala Thr Val Trp Ser Leu Gly Ile Leu
 65 70 75 80

Leu Tyr Asp Met Val Cys Gly Asp Ile Pro Phe Glu Arg Asp Gln Glu
 85 90 95

Ile Leu Glu Ala Glu Leu His Phe Pro Ser Pro Cys Phe Pro Gln Asp
 100 105 110

Cys Cys Ala Leu Ile Arg Arg Cys Leu Ala Pro Lys Pro Ser Ser Arg
 115 120 125

Pro Ser Leu Glu Glu Ile Leu Leu Asp Pro Trp Met Gln Thr Pro Ala
 130 135 140

Glu Asp Val Pro Leu Asn Pro Ser Lys Gly Gly Pro Ala Pro Leu Ala
 145 150 155 160

Trp Ser Leu Leu Pro
 165

```
<210> 2164
<211> 91
<212> PRT
<213> Homo sapiens
```

```

<400> 2164
Thr Tyr Ala Val Ala Val Pro Asn Ser Leu Ile Leu Val Leu Val Pro
          5              10              15
Cys Phe Met Met Asn Pro Thr Leu Thr Leu Met Gly Gln Gly Cys Thr
          20              25              30

```

Ala Pro Gln Ser Gly Ser Leu Asp Thr Ser Thr Met His Ser Arg Pro
 35 40 45

Leu Ser Gly His Trp Ala Ser Ser Ser Met Thr Trp Cys Val Gly Thr
 50 55 60

Phe Pro Leu Arg Gly Thr Arg Arg Phe Trp Lys Leu Ser Ser Thr Ser
 65 70 75 80

Gln Ala His Val Phe Pro Lys Ile Ala Val Pro
 85 90

<210> 2165
 <211> 66
 <212> PRT
 <213> Homo sapiens

<400> 2165
 Ser Ala Gly Ala Trp Pro Pro Asn Leu Leu Pro Asp Pro His Trp Lys
 5 10 15

Arg Ser Cys Trp Thr Pro Gly Cys Lys His Gln Pro Arg Met Tyr Pro
 20 25 30

Ser Thr Pro Pro Lys Glu Ala Leu Pro Leu Trp Pro Gly Pro Cys Cys
 35 40 45

Pro Lys Pro Gly Leu Ala Trp Pro Gly Pro Gln Trp Ser Glu Glu Pro
 50 55 60

Ser His
 65

<210> 2166
 <211> 82
 <212> PRT
 <213> Homo sapiens

<400> 2166
 Ala Pro Leu Pro Lys Pro Met Phe Ser Pro Arg Leu Leu Cys Pro Asn
 5 10 15

Pro Pro Val Pro Gly Pro Gln Thr Phe Phe Pro Thr Leu Thr Gly Arg
 20 25 30

Asp Pro Ala Gly Pro Leu Asp Ala Asn Thr Ser Arg Gly Cys Thr Pro
 35 40 45

Gln Pro Leu Gln Arg Arg Pro Cys Pro Phe Gly Leu Val Leu Ala Ala
 50 55 60

Leu Ser Leu Ala Trp Pro Gly Leu Ala Pro Asn Gly Gln Lys Ser His
 65 70 75 80

Pro Met

<210> 2167
 <211> 118
 <212> PRT

<213> Homo sapiens

<400> 2167

```

Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro
           5              10              15

Gly Ala Lys Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser
           20              25              30

Ala Ser Val Gly Asp Thr Val Thr Ile Ser Cys Arg Ala Ser Gln Asn
           35              40              45

Ile Asp Arg Trp Leu Ala Trp His Gln Gln Lys Pro Gly Lys Ala Pro
           50              55              60

Asn Val Leu Ile Tyr Ala Thr Ser Ser Leu Glu Glu Gly Val Ser Leu
           65              70              75              80

Arg Phe Thr Gly Ser Gly Ser Gly Thr Gln Phe Asn Leu Thr Ile Thr
           85              90              95

Ser Leu Gln Pro Asp Asp Ser Ala Thr Tyr Tyr Cys Gln His Tyr Ser
           100             105             110

Ala Ser Leu Arg Ser Phe
           115

```

<210> 2168

<211> 66

<212> PRT

<213> Homo sapiens

<400> 2168

```

Asp Ile Arg Gly Phe Ala Trp Phe Leu Leu Met Pro Gly Gln Pro Pro
           5              10              15

Ile Tyr Ile Leu Arg Gly Pro Thr Thr Tyr Cys Asn Cys Ile Ser Asp
           20              25              30

Arg Cys Arg Gln Gly Gly Arg Arg Leu Gly His Leu Asp Val Thr Phe
           35              40              45

Gly Thr Trp Glu Pro Glu Gln Gln Glu Pro Gln Glu Leu Ser Gly Asp
           50              55              60

Pro His
           65

```

<210> 2169

<211> 86

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(86)

<223> Xaa = Any amino acid

<400> 2169

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Gln Val Val Ala Xaa Ile Gln His Cys His Ser Arg Gly Val Val His
           5              10              15

```

Arg Asp Ile Lys Asp Glu Asn Ile Leu Ile Asp Leu Arg Arg Gly Cys
 20 25 30
 Ala Lys Leu Ile Asp Phe Gly Ser Gly Ala Leu Leu His Asp Glu Pro
 35 40 45
 Tyr Thr Asp Phe Asp Gly Thr Arg Val Tyr Ser Pro Pro Glu Trp Ile
 50 55 60
 Ser Arg His Gln Tyr His Ala Leu Pro Ala Thr Val Trp Ser Leu Gly
 65 70 75 80
 Ile Xaa Leu Tyr Asp Met
 85

<210> 2170
 <211> 60
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(60)
 <223> Xaa = Any amino acid

<400> 2170
 Thr Tyr Ala Val Ala Val Pro Asn Ser Leu Ile Leu Val Leu Val Pro
 5 10 15
 Cys Phe Met Met Asn Pro Thr Leu Thr Leu Met Gly Gln Gly Cys Thr
 20 25 30
 Ala Pro Gln Ser Gly Ser Leu Asp Thr Ser Thr Met His Ser Arg Pro
 35 40 45
 Leu Ser Gly His Trp Ala Ser Xaa Ser Met Thr Trp
 50 55 60

<210> 2171
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(51)
 <223> Xaa = Any amino acid

<400> 2171
 Pro Cys His Arg Xaa Gly Cys Pro Val Thr Arg Gln Trp Pro Gly Val
 5 10 15
 His Gly Thr Gly Val Glu Arg Ser Thr Leu Gly Gly Cys Thr Pro Leu
 20 25 30
 Ser His Gln Ser Gln Cys Arg Val His His Glu Ala Gly His Gln Asn
 35 40 45
 Gln Asn Gln
 50

<210> 2172
 <211> 121
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(121)
 <223> Xaa = Any amino acid

<400> 2172
 Gly His Ser Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu
 5 10 15
 Leu Leu Trp Leu Pro Gly Ala Lys Cys Asp Ile Gln Met Thr Gln Ser
 20 25 30
 Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Thr Val Thr Ile Ser Xaa
 35 40 45
 Arg Ala Ser Xaa Asn Ile Asp Arg Trp Leu Ala Trp His Gln Gln Lys
 50 55 60
 Pro Gly Lys Ala Pro Asn Val Leu Ile Tyr Ala Thr Ser Ser Leu Glu
 65 70 75 80
 Glu Gly Val Ser Leu Arg Phe Thr Gly Ser Gly Ser Gly Thr Gln Phe
 85 90 95
 Asn Leu Thr Ile Thr Ser Leu Gln Pro Asp Asp Ser Ala Thr Tyr Tyr
 100 105 110
 Cys Gln His Tyr Xaa Ala Ser Leu Xaa
 115 120

<210> 2173
 <211> 71
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(71)
 <223> Xaa = Any amino acid

<400> 2173
 Asp Ile Arg Gly Phe Ala Trp Phe Leu Leu Met Pro Gly Gln Pro Pro
 5 10 15
 Ile Tyr Ile Xaa Arg Gly Pro Xaa Thr Tyr Cys Asn Cys Ile Ser Asp
 20 25 30
 Arg Cys Arg Gln Gly Gly Arg Arg Leu Gly His Leu Asp Val Thr Phe
 35 40 45
 Gly Thr Trp Glu Pro Glu Gln Gln Glu Pro Gln Glu Leu Ser Gly Asp
 50 55 60
 Pro His Val His Ala Val Ser
 65 70

```
<210> 2174
<211> 122
<212> PRT
<213> Homo sapiens
```

```

<400> 2174
Ser Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu
          5                                10                                15

Trp Leu Pro Gly Ala Lys Cys Asp Ile Gln Met Thr Gln Ser Pro Ser
          20                                25                                30

Thr Leu Ser Ala Ser Val Gly Asp Thr Val Thr Ile Ser Cys Arg Ala
          35                                40                                45

Ser Gln Asn Ile Asp Arg Trp Leu Ala Trp His Gln Gln Lys Pro Gly
          50                                55                                60

Lys Ala Pro Asn Val Leu Ile Tyr Ala Thr Ser Ser Leu Glu Glu Gly
          65                                70                                75                                80

Val Ser Leu Arg Phe Thr Gly Ser Gly Ser Gly Thr Gln Phe Asn Leu
          85                                90                                95

Thr Ile Thr Ser Leu Gln Pro Asp Asp Ser Ala Thr Tyr Tyr Cys Ala
          100                                105                                110

Thr Leu Phe Cys Ile Ser Ser Gln Phe Trp
          115                                120

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<210> 2175
<211> 69
<212> PRT
<213> Homo sapiens
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```
<400> 2175
Asp Ile Arg Gly Phe Ala Trp Phe Leu Leu Met Pro Gly Gln Pro Pro
      5                                10                        15

Ile Tyr Ile Leu Arg Gly Pro Thr Thr Tyr Cys Asn Cys Ile Ser Asp
      20                                25                        30

Arg Cys Arg Gln Gly Gly Arg Arg Leu Gly His Leu Asp Val Thr Phe
      35                                40                        45

Gly Thr Trp Glu Pro Glu Gln Gln Glu Pro Gln Glu Leu Ser Gly Asp
      50                                55                        60

Pro His Val His Ala
      65
```

```
<210> 2176
<211> 64
<212> PRT
<213> Homo sapiens
```

<400> 2176
Glu Thr Thr Trp Ala Pro Pro Val Thr Pro Val Ser Gly Ala Pro Thr
 5 10 15

Cys Val Leu Arg Cys Arg Asn Cys Arg Trp Lys Leu Pro Thr Ser Ser
 20 25 30
 Trp Val Pro Leu Ala Val Cys Leu Ile Cys Leu Thr Gly Asp Thr Cys
 35 40 45
 Pro Pro Asn Thr Ser Arg Cys Leu Tyr Trp Met Lys Leu Thr Lys Cys
 50 55 60

<210> 2177
 <211> 179
 <212> PRT
 <213> Homo sapiens

<400> 2177
 Leu Val Leu Ala Pro Thr Arg Glu Leu Ala Gln Gln Ile Gln Lys Val
 5 10 15
 Val Met Ala Leu Gly Asp Tyr Met Gly Ala Ser Cys His Ala Cys Ile
 20 25 30
 Gly Gly Thr Asn Val Arg Ala Glu Val Gln Lys Leu Gln Met Glu Ala
 35 40 45
 Pro His Ile Ile Val Gly Thr Pro Gly Arg Val Phe Asp Met Leu Asn
 50 55 60
 Arg Arg Tyr Leu Ser Pro Lys Tyr Ile Lys Met Phe Val Leu Asp Glu
 65 70 75 80
 Ala Asp Glu Met Leu Ser Arg Gly Phe Lys Asp Gln Ile Tyr Asp Ile
 85 90 95
 Phe Gln Lys Leu Asn Ser Asn Thr Gln Val Val Leu Leu Ser Ala Thr
 100 105 110
 Met Pro Ser Asp Val Leu Glu Val Thr Lys Lys Phe Met Arg Asp Pro
 115 120 125
 Ile Arg Ile Leu Val Lys Lys Glu Glu Leu Thr Leu Glu Gly Ile Arg
 130 135 140
 Gln Phe Tyr Ile Asn Val Glu Arg Glu Glu Trp Lys Leu Asp Thr Leu
 145 150 155 160
 Cys Asp Leu Tyr Glu Thr Leu Thr Ile Thr Gln Ala Val Ile Phe Ile
 165 170 175
 Asn Thr Arg

<210> 2178
 <211> 64
 <212> PRT
 <213> Homo sapiens

<400> 2178
 His Phe Val Ser Phe Ile Gln Tyr Lys His Leu Asp Val Phe Gly Gly
 5 10 15

Gln Val Ser Pro Val Lys His Ile Lys His Thr Ala Arg Gly Thr His
 20 25 30
 Asp Asp Val Gly Ser Phe His Leu Gln Phe Leu His Leu Ser Thr His
 35 40 45
 Val Gly Ala Pro Asp Thr Gly Val Thr Gly Gly Ala His Val Val Ser
 50 55 60

<210> 2179
 <211> 52
 <212> PRT
 <213> Homo sapiens

<400> 2179
 Asn Trp Arg Ile Pro Ser Arg Val Asn Ser Ser Phe Leu Thr Arg Ile
 5 10 15
 Arg Met Gly Ser Leu Met Asn Phe Leu Val Thr Ser Ser Thr Ser Glu
 20 25 30
 Gly Ile Val Ala Asp Ser Lys Thr Thr Trp Val Leu Leu Leu Ser Phe
 35 40 45
 Trp Asn Met Ser
 50

<210> 2180
 <211> 64
 <212> PRT
 <213> Homo sapiens

<400> 2180
 Ile Trp Ser Leu Asn Pro Arg Leu Asn Ile Ser Ser Ala Ser Ser Ser
 5 10 15
 Thr Asn Ile Leu Met Tyr Leu Gly Asp Arg Tyr Leu Arg Leu Ser Ile
 20 25 30
 Ser Asn Thr Arg Pro Gly Val Pro Thr Met Met Trp Gly Ala Ser Ile
 35 40 45
 Cys Ser Phe Cys Thr Ser Ala Arg Thr Leu Val Pro Pro Ile Gln Ala
 50 55 60

<210> 2181
 <211> 134
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(134)
 <223> Xaa = Any amino acid

<400> 2181
 Val Ile Val Arg Leu Glu Ala Phe Ala Val Asp Asp Gly Gly Ala Gly
 5 10 15
 Leu Val Ile Leu Leu Leu Ala Asp Pro His Leu Leu Glu Gly Gly Gln

30

Ile Ala Asn Gly Asp Asp
130

Thr

<210> 2183
 <211> 129
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(129)
 <223> Xaa = Any amino acid

<400> 2183
 Val Ile Thr Ile Gly Asn Glu Arg Phe Arg Cys Pro Glu Ala Xaa Xaa
 5 10 15
 Gln Pro Ser Phe Leu Gly Met Glu Ser Cys Gly Ile His Glu Thr Thr
 20 25 30
 Phe Asn Ser Ile Met Lys Cys Asp Val Asp Ile Arg Lys Asp Leu Tyr
 35 40 45
 Ala Asn Xaa Val Leu Ser Gly Gly Thr Thr Met Tyr Pro Gly Ile Xaa
 50 55 60
 Asp Arg Met Gln Lys Glu Ile Xaa Ala Leu Ala Pro Ser Xaa Met Lys
 65 70 75 80
 Ile Lys Ile Ile Ala Pro Pro Glu Arg Lys Tyr Ser Val Trp Ile Gly
 85 90 95
 Gly Ser Ile Leu Ala Ser Leu Ser Thr Phe Gln Gln Met Trp Ile Ser
 100 105 110
 Lys Gln Glu Tyr Asp Glu Ser Gly Pro Ser Ile Val His Arg Lys Cys
 115 120 125
 Phe

<210> 2184
 <211> 55
 <212> PRT
 <213> Homo sapiens

<400> 2184
 Arg Ser Arg Ser Leu Leu Leu Leu Ser Ala Ser Thr Pro Cys Gly Ser
 5 10 15
 Ala Ala Pro Ser Trp Pro Arg Cys Pro Pro Ser Ser Arg Cys Gly Ser
 20 25 30
 Ala Ser Arg Ser Met Thr Ser Pro Ala Pro Pro Ser Ser Thr Ala Asn
 35 40 45
 Ala Ser Arg Arg Thr Met Thr
 50 55

<210> 2185
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 2185

Ser Gly His Ser Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu
 5 10 15

Leu Leu Leu Trp Leu Pro Gly Ala Lys Cys Asp Ile Gln Met Thr Gln
 20 25 30

Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Thr Val Thr Ile Ser
 35 40 45

Cys Arg Ala Ser Gln Asn Ile Asp Arg Trp Leu Ala Trp His Gln Gln
 50 55 60

Lys Pro Gly Lys Ala Pro Asn Val Leu Ile Tyr Ala Thr Ser Ser Leu
 65 70 75 80

Glu Glu Gly Val Ser Leu Arg Phe Thr Gly Ser Gly Ser Gly Thr Gln
 85 90 95

Phe Asn Leu Thr Ile Thr Ser Leu Gln Pro Asp Asp Ser Ala Thr Tyr
 100 105 110

Tyr Cys Gln His Tyr Ser Ala Ser Leu Arg Ser Phe
 115 120

<210> 2186

<211> 71

<212> PRT

<213> Homo sapiens

<400> 2186

Asp Ile Arg Gly Phe Ala Trp Phe Leu Leu Met Pro Gly Gln Pro Pro
 5 10 15

Ile Tyr Ile Leu Arg Gly Pro Thr Ala Tyr Cys Asn Cys Ile Ser Asp
 20 25 30

Arg Cys Arg Gln Gly Gly Arg Arg Leu Gly His Leu Asp Val Thr Phe
 35 40 45

Gly Thr Trp Glu Pro Glu Gln Gln Glu Pro Gln Glu Leu Ser Gly Asp
 50 55 60

Pro His Val His Ala Val Ser
 65 70

<210> 2187

<211> 64

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(64)

<223> Xaa = Any amino acid

<400> 2187

Glu Pro Xaa Pro Leu Arg Pro Ile Glu Glu Met Thr Leu Arg Arg Arg
 5 10 15

Val Leu Gln Glu Thr Trp Xaa Gly Val Pro Ser Gln Ser Gln Trp Gly

	20		25		30
Ala Xaa His His Xaa Cys His Xaa Gln Asn Xaa His Ala Gly Thr Ser					
35		40		45	
Arg Glu Pro Xaa Thr His His Ala Gly Xaa Gln Asp Arg Thr Arg Gly					
50		55		60	

<210> 2188
 <211> 53
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(53)
 <223> Xaa = Any amino acid

<400> 2188	
His Ser Asp Val Glu Tyr Ser Lys Lys Arg Xaa Leu Val Ser Pro Ala	
5	10 15
Lys Ala Ser Gly Glu Leu Xaa Thr Ile Xaa Val Thr Xaa Arg Thr Xaa	
20	25 30
Met Gln Glu Pro Pro Gly Ser Xaa Arg His Thr Met Leu Xaa Asn Arg	
35	40 45
Thr Gly Pro Gly Ala	
50	

<210> 2189
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(51)
 <223> Xaa = Any amino acid

<400> 2189	
Gly Pro Trp Ser Cys Pro Val Xaa Gln His Gly Val Ser Xaa Ala Pro	
5	10 15
Trp Arg Phe Leu His Xaa Ser Ser Xaa Ser Asp Xaa Asp Gly Xaa Glu	
20	25 30
Leu Pro Thr Gly Phe Gly Trp Gly His Gln Xaa Thr Phe Leu Gly Val	
35	40 45
Leu Tyr Val	
50	

<210> 2190
 <211> 64
 <212> PRT
 <213> Homo sapiens

<220>

<221> variant
<222> (1)...(64)
<223> Xaa = Any amino acid

<400> 2190
Ala Pro Gly Pro Val Leu Xaa Ser Ser Met Val Cys Xaa Arg Leu Pro
 5 10 15

Gly Gly Ser Cys Met Xaa Val Leu Xaa Val Thr Xaa Met Val Xaa Ser
 20 25 30

Ser Pro Leu Ala Leu Ala Gly Asp Thr Xaa Pro Arg Phe Leu Glu Tyr
 35 40 45

Ser Thr Ser Glu Cys His Phe Phe Asn Gly Thr Glu Arg Xaa Arg Phe
 50 55 60

<210> 2191
<211> 94
<212> PRT
<213> Homo sapiens

<400> 2191
Pro Ile Ile Glu Ile Ser Ala Pro Ala Cys Lys Ala Ser Met Asn Ala
 5 10 15

Leu Val Pro Asp Leu Ala Ile Val Pro Arg Leu Leu Ile Lys Ser Ala
 20 25 30

Leu Val Ile Pro Ile Pro Val Ser Thr Ile Val Arg Val Arg Ser Cys
 35 40 45

Leu Phe Gly Ile Arg Leu Ile Cys Ser Ser Phe Ser Glu Ser Asn Leu
 50 55 60

Leu Gly Ser Val Lys Leu Ser Tyr Arg Ile Leu Ser Asn Ala Ser Asp
 65 70 75 80

Glu Phe Glu Met Ser Ser Leu Arg Lys Ile Ser Leu Phe Glu
 85 90

<210> 2192
<211> 61
<212> PRT
<213> Homo sapiens

<400> 2192
Asn His Arg Asp Ile Cys Thr Ser Leu Gln Ser Phe His Glu Arg Phe
 5 10 15

Gly Pro Arg Leu Gly Asp Ser Thr Lys Val Ile Asp Gln Val Ser Leu
 20 25 30

Gly His Ser Asn Ser Ser Ile His Asn Ser Glu Ser Ser Ile Leu Phe
 35 40 45

Val Arg Tyr Lys Val Asn Met Gln Leu Phe Leu Arg Val
 50 55 60

<210> 2193

<211> 58
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(58)
 <223> Xaa = Any amino acid

<400> 2193
 Gly Asn Pro Asp Pro Arg Pro Thr Asp Gly Gly Xaa Gly Gly Xaa Xaa
 5 10 15
 Val Arg Leu Ser Gly Arg Asn Cys Pro Val Asp Val Ile Asp His Gln
 20 25 30
 Tyr Phe Leu Leu Glu Gln Arg Asp Leu Ser Glu Arg Ala His Phe Lys
 35 40 45
 Phe Ile Arg Cys Ile Gly Gln Asn Pro Val
 50 55

<210> 2194
 <211> 139
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(139)
 <223> Xaa = Any amino acid

<400> 2194
 Xaa Thr Gly Ala Val Ser Phe Xaa Met Xaa Glu Glu Thr Gln Thr Gln
 5 10 15
 Asp Gln Pro Met Glu Glu Xaa Glu Val Xaa Thr Phe Ala Phe Gln Ala
 20 25 30
 Glu Ile Ala Gln Leu Met Ser Leu Ile Ile Asn Thr Phe Tyr Ser Asn
 35 40 45
 Lys Glu Ile Phe Leu Arg Glu Leu Ile Ser Asn Ser Ser Asp Ala Leu
 50 55 60
 Asp Lys Ile Arg Tyr Glu Ser Leu Thr Asp Pro Ser Lys Leu Asp Ser
 65 70 75 80
 Glu Lys Glu Leu His Ile Asn Leu Ile Pro Asn Lys Gln Asp Arg Thr
 85 90 95
 Leu Thr Ile Val Asp Thr Gly Ile Gly Met Thr Lys Ala Asp Leu Ile
 100 105 110
 Asn Asn Leu Gly Thr Ile Ala Lys Ser Gly Thr Lys Ala Phe Met Glu
 115 120 125
 Ala Leu Gln Ala Gly Ala Asp Ile Ser Met Ile
 130 135

<210> 2195

<211> 123
 <212> PRT
 <213> Homo sapiens

<400> 2195
 Gly His Ser Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu
 5 10 15
 Leu Leu Trp Leu Pro Gly Ala Lys Cys Asp Ile Gln Met Thr Gln Ser
 20 25 30
 Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Thr Val Thr Ile Ser Cys
 35 40 45
 Arg Ala Ser Gln Asn Ile Asp Arg Trp Leu Ala Trp His Gln Gln Lys
 50 55 60
 Pro Gly Lys Ala Pro Asn Val Leu Ile Tyr Ala Thr Ser Ser Leu Glu
 65 70 75 80
 Glu Gly Val Ser Leu Arg Phe Thr Gly Ser Gly Ser Gly Thr Gln Phe
 85 90 95
 Asn Leu Thr Ile Thr Ser Leu Gln Pro Asp Asp Ser Ala Thr Tyr Tyr
 100 105 110
 Cys Gln His Tyr Ser Ala Ser Leu Arg Ser Phe
 115 120

<210> 2196
 <211> 71
 <212> PRT
 <213> Homo sapiens

<400> 2196
 Asp Ile Arg Gly Phe Ala Trp Phe Leu Leu Met Pro Gly Gln Pro Pro
 5 10 15
 Ile Tyr Ile Leu Arg Gly Pro Thr Thr Tyr Cys Asn Cys Ile Ser Asp
 20 25 30
 Arg Cys Arg Gln Gly Gly Arg Arg Leu Gly His Leu Asp Val Thr Phe
 35 40 45
 Gly Thr Trp Glu Pro Glu Gln Gln Glu Pro Gln Glu Leu Ser Gly Asp
 50 55 60
 Pro His Val His Ala Val Ser
 65 70

<210> 2197
 <211> 71
 <212> PRT
 <213> Homo sapiens

<400> 2197
 Asp Ile Arg Gly Phe Ala Trp Phe Leu Leu Met Pro Gly Gln Pro Pro
 5 10 15
 Ile Tyr Ile Leu Arg Gly Pro Thr Thr Tyr Cys Asn Cys Ile Ser Asp
 20 25 30

Arg Cys Arg Gln Gly Gly Arg Arg Leu Gly His Leu Asp Val Thr Phe
 35 40 45
 Gly Thr Trp Glu Pro Glu Gln Gln Glu Pro Gln Glu Leu Ser Gly Asp
 50 55 60
 Pro His Val His Ala Val Ser
 65 70

<210> 2198
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 2198
 Ser Gly His Ser Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu
 5 10 15
 Leu Leu Leu Trp Leu Pro Gly Ala Lys Cys Asp Ile Gln Met Thr Gln
 20 25 30
 Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Thr Val Thr Ile Ser
 35 40 45
 Cys Arg Ala Ser Gln Asn Ile Asp Arg Trp Leu Ala Trp His Gln Gln
 50 55 60
 Lys Pro Gly Lys Ala Pro Asn Val Leu Ile Tyr Ala Thr Ser Ser Leu
 65 70 75 80
 Glu Glu Gly Val Ser Leu Arg Phe Thr Gly Ser Gly Ser Gly Thr Gln
 85 90 95
 Phe Asn Leu Thr Ile Thr Ser Leu Gln Pro Asp Asp Ser Ala Thr Tyr
 100 105 110
 Tyr Cys Gln His Tyr Ser Ala Ser Leu Arg Ser Phe
 115 120

<210> 2199
 <211> 85
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(85)
 <223> Xaa = Any amino acid

<400> 2199
 Ser Gln Glu Ser Val Gln Glu Pro Phe Leu Thr Pro Val Met Asp Asn
 5 10 15
 Lys Ala Xaa Pro Glu Glu Asp Glu Pro Gln His Glu Ala Ser Asn Ala
 20 25 30
 Thr Gln His Leu Ala Leu Gly Arg Phe Arg Leu Ser Pro Pro Leu His
 35 40 45
 Gly Asp Gly Val Leu Glu Ala Gly Val Leu His Val Ala Gly Val Asp

50 55 60
 Val Ser Met Leu Gly Ser His Phe Gln His His Gln Asp Leu Glu Xaa
 65 70 75 80

Pro Val Thr Xaa Ser
 85

<210> 2200
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 2200
 Asp Tyr Phe Asn Trp Asp Trp Leu Ser Leu Phe Cys Asn Ala Cys Leu
 5 10 15

Ser Leu Pro Arg Ile Pro Asn Cys Leu Cys Gln Pro Val Pro Leu Arg
 20 25 30

Ser Glu Ser Tyr Ser Gly Cys His Ala Ala Thr Arg Ser Ser Pro Phe
 35 40 45

Ile Pro Thr Pro Arg Arg Trp Leu
 50 55

<210> 2201
 <211> 70
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(70)
 <223> Xaa = Any amino acid

<400> 2201
 Ile Cys Pro Glu Gln Asp Ala Glu Trp His Trp Arg Leu Arg Ala Gly
 5 10 15

Ala His Leu Pro Arg Xaa Gly Pro Tyr Tyr Pro Ser Gln Glu Ser Glu
 20 25 30

Arg Ala Pro Ala Leu Thr Pro Glu Thr Ile Leu Thr Gly Ile Gly Tyr
 35 40 45

His Phe Ser Val Thr Pro Ala Cys Pro Cys Pro Glu Phe Pro Thr Ala
 50 55 60

Cys Val Ser Leu Ser Pro
 65 70

<210> 2202
 <211> 82
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(82)

<223> Xaa = Any amino acid

<400> 2202

Leu Gly Xaa Gly Asp Trp Xaa Phe Gln Ile Leu Val Met Leu Glu Met
5 10 15

Thr Pro Gln His Gly Asp Val Tyr Thr Cys His Val Glu His Pro Ser
20 25 30

Leu Gln Asn Pro Ile Thr Val Glu Trp Arg Ala Gln Ser Glu Ser Ala
35 40 45

Gln Ser Lys Met Leu Ser Gly Ile Gly Gly Phe Val Leu Gly Leu Ile
50 55 60

Phe Leu Gly Xaa Gly Leu Ile Ile His His Arg Ser Gln Lys Gly Leu
65 70 75 80

Leu His

<210> 2203

<211> 56

<212> PRT

<213> Homo sapiens

<400> 2203

Arg Leu Leu Val Pro Ala Gln Asn Ser Gln Leu Pro Val Ser Ala Cys
5 10 15

Pro Pro Glu Ile Arg Val Leu Gln Trp Leu Ser Arg Ser His Gln Val
20 25 30

Ile Ser Phe His Pro His Pro Lys Ala Leu Ala Val Thr Leu Leu Pro
35 40 45

Ala Leu Thr Gln Ser Leu Cys Leu
50 55

<210> 2204

<211> 57

<212> PRT

<213> Homo sapiens

<400> 2204

Ser Ile Pro Gly Gly Tyr Asn Thr Asp Ile Ser Arg Val Phe Asn Gly
5 10 15

Asn Asn Cys Thr Ser Cys Gln Gln Lys Leu Leu Pro Gly Pro Leu Glu
20 25 30

Ile Tyr Asp Ile Asp Ala Ile Thr Phe Pro Phe Ile Asp Val Leu Phe
35 40 45

His Leu Glu Val Lys Ile Gly Ala Thr
50 55

<210> 2205

<211> 78

<212> PRT

<213> Homo sapiens

<400> 2205

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Leu Asp Val Leu Gln Met Lys Glu Glu Asp Val Leu Lys Phe Leu Ala
      5                      10                      15
Ala Gly Thr His Leu Gly Gly Thr Asn Leu Asp Phe Gln Met Glu Gln
      20                      25                      30
Tyr Ile Tyr Lys Arg Lys Ser Asp Gly Ile Tyr Ile Ile Asn Leu Lys
      35                      40                      45
Arg Thr Trp Glu Lys Leu Leu Leu Ala Ala Arg Ala Ile Val Ala Ile
      50                      55                      60
Glu Asn Pro Ala Asp Val Ser Val Ile Ser Ser Arg Asn Thr
      65                      70                      75

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<210> 2206

<211> 63

<212> PRT

<213> Homo sapiens

<400> 2206

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Tyr Cys Lys Gly Pro Leu Glu Phe Leu Lys Trp Leu His Arg Ile Glu
      5                      10                      15
Ile Ile Ser Asn Asn Cys Lys Gly Thr Glu Asn Leu His Arg Asp Glu
      20                      25                      30
Val Gly Phe Pro Leu Gly Ala Leu Lys Phe Asp Asn Lys Ser Ser Thr
      35                      40                      45
Ser Thr Gly Gln Tyr Ile Asp Phe Gly Cys Leu Arg Pro Gln Asp
      50                      55                      60

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<210> 2207

<211> 87

<212> PRT

<213> Homo sapiens

<400> 2207

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Thr Leu Lys Tyr Phe Ile Ile Gly Gly Asn Leu Trp Arg Leu Val Ala
      5                      10                      15
Ser Asn Leu Gly Ala Ser Asp Thr Gln Asn Leu Tyr Ile Asp Gln Trp
      20                      25                      30
Lys Leu Met Ile Cys Tyr Gln Ile Ser Lys His Leu Met Glu Thr Pro
      35                      40                      45
Leu His Leu Cys Glu Asp Phe Gln Phe Leu Tyr Ser Tyr Leu Lys Leu
      50                      55                      60
Phe Gln Phe Cys Gly Ala Thr Ser Glu Thr Pro Met Gly Leu Cys Asn
      65                      70                      75                      80
Ile Lys Met Trp Arg Met His
      85

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<210> 2208
 <211> 174
 <212> PRT
 <213> Homo sapiens

<400> 2208
 Ala Leu Ala Pro Gly Pro Val Leu Phe Ser Ser Met Val Cys Leu Arg
 5 10 15
 Leu Pro Gly Gly Ser Cys Met Ala Val Leu Thr Val Thr Leu Met Val
 20 25 30
 Leu Ser Ser Pro Leu Ala Leu Ala Gly Asp Thr Arg Pro Arg Phe Leu
 35 40 45
 Glu Tyr Ser Thr Ser Glu Cys His Phe Phe Asn Gly Thr Glu Arg Val
 50 55 60
 Arg Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu Tyr Val Arg Phe
 65 70 75 80
 Asp Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu Leu Gly Arg Pro
 85 90 95
 Asp Glu Glu Tyr Trp Asn Ser Gln Lys Asp Phe Leu Glu Asp Arg Arg
 100 105 110
 Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly Val Val Glu Ser
 115 120 125
 Phe Thr Val Gln Arg Arg Val His Pro Lys Val Thr Val Tyr Pro Ser
 130 135 140
 Lys Thr Gln Pro Leu Gln His His Asn Leu Leu Val Cys Ser Val Ser
 145 150 155 160
 Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp Phe Arg Asn
 165 170

<210> 2209
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 2209
 Ala Pro His Trp Leu Trp Leu Gly Thr Pro Asp His Val Ser Trp Ser
 5 10 15
 Thr Leu Arg Leu Ser Val Ile Ser Ser Met Gly Arg Ser Gly Cys Gly
 20 25 30
 Ser Trp Thr Asp Thr Ser Ile Thr Lys Arg Ser Thr Cys Ala Ser Thr
 35 40 45
 Ala Thr Trp Gly Ser Ser Gly Arg
 50 55

<210> 2210
 <211> 52
 <212> PRT
 <213> Homo sapiens

<400> 2210
 Ser Gly Pro Trp Ser Cys Pro Val Leu Gln His Gly Val Ser Glu Ala
 5 10 15
 Pro Trp Arg Leu Leu His Gly Ser Ser Asp Ser Asp Thr Asp Gly Ala
 20 25 30
 Glu Leu Pro Thr Gly Phe Gly Trp Gly His Gln Thr Thr Phe Leu Gly
 35 40 45
 Val Leu Tyr Val
 50

<210> 2211
 <211> 54
 <212> PRT
 <213> Homo sapiens

<400> 2211
 His Ser Asp Val Glu Tyr Ser Lys Lys Arg Gly Leu Val Ser Pro Ala
 5 10 15
 Lys Ala Ser Gly Glu Leu Ser Thr Ile Ser Val Thr Val Arg Thr Ala
 20 25 30
 Met Gln Glu Pro Pro Gly Ser Leu Arg His Thr Met Leu Glu Asn Arg
 35 40 45
 Thr Gly Pro Gly Ala Arg
 50

<210> 2212
 <211> 70
 <212> PRT
 <213> Homo sapiens

<400> 2212
 Ser Ser Pro Gln Pro Arg Ser Cys Val Cys Ser Arg Cys Pro Pro Arg
 5 10 15
 Pro Ala Cys Leu Pro Gly Ser Pro Ser Gly Cys Ser Ser Thr Pro His
 20 25 30
 Gln Ala Ala Pro Ala Pro Ser Pro Pro Gly Thr Pro Pro Arg Arg Cys
 35 40 45
 Arg Ser Ala Arg Thr Pro Leu Gly Tyr Arg Ser Ile Cys Pro Gly Thr
 50 55 60
 Ala Pro Ala Pro Ser His
 65 70

<210> 2213
 <211> 50
 <212> PRT
 <213> Homo sapiens

<400> 2213
 Ser Thr Pro Arg Asn Val Val Trp Cys Pro Gln Pro Lys Pro Val Gly

5 10 15
 Ser Ser Ala Pro Ser Val Ser Leu Ser Glu Leu Pro Cys Arg Ser Leu
 20 25 30
 Gln Gly Ala Ser Asp Thr Pro Cys Trp Arg Thr Gly Gln Asp Gln Gly
 35 40 45
 Pro Glu
 50

<210> 2214
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 2214
 Arg Ile His Ser His Leu Arg Met Asp Ser Pro Leu His Cys Glu Ala
 5 10 15
 Leu His Asn Pro Val Val Val Ser Ala Val Gly Val His Arg Gly Pro
 20 25 30
 Pro Val Phe Gln Glu Val Leu Leu Ala Val Pro Val Leu Leu Ile Arg
 35 40 45
 Pro Pro Gln Leu Arg His Arg Pro Glu Leu Pro His Val Ala Val Glu
 50 55 60
 Ala His Val Leu Leu Leu Val Ile Glu Val Ser Val Gln Glu Pro His
 65 70 75 80
 Pro Leu Arg Pro Ile Glu Glu Met Thr Leu Arg Arg Arg Val Leu Gln
 85 90 95
 Glu Thr Trp Ser Gly Val Pro Ser Gln Ser Gln Trp Gly Ala Gln His
 100 105 110
 His Gln Cys His Cys Gln Asn Cys His Ala Gly Ala Ser Arg Glu Pro
 115 120 125
 Gln Thr His His Ala Gly Glu Gln Asp Arg Thr Arg Gly Gln Ser
 130 135 140

<210> 2215
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 2215
 Thr Leu Pro Pro Asp Arg Met Lys Phe Ile Ser Thr Ser Leu Leu Leu
 5 10 15
 Met Leu Leu Val Ser Ser Leu Ser Pro Val Gln Gly Val Leu Glu Val
 20 25 30
 Tyr Tyr Thr Ser Leu Arg Cys Arg Cys Val Gln Glu Ser Ser Val Phe
 35 40 45
 Ile Pro Arg Arg Phe Ile Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn
 50 55 60

Gly Cys Pro Arg Lys Glu Ile Ile Val Trp Lys Lys Asn Lys Ser Ile
 65 70 75 80
 Val Cys Val Asp Pro Gln Ala Glu Trp Ile Gln Arg Met Met Glu Val
 85 90 95
 Leu Arg Lys Arg Ser Ser Ser Thr Leu Pro Val Pro Val Phe Lys Arg
 100 105 110
 Lys Ile Pro
 115

<210> 2216
 <211> 55
 <212> PRT
 <213> Homo sapiens

<400> 2216
 Glu Lys Glu Val Leu Gln Leu Tyr Gln Phe Gln Cys Leu Arg Glu Arg
 5 10 15
 Phe Pro Asp Ala Asp Ile Ser Thr Lys Asn Thr Cys Ile Leu Pro Leu
 20 25 30
 Ser Leu Leu Trp Ile Leu Val Leu Cys Leu Val Lys Ser Phe Pro Gly
 35 40 45
 Lys Arg Thr Ser Pro Tyr Lys
 50 55

<210> 2217
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 2217
 Ser His Ala Tyr Leu Tyr Gly Glu Val Leu Phe Pro Gly Lys Asp Leu
 5 10 15
 Thr Lys His Lys Thr Lys Ile Gln Ser Arg Asp Lys Gly Arg Met Gln
 20 25 30
 Val Phe Leu Val Glu Ile Ser Ala Ser Gly Asn Leu Ser Leu Lys His
 35 40 45
 Trp Asn Trp
 50

<210> 2218
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 2218
 Ala Ala Met Ala Arg Gly Pro Lys Lys His Leu Lys Arg Val Ala Ala
 5 10 15
 Pro Lys His Trp Met Leu Asp Lys Leu Thr Gly Val Phe Ala Pro Arg
 20 25 30

Pro Ser Thr Gly Pro His Lys Leu Arg Glu Cys Leu Pro Leu Ile Ile
 35 40 45
 Phe Leu Arg Asn Arg Leu Lys Tyr Ala Leu Thr Gly Asp Glu Val Lys
 50 55 60
 Lys Ile Cys Met Gln Arg Phe Ile Lys Ile Asp Gly Lys Val Arg Thr
 65 70 75 80
 Asp Ile Thr Tyr Pro Ala Gly Phe Met Asp Val Ile Ser Ile Asp Lys
 85 90 95
 Thr Gly Glu Asn Phe Arg Leu Ile Tyr Asp Thr Lys Gly Arg Phe Ala
 100 105 110
 Val His Arg Ile Thr
 115

<210> 2219
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 2219
 Cys Asn Thr Met Tyr Ser Lys Ala Thr Leu Gly Val Ile Asp Gln Thr
 5 10 15
 Glu Ile Leu Ser Arg Leu Val Asn Ala Asp Asp Ile His Glu Ser Ser
 20 25 30
 Arg Val Gly Tyr Ile Ser Ser Asp Leu Ala Ile Asp Phe Asn Glu Pro
 35 40 45
 Leu His Ala Asn Leu Leu Tyr Phe Ile Ser Cys Gln Gly Ile Leu Lys
 50 55 60
 Ser Val Pro Gln Glu Asn Asp Glu Gly Glu Thr Leu Ser Gln Leu Val
 65 70 75 80
 Gly Thr Gly Gly Trp Thr Arg Ser Lys His Thr Gly Gln Phe Ile Gln
 85 90 95
 His Pro Met Leu Trp Ser Cys His Pro Leu Gln Met Leu Leu Gly Thr
 100 105 110
 Thr Ser His Gly Cys
 115

<210> 2220
 <211> 83
 <212> PRT
 <213> Homo sapiens

<400> 2220
 Val Ile Ser Val Arg Thr Leu Pro Ser Ile Leu Met Asn Arg Cys Met
 5 10 15
 Gln Ile Phe Phe Thr Ser Ser Pro Val Arg Ala Tyr Leu Ser Leu Phe
 20 25 30

Leu Arg Lys Met Met Arg Gly Arg His Ser Leu Asn Leu Trp Gly Pro
 35 40 45
 Val Asp Gly Arg Gly Ala Asn Thr Pro Val Asn Leu Ser Ser Ile Gln
 50 55 60
 Cys Phe Gly Ala Ala Thr Arg Phe Arg Cys Phe Leu Gly Pro Arg Ala
 65 70 75 80
 Met Ala Ala

<210> 2221
 <211> 70
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(70)
 <223> Xaa = Any amino acid

<400> 2221
 Leu Pro Pro Phe Leu Ser Glu Leu Phe Leu Leu His Ile Thr Ala Ala
 5 10 15
 Thr Thr Ala Pro Val Ile Thr Ala Pro Arg Arg Thr Arg Pro Ala Met
 20 25 30
 Met Pro Thr Met Gly Met Val Gly Trp Glu Asp Ser Ser His Leu Xaa
 35 40 45
 Val Arg Gly Leu Gly Arg Pro Ser Cys Cys Thr Trp Gln Val Tyr Leu
 50 55 60
 Cys Ser Ser Pro Glu Gly
 65 70

<210> 2222
 <211> 63
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(63)
 <223> Xaa = Any amino acid

<400> 2222
 Ala Leu Pro Pro Pro His His Gly Ser Asp His Ser Ser Ser Asp His
 5 10 15
 Ser Ser Lys Glu Asn Gln Ala Ser Asn Asp Ala His Asp Gly Asp Gly
 20 25 30
 Gly Leu Gly Arg Gln Leu Pro Ser Xaa Gly Glu Gly Leu Gly Gln Thr
 35 40 45
 Leu Met Leu His Met Ala Gly Val Ser Leu Leu Leu Ser Arg Arg
 50 55 60

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<210> 2223
<211> 50
<212> PRT
<213> Homo sapiens
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<220>  
<221> variant  
<222> (1)...(50)  
<223> Xaa = Any amino acid
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<400> 2223
Gly Ser Ala Gln Ala Pro His Xaa Glu Met Gly Ala Val Phe Pro Ala
      5              10              15
His His Pro His Arg Gly His His Cys Trp Pro Gly Ser Pro Trp Ser
      20              25              30
Cys Asp His Trp Ser Cys Gly Arg Cys Arg Asp Val Glu Glu Glu Glu
      35              40              45
Leu Arg
      50

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<210> 2224
<211> 92
<212> PRT
<213> Homo sapiens
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<220>  
<221> variant  
<222> (1)...(92)  
<223> Xaa = Any amino acid
```

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<400> 2224
Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys His Val Gln His Glu Gly
          5                      10                      15
Leu Pro Lys Pro Leu Thr Xaa Arg Trp Glu Leu Ser Ser Gln Pro Thr
          20                      25                      30
Ile Pro Ile Val Gly Ile Ile Ala Gly Leu Val Leu Leu Gly Ala Val
          35                      40                      45
Ile Thr Gly Ala Val Val Ala Ala Val Met Trp Arg Arg Lys Ser Ser
          50                      55                      60
Asp Arg Lys Gly Gly Ser Tyr Thr Gln Ala Ala Ser Ser Asp Ser Ala
          65                      70                      75                      80
Gln Gly Ser Asp Val Ser Leu Thr Ala Cys Lys Val
          85                      90

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<210> 2225
<211> 50
<212> PRT
<213> Homo sapiens
```

<400> 2225
Arg Ile Gly Phe Ser His Gln Gly Tyr Asn Cys Trp Trp Trp Cys His
 5 10 15

Ser Thr His Pro Gln Ile Ser Asp Trp Glu Glu Arg Thr Thr Glu Asp
 20 25 30

Cys Leu Lys Asp Ala Trp Ile Pro Cys Tyr Leu Arg Thr Leu Asn Thr
 35 40 45

Leu Thr
 50

<210> 2226
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 2226
 Ala Ser Ala Glu Phe Glu Met Ala Gly Gly Lys Ala Gly Lys Asp Ser
 5 10 15

Gly Lys Ala Lys Thr Lys Ala Val Ser Arg Ser Gln Arg Ala Gly Leu
 20 25 30

Gln Phe Pro Val Gly Arg Ile His Arg His Leu Lys Ser Arg Thr Thr
 35 40 45

Ser His Gly Arg Val Gly Ala Thr Ala Ala Val Tyr Ser Ala Ala Ile
 50 55 60

Leu Glu Tyr Leu Thr Ala Glu Val Leu Glu Leu Ala Gly Asn Ala Ser
 65 70 75 80

Lys Asp Leu Lys Val Lys Arg Ile Thr Pro Arg His Leu Gln Leu Ala
 85 90 95

Ile Arg Gly Asp Glu Glu Leu Asp Ser Leu Ile Lys Ala Thr Ile Ala
 100 105 110

Gly Gly Gly Val Ile Pro His Ile His Lys Ser Leu Ile Gly Lys Lys
 115 120 125

Gly Gln Gln Lys Thr Val
 130

<210> 2227
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 2227
 Arg Cys Asp Glu Gly Val Gly Gly Gly Ile Ser Pro Trp Val Arg Leu
 5 10 15

Ala Phe Ser Leu Pro Cys Leu Leu Glu Leu Gln Arg Asn Ser Lys Trp
 20 25 30

Leu Ala Val Arg Leu Glu Arg Thr Pro Glu Arg Pro Arg Gln Arg Arg
 35 40 45

Phe Pro Ala Arg Arg Glu Pro Ala Cys Ser Ser Gln Trp Ala Val Phe
 50 55 60

Ile Asp Thr
65

<210> 2228
<211> 60
<212> PRT
<213> Homo sapiens

<400> 2228
Asp Asn Lys Glu Ser Arg His Pro Leu Asp Ser Leu Leu Leu Ser Phe
 5 10 15
Leu Pro Asn Gln Arg Phe Val Asp Val Trp Asn Asp Thr Thr Thr Ser
 20 25 30
Asn Cys Ser Leu Asp Glu Arg Ile Gln Phe Phe Ile Ser Thr Asn Ser
 35 40 45
Lys Leu Gln Val Thr Arg Gly Asn Thr Leu Tyr Leu
 50 55 60

<210> 2229
<211> 64
<212> PRT
<213> Homo sapiens

<400> 2229
Ile Arg Pro Thr Gly Asn Cys Lys Pro Ala Leu Cys Glu Arg Glu Thr
 5 10 15
Ala Phe Val Leu Ala Phe Pro Glu Ser Phe Pro Ala Leu Pro Pro Ala
 20 25 30
Ile Ser Asn Ser Ala Glu Ala Gln Ala Ser Lys Ala Glu Lys Arg Leu
 35 40 45
Ile Gly Pro Thr Val Arg Ser His His Leu Leu Leu Arg Arg Thr Ala
 50 55 60

<210> 2230
<211> 53
<212> PRT
<213> Homo sapiens

<400> 2230
Ile Leu Gly Val Asp Glu Tyr Gly Pro Leu Gly Thr Ala Ser Arg Leu
 5 10 15
Ser Ala Ser Gly Lys Pro Pro Leu Ser Trp Pro Phe Arg Ser Pro Phe
 20 25 30
Gln Pro Tyr Arg Gln Pro Phe Arg Ile Pro Leu Lys Leu Lys Gln Ala
 35 40 45
Arg Gln Arg Lys Gly
 50

<210> 2231
<211> 185

<212> PRT

<213> Homo sapiens

<400> 2231

Phe Asp Asp Arg Arg Gly Arg Pro Val Gly Phe Pro Met Arg Gly Arg
 5 10 15

Gly Gly Phe Asp Arg Met Pro Pro Gly Arg Gly Gly Arg Pro Met Pro
 20 25 30

Pro Ser Arg Arg Asp Tyr Asp Asp Met Ser Pro Arg Arg Gly Pro Pro
 35 40 45

Pro Pro Pro Pro Gly Arg Gly Gly Arg Gly Gly Ser Arg Ala Arg Asn
 50 55 60

Leu Pro Leu Pro Pro Pro Pro Pro Arg Gly Gly Asp Leu Met Ala
 65 70 75 80

Tyr Asp Arg Arg Gly Arg Pro Gly Asp Arg Tyr Asp Gly Met Val Gly
 85 90 95

Phe Ser Ala Asp Glu Thr Trp Asp Ser Ala Ile Asp Thr Trp Ser Pro
 100 105 110

Ser Glu Trp Gln Met Ala Tyr Glu Pro Gln Gly Gly Ser Gly Tyr Asp
 115 120 125

Tyr Ser Tyr Ala Gly Gly Arg Gly Ser Tyr Gly Asp Leu Gly Gly Pro
 130 135 140

Ile Ile Thr Thr Gln Val Thr Ile Pro Lys Asp Leu Ala Gly Ser Ile
 145 150 155 160

Ile Gly Lys Gly Gly Gln Arg Ile Lys Gln Ile Arg His Glu Ser Gly
 165 170 175

Ala Ser Ile Lys Ile Asp Glu Pro Leu
 180 185

<210> 2232

<211> 65

<212> PRT

<213> Homo sapiens

<400> 2232

Ala Leu Val Glu Asp His Leu Pro Leu Leu Pro Asp Glu Ala Ala Gly
 5 10 15

Val Val Ala Glu Leu Gly Ile Phe Leu Phe Leu His His His His Leu
 20 25 30

Glu Gly Glu Thr Ser Trp Pro Met Thr Glu Glu Gly Asp Leu Glu Thr
 35 40 45

Val Thr Thr Ala Trp Leu Val Ser Val Leu Met Lys Leu Gly Thr Leu
 50 55 60

Gln
 65

<210> 2233
 <211> 112
 <212> PRT
 <213> Homo sapiens

<400> 2233
 Trp Ala Pro Cys Ile Tyr Cys Arg Val Pro Ser Phe Ile Ser Thr Glu
 5 10 15
 Thr Asn His Ala Val Val Thr Val Ser Arg Ser Pro Ser Ser Val Ile
 20 25 30
 Gly His Glu Val Ser Pro Ser Arg Trp Trp Trp Trp Arg Lys Arg Lys
 35 40 45
 Ile Pro Ser Ser Ala Thr Thr Pro Ala Ala Ser Ser Gly Arg Arg Gly
 50 55 60
 Arg Trp Ser Ser Thr Arg Ala His Ile Ile Ile Ile Ser Ser Arg Trp
 65 70 75 80
 Arg His Gly Thr Pro Thr Pro Thr Arg Arg His Ser Val Lys Thr Thr
 85 90 95
 Ser Ser Pro His Gly Lys Ser His Trp Ala Ser Ala Thr Val Ile Lys
 100 105 110

<210> 2234
 <211> 199
 <212> PRT
 <213> Homo sapiens

<400> 2234
 His Leu Ile Tyr Lys Cys Gly Gly Ile Asp Lys Arg Thr Ile Glu Lys
 5 10 15
 Phe Gly Lys Glu Ala Ala Glu Met Gly Lys Gly Ser Phe Lys Tyr Ala
 20 25 30
 Trp Val Leu Asp Lys Leu Lys Ala Glu Arg Glu Arg Gly Ile Thr Ile
 35 40 45
 Asp Ile Ser Leu Trp Lys Phe Glu Thr Ser Lys Tyr Tyr Val Thr Ile
 50 55 60
 Ile Asp Ala Pro Gly His Arg Asp Phe Ile Lys Asn Met Ile Thr Gly
 65 70 75 80
 Thr Ser Gln Ala Asp Cys Ala Val Leu Ile Val Ala Ala Gly Val Gly
 85 90 95
 Glu Phe Glu Ala Gly Ile Ser Lys Asn Gly Gln Thr Arg Glu His Ala
 100 105 110
 Leu Leu Ala Tyr Thr Leu Gly Val Lys Gln Leu Ile Val Gly Val Asn
 115 120 125
 Lys Met Asp Ser Thr Glu Pro Pro Tyr Ser Gln Lys Arg Tyr Glu Glu
 130 135 140
 Ile Val Lys Glu Val Ser Thr Tyr Ile Lys Lys Ile Gly Tyr Asn Pro
 145 150 155 160

Asp Thr Val Ala Phe Val Pro Ile Ser Gly Trp Asn Gly Asp Asn Met
165 170 175

Leu Glu Pro Ser Ala Asn Met Pro Trp Phe Lys Gly Trp Lys Val Thr
180 185 190

Arg Lys Asp Gly Asn Ala Ser
195

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<210> 2235
<211> 76
<212> PRT
<213> Homo sapiens
```

<400> 2235
 Thr Gly Ile Ala Ile Leu Thr Gly Asp Phe Pro Ser Leu Glu Pro Arg
 5 10 15

His Val Ser Thr Trp Leu Gln His Val Val Thr Ile Pro Thr Arg Asn
20 25 30

Trp His Lys Cys Tyr Cys Val Gly Val Val Ala Asn Phe Leu Asn Val
35 40 45

Ser Ala Asp Phe Leu Asn Asn Phe Leu Ile Ser Leu Leu Ala Val Gly
50 55 60

Trp Leu Ser Gly Ile His Phe Val Asn Thr Asp Asn
65 70 75

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<210> 2236
<211> 122
<212> PRT
<213> Homo sapiens
```

<400> 2236
Leu Phe His Thr Gln Cys Val Ser Gln Lys Gly Met Leu Ser Gly Leu
 5 10 15

Pro Ile Leu Gly Asp Thr Ser Phe Lys Phe Thr Asn Thr Ser Ser Asn
20 25 30

Asn Gln Asp Ser Thr Val Ser Leu Arg Cys Pro Cys Asn His Val Phe
35 40 45

Asp Lys Val Ser Val Ser Trp Gly Ile Asn Asp Ser His Ile Val Leu
50 55 60

Ala Gly Leu Lys Phe Pro Gln Gly Asp Ile Asn Gly Asp Thr Thr Phe
65 70 75 80

Thr Leu Ser Phe Gln Phe Ile Gln Asp Pro Gly Ile Leu Glu Gly Ala
85 90 95

Leu Ser His Leu Ser Ser Leu Leu Pro Lys Phe Phe Asn Gly Ser Phe
100 105 110

Val Asp Ala Thr Ala Phe Ile Asp Gln Met
115 120

<210> 2237
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 2237
 Tyr Leu Leu Val Ser Asn Phe His Lys Glu Ile Ser Met Val Ile Pro
 5 10 15
 Arg Ser Arg Ser Ala Phe Ser Leu Ser Lys Thr Gln Ala Tyr Leu Lys
 20 25 30
 Glu Pro Phe Pro Ile Ser Ala Ala Ser Phe Pro Asn Phe Ser Met Val
 35 40 45
 Leu Leu Ser Met Pro Pro His Leu
 50 55

<210> 2238
 <211> 50
 <212> PRT
 <213> Homo sapiens

<400> 2238
 Leu Arg Glu Gly Ser Gly Trp Val Arg Gly Asp Gly Glu Gly Lys Gly
 5 10 15
 Gly Val Ser Ile Phe Ile Leu Arg Ile Gly Val Gln Ser Thr Ser Gly
 20 25 30
 Val Ser Ala Pro Pro Cys Pro Pro Val Gly Leu Arg Arg Thr Gly Lys
 35 40 45
 Arg Thr
 50

<210> 2239
 <211> 50
 <212> PRT
 <213> Homo sapiens

<400> 2239
 Arg Ala Leu Thr Glu Ser Ser Arg Asn Ser Gly Thr Val Ser Arg Gly
 5 10 15
 Pro Ala Leu His Gly Pro Gly Pro Pro Pro Ser Pro Ser Pro Arg Pro
 20 25 30
 Glu Pro Arg Ala Thr Arg Ser Ala Ala Ala Ala Ala Trp Pro Gly Thr
 35 40 45
 Ile Ser
 50

<210> 2240
 <211> 55
 <212> PRT
 <213> Homo sapiens

<220>

<221> variant

<222> (1)...(55)

<223> Xaa = Any amino acid

<400> 2240

Ser Arg Pro Pro Ala Leu Pro Gly Ser Thr Ser Pro Val His Val Leu
 5 10 15

Ile Leu His Phe Ala Phe Tyr His Lys Ile Phe Leu Trp Pro Gly Ala
 20 25 30

Phe Gly Pro Ser Ala Ser Ser Cys His Gln Arg Gly Pro Ser Gly Ser
 35 40 45

Thr Trp Arg Pro Xaa Val Gln
 50 55

<210> 2241

<211> 75

<212> PRT

<213> Homo sapiens

<400> 2241

Gln Arg Ala Ala Glu Thr Leu Glu Leu Phe Pro Glu Gly Leu His Cys
 5 10 15

Met Asp Gln Gly His His Leu Leu Leu His Pro Gly Gln Asn Pro Val
 20 25 30

Pro Pro Gly Leu Gln Pro Leu Gln His Gly Leu Glu Pro Ser His Asp
 35 40 45

Leu Val Thr Lys Ala Leu Pro Arg Leu Leu Gly Cys Gly Ile Leu Asn
 50 55 60

Ile Arg Asp Arg Gly Ser Val Ala Ser Ala Pro
 65 70 75

<210> 2242

<211> 103

<212> PRT

<213> Homo sapiens

<400> 2242

Asp Trp Lys Glu Asp Met Lys Ser Ser Asp Arg Glu Gln Gln Lys Leu
 5 10 15

Trp Asn Cys Phe Gln Arg Ala Cys Thr Ala Trp Thr Arg Ala Thr Thr
 20 25 30

Phe Ser Phe Thr Gln Ala Arg Thr Pro Cys His Gln Val Cys Ser Arg
 35 40 45

Cys Ser Met Ala Trp Asn His Leu Met Thr Leu Ser Gln Lys Leu Ser
 50 55 60

Pro Gly Ser Ser Val Ala Gly Ser Ser Thr Ser Gly Thr Gly Asp Leu
 65 70 75 80

Leu Pro Arg His Arg Asn Pro Ser Leu Ser Phe Ser Ser Arg Gly Val

805

85

90

95

Ser Ser Arg Cys Cys Ser Ser
100

<210> 2243
<211> 76
<212> PRT
<213> Homo sapiens

<400> 2243
Gln Gly His Glu Met Val Pro Gly His Ala Ala Ala Ala Asp Leu
5 10 15
Val Ala Arg Gly Ser Gly Leu Gly Glu Gly Glu Gly Gly Pro Gly
20 25 30
Pro Cys Ser Ala Gly Pro Leu Glu Thr Val Pro Glu Phe Leu Leu Leu
35 40 45
Ser Val Arg Ala Leu His Val Leu Phe Pro Val Leu Arg Ser Pro Thr
50 55 60
Gly Gly Gln Gly Gly Ala Asp Thr Pro Glu Val Leu
65 70 75

<210> 2244
<211> 194
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(194)
<223> Xaa = Any amino acid

<400> 2244
Leu Glu Xaa Leu Ala Ala Met Cys Phe Pro Lys Val Leu Ser Asp Asp
5 10 15
Met Lys Lys Leu Lys Ala Arg Met His Gln Ala Ile Glu Arg Phe Tyr
20 25 30
Asp Lys Met Gln Asn Ala Glu Ser Gly Arg Gly Gln Val Met Ser Ser
35 40 45
Leu Ala Glu Leu Glu Asp Asp Phe Lys Glu Gly Tyr Leu Glu Thr Val
50 55 60
Ala Ala Tyr Tyr Glu Glu Gln His Leu Glu Leu Thr Pro Leu Leu Glu
65 70 75 80
Lys Glu Arg Asp Gly Leu Arg Cys Arg Gly Asn Arg Ser Pro Val Pro
85 90 95
Asp Val Glu Asp Pro Ala Thr Glu Glu Pro Gly Glu Ser Phe Cys Asp
100 105 110
Lys Val Met Arg Trp Phe Gln Ala Met Leu Gln Arg Leu Gln Thr Trp
115 120 125

Trp His Gly Val Leu Ala Trp Val Lys Glu Lys Val Val Ala Leu Val
130 135 140

His Ala Val Gln Ala Leu Trp Lys Gln Phe Gln Ser Phe Cys Cys Ser
145 150 155 160

Leu Ser Glu Leu Phe Met Ser Ser Phe Gln Ser Tyr Gly Ala Pro Arg
165 170 175

Gly Asp Lys Glu Glu Leu Thr Pro Gln Lys Cys Ser Glu Pro Gln Ser
180 185 190

Ser Lys

<210> 2245
<211> 87
<212> PRT
<213> Homo sapiens

<400> 2245
Ile Leu Thr Leu Tyr Ser Glu Pro Ser Phe Asn Thr Met Val Ser Phe
5 10 15

Leu Arg Ala Ser Arg Ser Pro Val Arg Ser Met Val Ile Gly Pro Gly
20 25 30

Ala Leu Ser Gln Thr Arg Val Ser Arg Val Thr Thr Thr Leu Gly Ala
35 40 45

Phe Gly Ser Val Thr Thr Gly Pro Ser Pro Ser Ser Val Phe Leu Tyr
50 55 60

Leu Ile Arg Leu Ser Ser Ser Leu Ser Ile Ser Cys Ser Ser Phe Arg
65 70 75 80

Asp Phe Cys Gly Gly Gly Leu
85

<210> 2246
<211> 55
<212> PRT
<213> Homo sapiens

<400> 2246
His Asn Gly Phe Leu Phe Glu Gly Phe Gln Ile Ser Ser Lys Val His
5 10 15

Gly Asp Trp Ser Arg Gly Thr Leu Thr Asn Gln Gly Glu Pro Gly Asp
20 25 30

Asn Asp Ile Gly Gly Phe Arg Ile Cys His His Arg Thr Ile Ser Gln
35 40 45

Gln Arg Phe Leu Val Leu Asn
50 55

<210> 2247
<211> 119
<212> PRT

<213> Homo sapiens

<400> 2247

Glu Lys Ala Pro Glu Pro His Val Glu Glu Asp Asp Asp Asp Glu Leu
5 10 15

Asp Ser Lys Leu Asn Tyr Lys Pro Pro Pro Gln Lys Ser Leu Lys Glu
20 25 30

Leu Gln Glu Met Asp Lys Asp Asp Glu Ser Leu Ile Lys Tyr Lys Lys
35 40 45

Thr Leu Leu Gly Asp Gly Pro Val Val Thr Asp Pro Lys Ala Pro Asn
50 55 60

Val Val Val Thr Arg Leu Thr Leu Val Cys Glu Ser Ala Pro Gly Pro
65 70 75 80

Ile Thr Met Asp Leu Thr Gly Asp Leu Glu Ala Leu Lys Lys Glu Thr
85 90 95

Ile Val Leu Lys Glu Gly Ser Glu Tyr Arg Val Lys Ile His Phe Lys
100 105 110

Val Asn Arg Asp Ile Val Ser
115

<210> 2248

<211> 55

<212> PRT

<213> Homo sapiens

<400> 2248

Pro Arg Leu Leu Pro Ala Pro Pro Trp Arg Arg Ala Thr Ser Cys Leu
5 10 15

Thr Ala Arg Ser Ser Pro Leu Ala Met Ser Gly Ser Ala Ala Leu Arg
20 25 30

His Ser Ser Ser Leu Pro Ser Trp Ala Trp Ser Pro Val Ala Ser Thr
35 40 45

Lys Leu Pro Ser Thr Pro Ser
50 55

<210> 2249

<211> 54

<212> PRT

<213> Homo sapiens

<400> 2249

Arg Ser Arg Ser Leu Leu Leu Leu Ser Ala Ser Thr Pro Cys Gly Ser
5 10 15

Ala Ala Pro Ser Trp Pro Arg Cys Pro Pro Ser Ser Arg Cys Gly Ser
20 25 30

Ala Ser Arg Ser Met Thr Ser Pro Ala Pro Pro Ser Ser Thr Ala Asn
35 40 45

Ala Ser Arg Arg Thr Met

50

<210> 2250
<211> 147
<212> PRT
<213> Homo sapiens

<400> 2250
Thr Ala Ala Ser Ser Ser Ser Leu Glu Lys Ser Tyr Glu Leu Pro Asp
 5 10 15

Gly Gln Val Ile Thr Ile Gly Asn Glu Arg Phe Arg Cys Pro Glu Ala
 20 25 30

Leu Phe Gln Pro Ser Phe Leu Gly Met Glu Ser Cys Gly Ile His Glu
 35 40 45

Thr Thr Phe Asn Ser Ile Met Lys Cys Asp Val Asp Ile Arg Lys Asp
 50 55 60

Leu Tyr Ala Asn Thr Val Leu Ser Gly Gly Thr Thr Met Tyr Pro Gly
 65 70 75 80

Ile Ala Asp Arg Met Gln Lys Glu Ile Thr Ala Leu Ala Pro Ser Thr
 85 90 95

Met Lys Ile Lys Ile Ile Ala Pro Pro Glu Arg Lys Tyr Ser Val Trp
 100 105 110

Ile Gly Gly Ser Ile Leu Ala Ser Leu Ser Thr Phe Gln Gln Met Trp
 115 120 125

Ile Ser Lys Gln Glu Tyr Asp Glu Ser Gly Pro Ser Ile Val His Arg
 130 135 140

Lys Cys Phe
145

<210> 2251
<211> 135
<212> PRT
<213> Homo sapiens

<400> 2251
Lys His Leu Arg Trp Thr Met Glu Gly Pro Asp Ser Ser Tyr Ser Cys
 5 10 15

Leu Leu Ile His Ile Cys Trp Lys Val Asp Ser Glu Ala Arg Met Glu
 20 25 30

Pro Pro Ile His Thr Glu Tyr Leu Arg Ser Gly Gly Ala Met Ile Leu
 35 40 45

Ile Phe Ile Val Leu Gly Ala Arg Ala Val Ile Ser Phe Cys Ile Leu
 50 55 60

Ser Ala Met Pro Gly Tyr Met Val Val Pro Pro Asp Ser Thr Val Leu
 65 70 75 80

Ala Tyr Arg Ser Leu Arg Met Ser Thr Ser His Phe Met Met Glu Leu
 85 90 95

Lys Val Val Ser Trp Met Pro Gln Asp Ser Met Pro Arg Lys Glu Gly
 100 105 110
 Trp Lys Ser Ala Ser Gly Gln Arg Asn Arg Ser Leu Pro Met Val Met
 115 120 125
 Thr Trp Pro Ser Gly Ser Ser
 130 135

<210> 2252
 <211> 151
 <212> PRT
 <213> Homo sapiens

<400> 2252
 Ile Val Arg Leu Glu Ala Phe Ala Val Asp Asp Gly Gly Ala Gly Leu
 5 10 15
 Val Ile Leu Leu Leu Ala Asp Pro His Leu Leu Glu Gly Gly Gln Arg
 20 25 30
 Gly Gln Asp Gly Ala Ala Asp Pro His Gly Val Leu Ala Leu Arg Arg
 35 40 45
 Ser Asn Asp Leu Asp Leu His Cys Ala Gly Cys Gln Gly Ser Asp Leu
 50 55 60
 Leu Leu His Pro Val Gly Asn Ala Arg Val His Gly Gly Ala Ala Arg
 65 70 75 80
 Gln His Cys Val Gly Val Gln Val Phe Ala Asp Val His Val Thr Leu
 85 90 95
 His Asp Gly Val Glu Gly Ser Phe Val Asp Ala Thr Gly Leu His Ala
 100 105 110
 Gln Glu Gly Arg Leu Glu Glu Cys Leu Arg Ala Ala Glu Pro Leu Ile
 115 120 125
 Ala Asn Gly Asp Asp Leu Ala Val Arg Gln Leu Val Ala Leu Leu Gln
 130 135 140
 Gly Gly Ala Gly Ser Ser Arg
 145 150

<210> 2253
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 2253
 Ser His Arg Leu Leu Gly Cys Cys Glu Pro Arg Ala Leu Leu Ser Ser
 5 10 15
 Gln Leu Ala Arg Arg Ala Glu Gln Pro Phe Gly Pro Ser His Pro Arg
 20 25 30
 Ser Leu Tyr Arg Ser Phe Leu Asn Leu Arg Asp Pro Phe Pro Ala Leu
 35 40 45

Leu Lys Phe Pro Val Pro Thr Leu Gly Leu Ser Pro
 50 55 60

<210> 2254
 <211> 70
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(70)
 <223> Xaa = Any amino acid

<400> 2254
 Gly Ile Arg Ser Gln Leu Ser Leu Asn Ser Gln Ser Pro Pro Trp Ala
 5 10 15
 Ser Leu Pro Asn Asp Leu Val Ala Leu Gly Ala Ser Glu Val Asn Pro
 20 25 30
 Glu Ile Leu Pro Pro Ser Thr Leu Gly Ser Asp Leu Cys Pro Ser Leu
 35 40 45
 Xaa His Lys Glu Ile Ser Val Lys Xaa Val Gly Thr Gly Gly Phe Arg
 50 55 60
 Pro Cys Ser Lys Ala Thr
 65 70

<210> 2255
 <211> 77
 <212> PRT
 <213> Homo sapiens

<400> 2255
 Gly Glu Arg Pro Arg Val Gly Thr Gly Asn Leu Arg Arg Ala Gly Asn
 5 10 15
 Gly Ser Leu Arg Phe Arg Lys Leu Leu Tyr Lys Leu Arg Gly Trp Leu
 20 25 30
 Gly Pro Lys Gly Cys Ser Ala Arg Arg Ala Ser Cys Glu Leu Ser Lys
 35 40 45
 Ala Leu Gly Ser Gln His Pro Lys Ser Leu Trp Leu Gln Ser Cys Val
 50 55 60
 Cys Thr Thr Gln Ser Lys Gly Ser Phe Cys Phe Val Phe
 65 70 75

<210> 2256
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 2256
 Thr Leu Pro Pro Asp Arg Met Lys Phe Ile Ser Thr Ser Leu Leu Leu
 5 10 15
 Met Leu Leu Val Ser Ser Leu Ser Pro Val Gln Gly Val Leu Glu Val

20 25 30
 Tyr Tyr Thr Ser Leu Arg Cys Arg Cys Val Gln Glu Ser Ser Val Phe
 35 40 45
 Ile Pro Arg Arg Phe Ile Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn
 50 55 60
 Gly Cys Pro Arg Lys Glu Ile Ile Val Trp Lys Lys Asn Lys Ser Ile
 65 70 75 80
 Val Cys Val Asp Pro Gln Ala Glu Trp Ile Gln Arg Met Met Glu Val
 85 90 95
 Leu Arg Lys Arg Ser Ser Ser Thr Leu Pro Val Pro Val Phe Lys Arg
 100 105 110
 Lys Ile Pro
 115

<210> 2257
 <211> 55
 <212> PRT
 <213> Homo sapiens

<400> 2257
 Glu Lys Glu Val Leu Gln Leu Tyr Gln Phe Gln Cys Leu Arg Glu Arg
 5 10 15
 Phe Pro Asp Ala Asp Ile Ser Thr Lys Asn Thr Cys Ile Leu Pro Leu
 20 25 30
 Ser Leu Leu Trp Ile Leu Val Leu Cys Leu Val Lys Ser Phe Pro Gly
 35 40 45
 Lys Arg Thr Ser Pro Tyr Lys
 50 55

<210> 2258
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(51)
 <223> Xaa = Any amino acid

<400> 2258
 Xaa His Ala Tyr Leu Tyr Gly Glu Val Leu Phe Pro Gly Lys Asp Leu
 5 10 15
 Thr Lys His Lys Thr Lys Ile Gln Ser Arg Asp Lys Gly Arg Met Gln
 20 25 30
 Val Phe Leu Val Glu Ile Ser Ala Ser Gly Asn Leu Ser Leu Lys His
 35 40 45
 Trp Asn Trp
 50

<210> 2259
<211> 69
<212> PRT
<213> Homo sapiens

<400> 2259
Leu Cys Leu Arg Ala Leu Ala Gly Gln Glu Gln Asp Ser Trp Asp Gly
5 10 15
Ala Ala Gln Ala Trp Phe Leu Leu Pro Val Ala Ala Asp Asn Leu Gly
20 25 30
Gly Asn Leu Pro Leu Ala Val Leu Glu Ala Thr Val Leu Ser Pro Ser
35 40 45
Ile Thr Ala Leu Gly Pro Gly Asp Ala Lys Gly Gln Asn Gln Asp Lys
50 55 60
Glu Ala Gln Ser Gln
65

<210> 2260
<211> 102
<212> PRT
<213> Homo sapiens

<400> 2260
Leu Pro Thr Ser Pro Ser Ala Leu Ala Ser Tyr Ser Pro Ser Thr Thr
5 10 15
Asp Met Ala Gln Ser Leu Ala Leu Ser Leu Leu Ile Leu Val Leu Ala
20 25 30
Phe Gly Ile Pro Arg Thr Gln Gly Ser Asp Gly Gly Ala Gln Asp Cys
35 40 45
Cys Leu Lys Tyr Ser Gln Arg Lys Ile Pro Ala Lys Val Val Arg Ser
50 55 60
Tyr Arg Lys Gln Glu Pro Ser Leu Gly Cys Ser Ile Pro Ala Ile Leu
65 70 75 80
Phe Leu Pro Arg Lys Arg Ser Gln Ala Glu Leu Cys Ala Asp Pro Lys
85 90 95
Glu Leu Trp Val Gln Gln
100

<210> 2261
<211> 77
<212> PRT
<213> Homo sapiens

<400> 2261
Ala Ser Leu Ser Trp Phe Trp Pro Leu Ala Ser Pro Gly Pro Lys Ala
5 10 15
Val Met Glu Gly Leu Arg Thr Val Ala Ser Ser Thr Ala Lys Gly Arg
20 25 30

Phe Pro Pro Arg Leu Ser Ala Ala Thr Gly Ser Arg Asn Gln Ala Trp
 35 40 45

Ala Ala Pro Ser Gln Leu Ser Cys Ser Cys Pro Ala Ser Ala Leu Arg
 50 55 60

Gln Ser Tyr Val Gln Thr Gln Arg Ser Ser Gly Cys Ser
 65 70 75

<210> 2262

<211> 60

<212> PRT

<213> Homo sapiens

<400> 2262

Trp Arg Gly Ser Gly Leu Leu Pro Gln Val Gln Pro Lys Glu Asp Ser
 5 10 15

Arg Gln Gly Cys Pro Gln Leu Pro Glu Ala Gly Thr Lys Leu Gly Leu
 20 25 30

Leu His Pro Ser Tyr Pro Val Leu Ala Pro Gln Ala Leu Ser Gly Arg
 35 40 45

Ala Met Cys Arg Pro Lys Gly Ala Leu Gly Ala Ala
 50 55 60

<210> 2263

<211> 60

<212> PRT

<213> Homo sapiens

<400> 2263

Ser His Arg Leu Leu Gly Cys Cys Glu Pro Arg Ala Leu Leu Ser Ser
 5 10 15

Gln Leu Ala Arg Arg Ala Glu Gln Pro Phe Gly Pro Ser His Pro Arg
 20 25 30

Ser Leu His Arg Ser Phe Leu Asn Leu Arg Asp Pro Phe Pro Ala Leu
 35 40 45

Leu Lys Phe Pro Val Pro Thr Leu Gly Leu Ser Pro
 50 55 60

<210> 2264

<211> 55

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(55)

<223> Xaa = Any amino acid

<400> 2264

Gly Ile Arg Ser Gln Leu Ser Leu Asn Ser Gln Ser Pro Pro Trp Ala
 5 10 15

Ser Leu Pro Asn Asp Leu Val Ala Leu Gly Ala Pro Glu Xaa Asn Pro

20 25 30
 Glu Ile Leu Pro Pro Ser Thr Leu Gly Ser Asp Leu Cys Pro Ser Leu
 35 40 45

Cys His Lys Glu Ile Ser Val
 50 55

<210> 2265
 <211> 77
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(77)
 <223> Xaa = Any amino acid

<400> 2265
 Gly Glu Arg Pro Arg Val Gly Thr Gly Asn Leu Arg Arg Ala Gly Asn
 5 10 15

Gly Ser Leu Arg Phe Arg Lys Leu Leu Cys Lys Leu Arg Gly Trp Leu
 20 25 30

Gly Pro Lys Gly Cys Ser Ala Arg Arg Ala Ser Cys Glu Leu Ser Lys
 35 40 45

Ala Leu Gly Ser Gln His Pro Lys Ser Leu Trp Leu Gln Ser Cys Val
 50 55 60

Cys Xaa Thr His Ser Lys Gly Ser Phe Cys Phe Val Phe
 65 70 75

<210> 2266
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 2266
 Thr Leu Pro Pro Asp Arg Met Lys Phe Ile Ser Thr Ser Leu Leu Leu
 5 10 15

Met Leu Leu Val Ser Ser Leu Ser Pro Val Gln Gly Val Leu Glu Val
 20 25 30

Tyr Tyr Thr Ser Leu Arg Cys Arg Cys Val Gln Glu Ser Ser Val Phe
 35 40 45

Ile Pro Arg Arg Phe Ile Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn
 50 55 60

Gly Cys Pro Arg Lys Glu Ile Ile Val Trp Lys Lys Asn Lys Ser Ile
 65 70 75 80

Val Cys Val Asp Pro Gln Ala Glu Trp Ile Gln Arg Met Met Glu Val
 85 90 95

Leu Arg Lys Arg Ser Ser Ser Thr Leu Pro Val Pro Val Phe Lys Arg
 100 105 110

Lys Ile Pro
115

<210> 2267
<211> 55
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(55)
<223> Xaa = Any amino acid

<400> 2267
Glu Lys Glu Val Leu Gln Leu Tyr Gln Phe Gln Cys Leu Arg Glu Arg
5 10 15

Phe Pro Asp Ala Asp Ile Ser Thr Lys Asn Thr Cys Ile Leu Pro Leu
20 25 30

Ser Leu Leu Trp Ile Leu Val Leu Cys Leu Val Lys Ser Phe Pro Gly
35 40 45

Lys Arg Xaa Ser Pro Tyr Lys
50 55

<210> 2268
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(51)
<223> Xaa = Any amino acid

<400> 2268
Ser His Ala Tyr Leu Tyr Gly Glu Xaa Leu Phe Pro Gly Lys Asp Leu
5 10 15

Thr Lys His Lys Thr Lys Ile Gln Ser Arg Asp Lys Gly Arg Met Gln
20 25 30

Val Phe Leu Val Glu Ile Ser Ala Ser Gly Asn Leu Ser Leu Lys His
35 40 45

Trp Asn Trp
50

<210> 2269
<211> 101
<212> PRT
<213> Homo sapiens

<400> 2269
Ser His Leu Leu Glu Gly Gly Gln Arg Gly Gln Asp Gly Ala Ala Asp
5 10 15

Pro His Gly Val Leu Ala Leu Arg Arg Ser Asn Asp Leu Asp Leu His
20 25 30

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<400> 2271
Arg Cys Pro Glu Ala Leu Phe Gln Pro Ser Phe Leu Gly Met Glu Ser
          5                      10                      15

Cys Gly Ile His Glu Thr Thr Phe Asn Ser Ile Met Lys Cys Asp Val
          20                      25                      30

Asp Ile Arg Lys Asp Leu Tyr Ala Asn Thr Val Leu Ser Gly Gly Thr
          35                      40                      45

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Thr Met Tyr Pro Gly Ile Ala Asp Arg Met Gln Lys Glu Ile Thr Ala
50 55 60
Leu Ala Pro Ser Thr Met Lys Ile Lys Ile Ile Ala Pro Pro Glu Arg
65 70 75 80
Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser Leu Ser Thr
85 90 95
Phe Gln Gln Met
100

<210> 2272
<211> 54
<212> PRT
<213> Homo sapiens

<400> 2272
Arg Arg Thr Ser Gln Thr Asp Gly Thr Gln Ala Gly Trp Val Leu Tyr
5 10 15
Pro Arg Ser Gln Glu Gly Arg Val Ser Cys Thr Val Val Asn Arg Arg
20 25 30
Ala Ala Trp Arg Gln Trp Leu Ser Gln Lys Val Thr Gln Ser Ser Cys
35 40 45
Leu Glu Arg Glu Ser Leu
50

<210> 2273
<211> 72
<212> PRT
<213> Homo sapiens

<400> 2273
Leu Arg Ile Gln Arg Cys Trp Gly Glu Lys Ser Ser Ile Asp Ser Thr
5 10 15
Phe Gln Asp Val His Phe Gly Glu Arg Ser Arg Trp Asp Pro Gln Glu
20 25 30
Asn Asp Gly Glu His Pro Arg Gln Met Gly Leu Lys Gln Asp Gly Cys
35 40 45
Tyr Ile Gln Glu Ala Lys Lys Gly Glu Phe Arg Ala Leu Trp Leu Thr
50 55 60
Gly Gly Leu Pro Gly Gly Ser Gly
65 70

<210> 2274
<211> 55
<212> PRT
<213> Homo sapiens

<400> 2274
Val Pro Ser Val Trp Asp Val Leu Arg His Phe Leu Glu Gly Pro Thr
5 10 15

Cys Ser Ser Pro Arg Asn Gly His Pro Gly Arg Trp Ser Leu Tyr Cys
 20 25 30

Phe Ser Leu Pro Ser Asn Val Glu Ser Gly Val Ser Leu Gly Ser Ala
 35 40 45

Asn Asn Gly Cys His Leu Gln
 50 55

<210> 2275

<211> 74

<212> PRT

<213> Homo sapiens

<400> 2275

Pro Gln Cys Thr Lys Leu Ser Leu Leu Gly Phe Leu Asp Ile Ala Pro
 5 10 15

Ile Leu Leu Glu Ser His Leu Ser Gly Met Phe Ser Val Ile Phe Leu
 20 25 30

Arg Val Pro Pro Ala Pro Leu Pro Glu Met Asp Ile Leu Glu Gly Gly
 35 40 45

Val Tyr Thr Ala Phe Leu Ser Pro Ala Thr Leu Asn Pro Glu Ser Ala
 50 55 60

Trp Ala Pro Gln Thr Thr Ala Ala Ile Ser
 65 70

<210> 2276

<211> 69

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(69)

<223> Xaa = Any amino acid

<400> 2276

Ser Arg Trp Met Glu Gln Lys Ile Asn Leu Xaa Leu Val Arg Thr Pro
 5 10 15

Phe Trp Gly Cys Pro Leu Pro Ser Ala Lys Leu Val Pro Leu Arg Arg
 20 25 30

Gly Ser Pro Cys Thr Ala Thr Ser Leu Thr Trp Leu Ala Thr Leu Lys
 35 40 45

Ser Ser Cys Gln Ser Arg Arg Ser Met Ser Ser Met Ala Val Leu Met
 50 55 60

Leu Ala Thr Ser Trp
 65

<210> 2277

<211> 120

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(120)

<223> Xaa = Any amino acid

<400> 2277

Tyr Glu Ala Leu Glu Leu Arg Asp Asn Asp Lys Thr Arg Tyr Met Gly
 5 10 15

Lys Gly Val Ser Lys Ala Val Glu His Ile Asn Lys Thr Ile Ala Pro
 20 25 30

Ala Leu Val Ser Lys Lys Leu Asn Val Thr Glu Gln Glu Lys Ile Asp
 35 40 45

Lys Leu Met Ile Glu Met Asp Gly Thr Glu Asn Lys Ser Xaa Phe Gly
 50 55 60

Ala Asn Ala Ile Leu Gly Val Ser Leu Ala Val Cys Lys Ala Gly Ala
 65 70 75 80

Val Glu Lys Gly Val Pro Leu Tyr Arg His Ile Ala Asp Leu Ala Gly
 85 90 95

Asn Ser Glu Val Ile Leu Pro Val Pro Ala Phe Asn Val Ile Asn Gly
 100 105 110

Gly Ser His Ala Gly Asn Lys Leu
 115 120

<210> 2278

<211> 100

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(100)

<223> Xaa = Any amino acid

<400> 2278

Gln Leu Val Ala Ser Met Arg Thr Ala Ile Asp Asp Ile Glu Arg Arg
 5 10 15

Asp Trp Gln Asp Asp Phe Arg Val Ala Ser Gln Val Ser Asp Val Ala
 20 25 30

Val Gln Gly Asp Pro Leu Leu Asn Gly Thr Ser Phe Ala Asp Gly Lys
 35 40 45

Gly His Pro Gln Asn Gly Val Arg Thr Lys Xaa Arg Phe Ile Phe Cys
 50 55 60

Ser Ile His Leu Asp His Gln Phe Val Asn Leu Leu Phe Cys Asp
 65 70 75 80

Val Gln Phe Leu Ala Asn Gln Gly Arg Arg Asn Ser Phe Ile Asp Val
 85 90 95

Leu Asn Ser Leu
 100

<210> 2279
 <211> 100
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(100)
 <223> Xaa = Any amino acid

<400> 2279
 Glu Pro Pro Leu Met Thr Leu Asn Ala Gly Thr Gly Arg Met Thr Ser
 5 10 15
 Glu Leu Pro Ala Lys Ser Ala Met Trp Arg Tyr Arg Gly Thr Pro Phe
 20 25 30
 Ser Thr Ala Pro Ala Leu Gln Thr Ala Arg Asp Thr Pro Arg Met Ala
 35 40 45
 Phe Ala Pro Xaa Leu Asp Leu Phe Ser Val Pro Ser Ile Ser Ile Ile
 50 55 60
 Ser Leu Ser Ile Phe Ser Cys Ser Val Thr Phe Ser Phe Leu Leu Thr
 65 70 75 80
 Arg Ala Gly Ala Ile Val Leu Leu Met Cys Ser Thr Ala Phe Glu Thr
 85 90 95
 Pro Phe Pro Ile
 100

<210> 2280
 <211> 75
 <212> PRT
 <213> Homo sapiens

<400> 2280
 Leu Asp Asn Pro Gly Ser Gly Gly Gly Cys Lys Asn Leu Gln Lys Leu
 5 10 15
 Glu Gly Ala Pro Gln Glu Asn Lys Gln Gln Ala Leu Phe Pro Leu Ala
 20 25 30
 His Pro Pro Lys Asn His Pro Ser His Pro Ser Val Trp Trp Cys Pro
 35 40 45
 Val Val Ser Ile Phe His Ser Phe Pro Asn Tyr Gly Ser Lys Val Leu
 50 55 60
 Leu Thr Arg Ile Arg Ala Leu Gly Ile Thr Glu
 65 70 75

<210> 2281
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>

<221> variant

<222> (1)...(51)

<223> Xaa = Any amino acid

<400> 2281

Gly Pro Leu Thr Gln Lys Lys Lys Lys Lys Xaa Ser Leu Gly Val Thr
 5 10 15
 Thr Gly His Tyr Leu Pro Gln Asn Lys Glu Ser Trp Ala Glu Ala Gly
 20 25 30
 Lys Gln Leu Asp Pro Ile Trp Asp Pro Arg Leu Gly Glu Arg Val Pro
 35 40 45
 Leu Leu Lys
 50

<210> 2282

<211> 57

<212> PRT

<213> Homo sapiens

<400> 2282

Asn Asn Pro Gly Arg Arg Arg Glu Glu Gly Thr Leu Gly Thr Pro Leu
 5 10 15
 Pro Thr Ile Arg Asp Tyr Leu His Phe Ser Asn Trp Thr Ile Pro Ala
 20 25 30
 Gln Glu Glu Val Ala Arg Ile Cys Lys Ser Trp Arg Glu Arg Pro Arg
 35 40 45
 Arg Thr Asn Ser Lys Pro Tyr Phe Pro
 50 55

<210> 2283

<211> 68

<212> PRT

<213> Homo sapiens

<400> 2283

Ile Ile Gln Ala Gly Glu Glu Arg Arg Ala His Leu Glu Leu Pro Ser
 5 10 15
 Pro Gln Tyr Val Ile Ile Tyr Ile Leu Val Ile Gly Gln Ser Arg Leu
 20 25 30
 Arg Arg Arg Leu Gln Glu Ser Ala Lys Val Gly Gly Ser Ala Pro Gly
 35 40 45
 Glu Gln Thr Ala Ser Leu Ile Ser Pro Ser Pro Ser Pro Lys Lys Pro
 50 55 60
 Ser Ile Pro Ser
 65

<210> 2284

<211> 66

<212> PRT

<213> Homo sapiens

50

<210> 2287
<211> 87
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(87)
<223> Xaa = Any amino acid

<400> 2287
Pro Arg Val Pro Tyr Trp Val Lys Leu Leu Thr Cys Leu Ser Pro Gly
 5 10 15

Phe Phe Ile Leu Gly Glu Val Met Pro Cys Cys Tyr Pro Lys Ala Xaa
 20 25 30

Phe Phe Phe Phe Phe Leu Gly Glu Gly Thr Leu Leu Cys Tyr Pro Lys
 35 40 45

Cys Ser Tyr Ser Gly Glu Lys Asn Leu Thr Ser Ile Ile Trp Glu Gly
 50 55 60

Met Glu Asp Gly His His Arg Thr Pro Pro Asp Thr Arg Met Gly Trp
 65 70 75 80

Met Val Phe Trp Gly Met Gly
 85

<210> 2288
<211> 88
<212> PRT
<213> Homo sapiens

<400> 2288
Thr Ser Val Glu Pro Leu Ser Arg Gly Pro Trp Val Pro Asn Thr Lys
 5 10 15

Ile Pro Thr Ala Glu Arg Ala Ala Asp His Leu Val Arg Ile Pro Val
 20 25 30

Ala Phe Ile Ser Lys Ile Asn Ser Pro Phe Leu Arg Leu Ser Glu Ser
 35 40 45

Trp Val Tyr Ala Leu Lys Lys Ala Glu Leu Leu Asp Ser Leu Thr Ser
 50 55 60

Cys His Arg Val Leu Asn Val Ser Asp His Lys Gly Leu His Thr Phe
 65 70 75 80

Ala Val Cys Ser Gly Ala Thr Tyr
 85

<210> 2289
<211> 53
<212> PRT
<213> Homo sapiens

<400> 2289

Val Phe Leu Tyr Trp Glu Pro Lys Val Leu Cys Leu Val Ala Gln Arg
 5 10 15

Leu Ser Thr Phe Pro Arg Leu Asn Ala Cys Gly Ala Leu Ser Thr Ser
 20 25 30

Thr Cys Ser Gln Gly Pro Pro Ser Leu Ser Ser Asn Ala Gln Asp Arg
 35 40 45

Val Asp Leu Ile Gly
 50

<210> 2290

<211> 51

<212> PRT

<213> Homo sapiens

<400> 2290

Phe Ser Phe Phe Gln Gly Ile Asp Pro Arg Leu Arg Gln Pro Gln Glu
 5 10 15

Arg Gly Val Tyr Phe Gly Tyr Lys Gly Asn Arg Asn Pro Asp Gln Met
 20 25 30

Val Ser Ser Pro Leu Ser Ser Arg Tyr Phe Cys Ile Gly Asn Pro Arg
 35 40 45

Ser Ser Ala
 50

<210> 2291

<211> 81

<212> PRT

<213> Homo sapiens

<400> 2291

Thr Gln Asp Ser Asp Asn Leu Lys Lys Gly Glu Phe Ile Leu Asp Ile
 5 10 15

Lys Ala Thr Gly Ile Leu Thr Lys Trp Ser Ala Ala Leu Ser Ala Val
 20 25 30

Gly Ile Phe Val Leu Gly Thr Gln Gly Pro Leu Leu Ser Gly Ser Thr
 35 40 45

Leu Val Tyr Leu Ser Lys Ala Gln Arg Leu Trp Ser Leu Val His Lys
 50 55 60

His Leu Leu Pro Arg Ala Ser Leu Pro Glu Phe Lys Arg Pro Arg Gln
 65 70 75 80

Ser

<210> 2292

<211> 125

<212> PRT

<213> Homo sapiens

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<400> 2292
Arg Tyr Gln Trp Val Arg Cys Asn Pro Asp Ser Asn Ser Ala Asn Cys
          5                      10                      15

Leu Glu Glu Lys Gly Pro Met Phe Glu Leu Leu Pro Gly Glu Ser Asn
          20                      25                      30

Lys Ile Pro Arg Leu Arg Thr Asp Leu Phe Pro Lys Thr Arg Ile Gln
          35                      40                      45

Asp Leu Asn Arg Ile Phe Pro Leu Ser Glu Asp Tyr Ser Gly Ser Gly
          50                      55                      60

Phe Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Phe Leu
          65                      70                      75                      80

Thr Glu Met Glu Gln Asp Tyr Gln Leu Val Asp Glu Ser Asp Ala Phe
          85                      90                      95

His Asp Asn Leu Arg Ser Leu Asp Arg Asn Leu Pro Ser Asp Ser Gln
          100                     105                     110

Asp Leu Gly Gln His Gly Leu Glu Glu Asp Phe Met Leu
          115                     120                     125

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<210> 2293
<211> 59
<212> PRT
<213> Homo sapiens
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<400> 2293
Ser Ser Glu Ser Gly Lys Ile Arg Phe Lys Ser Trp Ile Leu Val Phe
              5              10              15

Gly Lys Arg Ser Val Leu Arg Arg Gly Ile Leu Leu Asp Ser Pro Gly
      20      25      30

Ser Ser Ser Asn Ile Gly Pro Phe Ser Ser Arg Gln Phe Ala Glu Leu
      35      40      45

Leu Ser Gly Leu Gln Arg Thr His Trp Tyr Leu
      50      55

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<210> 2294
<211> 100
<212> PRT
<213> Homo sapiens
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<400> 2294
Gly Cys His Gly Lys His His Phe Arg Leu Leu Val Gly Asn Pro Val
      5                      10                      15

Pro Phe Pro Leu Gly Ser His Ser Gln Ile Leu Ile Gln Ser Arg Ser
      20                      25                      30

Arg Ser Arg Ser Leu Ile Gln Ser Ser Pro Gln Lys Val Gly Arg Tyr
      35                      40                      45

Asp Ser Ser Pro Gly Phe Ser Ser Leu Glu Lys Gly Gln Ser Ser Asp
      50                      55                      60

```


Gly Gly Ser Cys Trp Ile His Leu Glu Val Val Arg Thr Leu Val Leu
 65 70 75 80

Phe Leu Gln Gly Ser Leu Gln Asn Tyr Cys Leu Asp Cys Ser Ala Pro
 85 90 95

Ile Gly Thr Trp
 100

<210> 2295
 <211> 50
 <212> PRT
 <213> Homo sapiens

<400> 2295
 Ser Trp Glu Pro Gly Gln Val Ser Val Gly Thr Ser Leu Ser Arg Trp
 5 10 15

Gln His Ser Asp Trp Pro Cys Arg Arg Gly Trp Leu Ser Pro Leu Glu
 20 25 30

Thr Lys Thr Gly Trp Leu Glu Thr Val Thr Thr Gln Val Leu Arg Trp
 35 40 45

Ser Leu
 50

<210> 2296
 <211> 131
 <212> PRT
 <213> Homo sapiens

<400> 2296
 Pro Asp Ser Thr Gly Glu Leu Val Leu Ser Gln Ser Pro Ala Thr Leu
 5 10 15

Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln
 20 25 30

Ser Val Ala Thr Tyr Leu Gly Trp Ser Gln Gln Lys Pro Gly Gln Ala
 35 40 45

Pro Arg Ile Ile Ile Tyr Asp Thr Ser Tyr Arg Ala Ala Gly Ile Pro
 50 55 60

Ala Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Val
 65 70 75 80

Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys His Gly Arg
 85 90 95

Ala Lys Trp Pro Pro Ser Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
 100 105 110

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
 115 120 125

Asp Glu Gln
 130

<210> 2297
 <211> 53
 <212> PRT
 <213> Homo sapiens

<400> 2297
 Arg Leu His Arg Arg Thr Cys Val Val Thr Val Ser Ser His Pro Val
 5 10 15
 Phe Val Ser Arg Gly Glu Ser His Pro Leu Leu Gln Gly Gln Ser Glu
 20 25 30
 Cys Cys His Leu Leu Arg Leu Val Pro Thr Glu Thr Trp Pro Gly Ser
 35 40 45
 Gln Asp His His Leu
 50

<210> 2298
 <211> 78
 <212> PRT
 <213> Homo sapiens

<400> 2298
 Cys Pro Arg Trp Gly Thr Pro Arg Tyr Trp Leu Gly Ala Leu Tyr Arg
 5 10 15
 Asn Gln Gln Ser Ser Pro Thr Ala Pro Pro Gly Leu Leu Pro Leu Glu
 20 25 30
 Tyr Phe Pro Ala Ala Pro His Cys Ser His Ser Arg Gln Trp Arg Cys
 35 40 45
 Ser Gln Thr His Arg Ile His His His Pro Gln Met Leu Gly Pro Cys
 50 55 60
 Arg Gln Glu Ile Cys Gly Glu Ile Gln Gly Cys Gly Trp Phe
 65 70 75

<210> 2299
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 2299
 Asn Leu Leu Ile Glu Pro Gln Gln Gly Ala Asp Asn Cys Asp Val Asn
 5 10 15
 Gln Cys His Ser Phe Ala His Gln Lys Ser Pro Arg Leu Gln Val Ser
 20 25 30
 Ile Gln Gln Pro Gln Asn Ser Pro His Phe Leu Leu Cys Ile Leu Ser
 35 40 45
 Gly Leu Phe Val Val Val His Asp Ala Gln Gly Gly Glu His Pro Gly
 50 55 60
 Thr Gly Trp Gly His Tyr Ile Gly Ile Ser Lys Ala His Pro Leu His
 65 70 75 80
 His Leu Gly Cys Cys Leu Trp Ser Thr Ser Pro Gln Leu Leu Ile Ala

85 90 95
 His Ile Val Gly Asn Gly Val Ala Leu Lys His Thr Glu Ser Ile Ile
 100 105 110
 Thr Leu Lys Cys Trp Asp Leu Ala Gly Arg Lys Phe Ala Glu Lys Phe
 115 120 125
 Arg Gly Ala Val Gly Leu
 130

<210> 2300
 <211> 66
 <212> PRT
 <213> Homo sapiens

<400> 2300
 Ala Ser Ser Ser Pro Arg Ile Arg Leu Thr Ser Ser Phe Ala Phe Ser
 5 10 15
 Val Ala Cys Leu Leu Trp Cys Met Met Pro Lys Val Gly Asn Thr Gln
 20 25 30
 Val Leu Ala Gly Gly Thr Ile Ser Glu Ser Ala Lys Leu Thr His Cys
 35 40 45
 Thr Thr Trp Ala Ala Ala Ser Gly Val Leu Pro Arg Ser Ser Ser Leu
 50 55 60
 Leu Thr
 65

<210> 2301
 <211> 141
 <212> PRT
 <213> Homo sapiens

<400> 2301
 Gln Thr Asn Arg Thr Pro Glu Phe Leu Arg Lys Phe Pro Ala Gly Lys
 5 10 15
 Val Pro Ala Phe Glu Gly Asp Asp Gly Phe Cys Val Phe Glu Ser Asn
 20 25 30
 Ala Ile Ala Tyr Tyr Val Ser Asn Glu Glu Leu Arg Gly Ser Thr Pro
 35 40 45
 Glu Ala Ala Ala Gln Val Val Gln Trp Val Ser Phe Ala Asp Ser Asp
 50 55 60
 Ile Val Pro Pro Ala Ser Thr Trp Val Phe Pro Thr Leu Gly Ile Met
 65 70 75 80
 His His Asn Lys Gln Ala Thr Glu Asn Ala Lys Glu Glu Val Arg Arg
 85 90 95
 Ile Leu Gly Leu Leu Asp Ala Tyr Leu Lys Thr Arg Thr Phe Leu Val
 100 105 110
 Gly Glu Arg Val Thr Leu Val Asp Ile Thr Val Val Cys Thr Leu Leu
 115 120 125

Trp Leu Tyr Lys Gln Val Leu Glu Pro Ser Phe His Gln
 130 135 140

<210> 2302
 <211> 50
 <212> PRT
 <213> Homo sapiens

<400> 2302
 Leu Arg Glu Gly Ser Gly Trp Val Arg Gly Asp Gly Glu Gly Lys Gly
 5 10 15

Gly Val Ser Ile Phe Ile Leu Arg Ile Gly Val Gln Ser Thr Ser Gly
 20 25 30

Val Ser Ala Pro Pro Cys Pro Pro Val Gly Leu Arg Arg Thr Gly Lys
 35 40 45

Arg Thr
 50

<210> 2303
 <211> 50
 <212> PRT
 <213> Homo sapiens

<400> 2303
 Arg Ala Leu Thr Glu Ser Ser Arg Asn Ser Gly Thr Val Ser Arg Gly
 5 10 15

Pro Ala Leu His Gly Pro Gly Pro Pro Pro Ser Pro Ser Pro Arg Pro
 20 25 30

Glu Pro Arg Ala Thr Arg Pro Ala Ala Ala Ala Ala Trp Pro Gly Thr
 35 40 45

Ile Ser
 50

<210> 2304
 <211> 75
 <212> PRT
 <213> Homo sapiens

<400> 2304
 Gln Arg Ala Ala Glu Thr Leu Glu Leu Phe Pro Glu Gly Leu His Cys
 5 10 15

Met Asp Gln Gly His His Leu Leu Leu His Pro Gly Gln Asn Pro Val
 20 25 30

Pro Pro Gly Leu Gln Pro Leu Gln His Gly Leu Glu Pro Ser His Asp
 35 40 45

Leu Val Thr Lys Ala Leu Pro Arg Leu Leu Gly Cys Gly Ile Leu Asn
 50 55 60

Ile Arg Asp Arg Gly Ser Val Ala Ser Ala Pro
 65 70 75

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<210> 2305
<211> 60
<212> PRT
<213> Homo sapiens
```

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<400> 2305
Arg Ser Glu Leu Trp Val Leu Leu Leu Ile Ile Ser Arg His Cys Leu
          5                      10                      15

Gln Val Ala Leu Phe Glu Val Val Leu Gln Leu Cys Gln Ala Arg His
          20                      25                      30

His His Ser Gly Leu Gln Leu Phe His Val Ile Arg Glu Asp Leu Arg
          35                      40                      45

Glu Ala His Gly Gly Gln Lys Phe Lys Glu Pro Arg
          50                      55                      60

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<210> 2306
<211> 103
<212> PRT
<213> Homo sapiens
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<400> 2306
Asp Trp Lys Glu Asp Met Lys Ser Ser Asp Arg Glu Gln Gln Lys Leu
          5                                10                    15

Trp Asn Cys Phe Gln Arg Ala Cys Thr Ala Trp Thr Arg Ala Thr Thr
          20                                25                    30

Phe Ser Phe Thr Gln Ala Arg Thr Pro Cys His Gln Ala Cys Ser Arg
          35                                40                    45

Cys Ser Met Ala Trp Asn His Leu Met Thr Leu Ser Gln Lys Leu Ser
          50                                55                    60

Pro Gly Ser Ser Val Ala Gly Ser Ser Thr Ser Gly Thr Gly Asp Leu
        65                                70                    75                        80

Leu Pro Arg His Arg Asn Pro Ser Leu Ser Phe Ser Ser Arg Gly Val
          85                                90                    95

Ser Ser Gly Cys Cys Ser Ser
          100
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<210> 2307
<211> 177
<212> PRT
<213> Homo sapiens
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<400> 2307
Pro Trp Leu Leu Glu Leu Leu Ala Ala Met Cys Phe Pro Lys Val Leu
          5                      10                      15

Ser Asp Asp Met Lys Lys Leu Lys Ala Arg Met Val Met Ser Ser Leu
          20                      25                      30

Ala Glu Leu Glu Asp Asp Phe Lys Glu Gly Tyr Leu Glu Thr Val Ala
          35                      40                      45

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Ala Tyr Tyr Glu Glu Gln His Pro Glu Leu Thr Pro Leu Leu Glu Lys
 50 55 60

Glu Arg Asp Gly Leu Arg Cys Arg Gly Asn Arg Ser Pro Val Pro Asp
 65 70 75 80

Val Glu Asp Pro Ala Thr Glu Glu Pro Gly Glu Ser Phe Cys Asp Lys
 85 90 95

Val Met Arg Trp Phe Gln Ala Met Leu Gln Arg Leu Gln Ala Trp Trp
 100 105 110

His Gly Val Leu Ala Trp Val Lys Glu Lys Val Val Ala Leu Val His
 115 120 125

Ala Val Gln Ala Leu Trp Lys Gln Phe Gln Ser Phe Cys Cys Ser Leu
 130 135 140

Ser Glu Leu Phe Met Ser Ser Phe Gln Ser Tyr Gly Ala Pro Arg Gly
 145 150 155 160

Asp Lys Glu Glu Leu Thr Pro Gln Lys Cys Ser Glu Pro Gln Ser Ser
 165 170 175

Lys

<210> 2308
 <211> 69
 <212> PRT
 <213> Homo sapiens

<400> 2308
 Cys Arg Ala Trp Gln Ser Trp Arg Thr Thr Ser Lys Arg Ala Thr Trp
 5 10 15

Arg Gln Trp Arg Leu Ile Met Arg Ser Ser Thr Gln Ser Ser Leu Leu
 20 25 30

Tyr Leu Lys Lys Lys Glu Met Asp Tyr Gly Ala Glu Ala Thr Asp Pro
 35 40 45

Leu Ser Arg Met Leu Arg Ile Pro Gln Pro Arg Ser Leu Gly Arg Ala
 50 55 60

Phe Val Thr Arg Ser
 65

<210> 2309
 <211> 76
 <212> PRT
 <213> Homo sapiens

<400> 2309
 Gln Gly His Glu Met Val Pro Gly His Ala Ala Ala Ala Ala Gly Leu
 5 10 15

Val Ala Arg Gly Ser Gly Leu Gly Glu Gly Glu Gly Gly Gly Pro Gly
 20 25 30

Pro Cys Ser Ala Gly Pro Leu Glu Thr Val Pro Glu Phe Leu Leu Leu
 35 40 45

Ser Val Arg Ala Leu His Val Leu Phe Pro Val Leu Arg Ser Pro Thr
 50 55 60

Gly Gly Gln Gly Gly Ala Asp Thr Pro Glu Val Leu
 65 70 75

<210> 2310
 <211> 50
 <212> PRT
 <213> Homo sapiens

<400> 2310
 Asp Arg Tyr Trp Tyr Ser Phe Ile Ile Glu Thr Lys Arg Ser Ala Leu
 5 10 15

Leu Asp Phe Pro Leu Phe Val Leu Lys Gly Ile Lys Asp Cys Arg Phe
 20 25 30

Pro Ala Leu Ser Ser Arg Gly His Tyr Glu Gln Ile Lys Trp Lys Asp
 35 40 45

Lys Phe
 50

<210> 2311
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 2311
 Trp Pro Arg Glu Asp Arg Ala Gly Asn Leu Gln Ser Leu Ile Pro Phe
 5 10 15

Arg Thr Lys Ser Gly Lys Ser Ser Lys Ala Asp Leu Leu Val Ser Ile
 20 25 30

Ile Lys Glu Tyr Gln Tyr Arg Ser Gln Lys Arg Ser Val Ser Leu Gln
 35 40 45

Gly Tyr Phe
 50

<210> 2312
 <211> 63
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(63)
 <223> Xaa = Any amino acid

<400> 2312
 Gly Gly Lys Met Ala Val Gln Ile Ser Lys Lys Arg Lys Phe Val Ala
 5 10 15

Asp Gly Ile Phe Lys Ala Glu Leu Asn Glu Phe Leu Thr Arg Glu Leu

833

20	25	30
Ala Glu Asp Gly Tyr Ser Gly Val Glu Gly Ala Ser Tyr Thr Asn Gln		
35	40	45

Asp Arg Asn His Tyr Leu Xaa His Gln Asn Thr Xaa Cys Ser Trp
50 55 60

<210> 2313
 <211> 70
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(70)
 <223> Xaa = Any amino acid

<400> 2313
Met Ser Phe Leu Leu Gly Ser Trp Leu Lys Met Ala Thr Leu Glu Leu
5 10 15

Arg Val Arg Val Thr Pro Thr Arg Thr Glu Ile Ile Ile Leu Xaa Thr
20 25 30

Arg Thr Xaa Asn Val Leu Gly Glu Lys Gly Arg Arg Ile Arg Glu Leu
35 40 45

Thr Ala Val Val Gln Lys Arg Phe Gly Phe Pro Glu Gly Ser Val Glu
50 55 60

Leu Tyr Ala Xaa Lys Val
65 70

<210> 2314
 <211> 76
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(76)
 <223> Xaa = Any amino acid

<400> 2314
Thr Thr Ala Val Ser Ser Arg Ile Arg Arg Pro Phe Ser Pro Arg Thr
5 10 15

Xaa Cys Val Leu Val Xaa Lys Ile Met Ile Ser Val Leu Val Gly Val
20 25 30

Thr Arg Thr Leu Asn Ser Arg Val Ala Ile Phe Ser Gln Leu Pro Ser
35 40 45

Lys Lys Leu Ile Gln Phe Ser Phe Glu Asp Ala Ile Ser Asp Lys Leu
50 55 60

Pro Leu Leu Gly Tyr Leu His Cys His Leu Ala Ala
65 70 75

<210> 2315
<211> 67
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(67)
<223> Xaa = Any amino acid

<400> 2315
Glu Xaa Ser Ser Gln Pro Thr Val Pro Ile Val Gly Ile Ile Ala Gly
 5 10 15
Leu Val Leu Leu Gly Ala Val Ile Thr Gly Ala Val Val Ala Ala Val
 20 25 30
Met Trp Arg Arg Asn Ser Ser Asp Arg Lys Gly Gly Ser Tyr Ser Gln
 35 40 45
Ala Ala Ser Ser Asp Ser Ala Gln Gly Ser Asp Val Ser Leu Thr Ala
 50 55 60
Cys Lys Val
 65

<210> 2316
<211> 62
<212> PRT
<213> Homo sapiens

<400> 2316
Val Ala Val Ser Ser Leu Arg His Gly Val Cys Ser Pro Thr Asp Ile
 5 10 15
Gly Val Leu Arg Lys Gly Gly Val Ile Trp Gln Lys Cys His Phe Ala
 20 25 30
Cys Cys Ile Gln Gly Ser Tyr Ser Thr Arg Tyr Cys Glu Leu Cys Ser
 35 40 45
His Gln Leu Ala Gln Lys Gln Gln Thr Ala Leu Cys Cys Gln
 50 55 60

<210> 2317
<211> 94
<212> PRT
<213> Homo sapiens

<400> 2317
Trp Leu Ser Pro Leu Ser Ala Met Ala Cys Ala Arg Pro Leu Ile Ser
 5 10 15
Val Tyr Ser Glu Lys Gly Glu Ser Ser Gly Lys Asn Val Thr Leu Pro
 20 25 30
Ala Val Phe Lys Ala Pro Ile Arg Pro Asp Ile Val Asn Phe Val His
 35 40 45
Thr Asn Leu Arg Lys Asn Asn Arg Gln Pro Tyr Ala Val Ser Glu Leu
 50 55 60

Ala Gly His Gln Thr Ser Ala Glu Ser Trp Gly Thr Gly Arg Ala Val
 65 70 75 80

Ala Arg Ile Pro Arg Val Arg Gly Gly Gly Thr His Arg Ser
 85 90

<210> 2318
 <211> 76
 <212> PRT
 <213> Homo sapiens

<400> 2318
 Thr Lys Leu Val Met Met Gln Lys Leu Leu Lys Cys Ser Arg Leu Val
 5 10 15

Leu Ala Leu Ala Leu Ile Leu Val Leu Glu Ser Ser Val Gln Gly Tyr
 20 25 30

Pro Thr Gln Arg Ala Arg Tyr Gln Trp Val Arg Cys Asn Pro Asp Ser
 35 40 45

Asn Ser Ala Asn Cys Leu Glu Glu Lys Gly Pro Met Phe Glu Leu Leu
 50 55 60

Pro Gly Glu Ser Asn Lys Ile Pro Arg Leu Arg Thr
 65 70 75

<210> 2319
 <211> 68
 <212> PRT
 <213> Homo sapiens

<400> 2319
 Cys Arg Ser Tyr Ser Asn Ala Val Gly Leu Ser Trp Leu Leu Pro Ser
 5 10 15

Ser Trp Phe Trp Asn Pro Gln Phe Lys Val Ile Leu Arg Arg Glu Pro
 20 25 30

Gly Thr Asn Gly Cys Ala Ala Ile Gln Thr Val Ile Leu Gln Thr Ala
 35 40 45

Leu Lys Lys Lys Asp Gln Cys Ser Asn Tyr Phe Gln Val Asn Pro Thr
 50 55 60

Arg Ser Pro Val
 65

<210> 2320
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 2320
 Glu Ser Asn Lys Ile Pro Arg Leu Arg Thr Asp Leu Phe Pro Lys Thr
 5 10 15

Arg Ile Gln Asp Leu Asn Arg Ile Phe Pro Leu Ser Glu Asp Tyr Ser
 20 25 30

Gly Ser Gly Phe Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
35 40 45

Gly Phe Leu Thr Glu Met Asp Lys Asp Ser Asn
50 55

<210> 2321
<211> 68
<212> PRT
<213> Homo sapiens

<400> 2321
Ser Trp Lys Ala Ser Leu Ser Ser Thr Ser Trp Asn Pro Cys Pro Phe
5 10 15

Pro Leu Gly Ser His Ser Gln Ile Leu Ile Gln Ser Arg Ser Arg Ser
20 25 30

Arg Ser Leu Ile Gln Ser Ser Pro Gln Lys Val Gly Arg Tyr Asp Ser
35 40 45

Ser Pro Gly Phe Ser Ser Leu Glu Lys Gly Gln Ser Ser Asp Gly Gly
50 55 60

Ser Cys Trp Ile
65

<210> 2322
<211> 58
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(58)
<223> Xaa = Any amino acid

<400> 2322
Ser Ala Thr Tyr Gly Xaa Gln Ala Gly Val Val Pro Trp Leu Ser Pro
5 10 15

Xaa Thr Ser Glu Arg Pro Thr Leu Ser Ser Ser Pro Xaa Ile Asn Pro
20 25 30

Glu Thr Gln Ala Ala Leu Ile Arg Gly Gln Asp Ser Thr Ile Ala Ala
35 40 45

Ser Glu Gln Gln Val Ala Xaa Xaa Asn Ser
50 55

<210> 2323
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(60)
<223> Xaa = Any amino acid

<400> 2323

Gln His Gln Asn Ser Lys Trp Xaa Xaa Arg Ile Leu Asp Ser Xaa Asp
 5 10 15

Xaa Ala Thr Val Asn Pro Val Glu Phe Asn Thr Glu Val Ala Thr Pro
 20 25 30

Pro Phe Ser Leu Leu Xaa Thr Ser Asn Glu Thr Xaa Phe Leu Ile Gly
 35 40 45

Ile Asn Glu Glu Xaa Leu Glu Gly Xaa Ala Ile Tyr
 50 55 60

<210> 2324

<211> 67

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(67)

<223> Xaa = Any amino acid

<400> 2324

Ile Asp Cys Xaa Ala Phe Gln Xaa Leu Phe Ile Asn Ala Asn Gln Glu
 5 10 15

Xaa Cys Phe Ile Arg Ser Xaa Gln Lys Gly Lys Trp Trp Cys Cys Asn
 20 25 30

Leu Ser Ile Lys Phe His Arg Val Tyr Cys Cys Xaa Ile Xaa Gly Ile
 35 40 45

Lys Asn Ser Xaa Xaa Pro Leu Ala Val Leu Met Leu Leu Ser Trp Asn
 50 55 60

Pro Ala Leu
 65

<210> 2325

<211> 158

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(158)

<223> Xaa = Any amino acid

<400> 2325

Met Met Gln Lys Leu Leu Lys Cys Ser Arg Val Val Leu Ala Leu Ala
 5 10 15

Leu Ile Leu Val Leu Glu Ser Ser Val Gln Gly Tyr Pro Thr Gln Arg
 20 25 30

Ala Arg Tyr Gln Trp Val Arg Cys Asn Pro Asp Ser Asn Ser Ala Asn
 35 40 45

Cys Leu Glu Glu Lys Gly Pro Met Phe Xaa Leu Leu Pro Gly Glu Ser

50 55 60
 Asn Lys Ile Pro Arg Leu Arg Thr Asp Leu Phe Pro Lys Thr Arg Ile
 65 70 75 80
 Gln Asp Leu Asn Arg Ile Phe Xaa Leu Ser Glu Asp Tyr Ser Gly Ser
 85 90 95
 Gly Phe Gly Ser Gly Ser Xaa Ser Gly Ser Gly Ser Gly Ser Gly Phe
 100 105 110
 Leu Thr Glu Met Glu Gln Asp Tyr Gln Leu Val Asp Gln Ser Asp Ala
 115 120 125
 Phe His Asp Asn Leu Arg Ser Leu Asp Arg Asn Leu Pro Ser Xaa Ser
 130 135 140
 Xaa Asp Leu Gly Gln His Gly Leu Glu Glu Asp Phe Met Leu
 145 150 155

<210> 2326

<211> 68

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(68)

<223> Xaa = Any amino acid

<400> 2326

Cys Arg Ser Tyr Ser Asn Ala Val Gly Leu Ser Trp Leu Leu Pro Ser
 5 10 15
 Ser Trp Phe Trp Asn Pro Gln Phe Lys Val Ile Leu Arg Arg Glu Pro
 20 25 30
 Gly Thr Asn Gly Cys Ala Ala Ile Gln Thr Val Ile Leu Gln Thr Ala
 35 40 45
 Leu Lys Lys Lys Asp Gln Cys Xaa Asn Tyr Phe Gln Val Asn Pro Thr
 50 55 60
 Arg Ser Pro Val
 65

<210> 2327

<211> 64

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(64)

<223> Xaa = Any amino acid

<400> 2327

Ser Ser Glu Xaa Gly Lys Ile Arg Phe Lys Ser Trp Ile Leu Val Phe
 5 10 15
 Gly Lys Arg Ser Val Leu Arg Arg Gly Ile Leu Leu Asp Ser Pro Gly

20 25 30
 Ser Ser Xaa Asn Ile Gly Pro Phe Ser Ser Arg Gln Phe Ala Glu Leu
 35 40 45
 Leu Ser Gly Leu Gln Arg Thr His Trp Tyr Leu Ala Leu Cys Val Gly
 50 55 60

<210> 2328
 <211> 103
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(103)
 <223> Xaa = Any amino acid

<400> 2328
 Gly Cys His Gly Lys His His Phe Gly Leu Leu Val Gly Asn Pro Val
 5 10 15
 Pro Phe Pro Leu Gly Ser His Ser Gln Ile Leu Ile Gln Xaa Arg Ser
 20 25 30
 Arg Ser Arg Ser Leu Ile Gln Ser Ser Pro Gln Lys Xaa Gly Arg Tyr
 35 40 45
 Asp Ser Ser Pro Gly Phe Trp Ser Leu Glu Lys Gly Gln Ser Ser Asp
 50 55 60
 Gly Gly Ser Cys Trp Ile His Leu Glu Val Val Xaa Thr Leu Val Leu
 65 70 75 80
 Phe Leu Gln Gly Ser Leu Gln Asn Tyr Cys Leu Asp Cys Ser Ala Pro
 85 90 95
 Ile Gly Thr Trp Leu Ser Ala
 100

<210> 2329
 <211> 123
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(123)
 <223> Xaa = Any amino acid

<400> 2329
 Val Met Met Gln Lys Leu Leu Lys Cys Ser Arg Leu Val Leu Ala Leu
 5 10 15
 Ala Leu Ile Leu Val Leu Glu Ser Ser Val Gln Gly Tyr Pro Thr Gln
 20 25 30
 Arg Ala Arg Tyr Gln Trp Val Arg Cys Asn Pro Asp Ser Asn Ser Ala
 35 40 45
 Asn Cys Leu Glu Glu Lys Gly Pro Met Phe Glu Leu Leu Pro Gly Glu

50 55 60
 Ser Asn Lys Ile Pro Arg Leu Arg Thr Asp Leu Phe Pro Lys Thr Arg
 65 70 75 80
 Ile Gln Asp Leu Asn Arg Ile Phe Xaa Leu Ser Glu Asp Tyr Ser Gly
 85 90 95
 Ser Gly Phe Gly Ser Arg Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
 100 105 110
 Phe Leu Thr Glu Met Glu Xaa Gly Leu Pro Asn
 115 120

<210> 2330
 <211> 68
 <212> PRT
 <213> Homo sapiens

<400> 2330
 Cys Arg Ser Tyr Ser Asn Ala Val Gly Leu Ser Trp Leu Leu Pro Ser
 5 10 15
 Ser Trp Phe Trp Asn Pro Gln Phe Lys Val Ile Leu Arg Arg Glu Pro
 20 25 30
 Gly Thr Asn Gly Cys Ala Ala Ile Gln Thr Val Ile Leu Gln Thr Ala
 35 40 45
 Leu Lys Lys Lys Asp Gln Cys Ser Asn Tyr Phe Gln Val Asn Pro Thr
 50 55 60
 Arg Ser Pro Val
 65

<210> 2331
 <211> 64
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(64)
 <223> Xaa = Any amino acid

<400> 2331
 Ser Ser Glu Xaa Gly Lys Ile Arg Phe Lys Ser Trp Ile Leu Val Phe
 5 10 15
 Gly Lys Arg Ser Val Leu Arg Arg Gly Ile Leu Leu Asp Ser Pro Gly
 20 25 30
 Ser Ser Ser Asn Ile Gly Pro Phe Ser Ser Arg Gln Phe Ala Glu Leu
 35 40 45
 Leu Ser Gly Leu Gln Arg Thr His Trp Tyr Leu Ala Leu Cys Val Gly
 50 55 60

<210> 2332
 <211> 104

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(104)

<223> Xaa = Any amino acid

<400> 2332

Gly Leu Ser Trp Lys Ala Ser Leu Ser Ser Thr Ser Trp Val Ile Xaa
 5 10 15

Val Pro Phe Pro Leu Gly Ser His Ser Gln Ile Leu Ile Gln Ser Arg
 20 25 30

Ser Gly Ser Arg Ser Leu Ile Gln Ser Ser Pro Gln Lys Xaa Gly Arg
 35 40 45

Tyr Asp Ser Ser Pro Gly Phe Ser Ser Leu Glu Lys Gly Gln Ser Ser
 50 55 60

Asp Gly Gly Ser Cys Trp Ile His Leu Glu Val Val Arg Thr Leu Val
 65 70 75 80

Leu Phe Leu Gln Gly Ser Leu Gln Asn Tyr Cys Leu Asp Cys Ser Ala
 85 90 95

Pro Ile Gly Thr Trp Leu Ser Ala
 100

<210> 2333

<211> 73

<212> PRT

<213> Homo sapiens

<400> 2333

Leu Ala Tyr Phe Met Tyr His Gly Tyr Thr Ile Asn Leu Gly Thr Lys
 5 10 15

Asn Phe Ile Glu Ile Phe Lys His Leu Lys Lys Lys Leu Lys Phe Tyr
 20 25 30

His Pro Phe Phe Ser His Glu Phe Leu Lys Asp Tyr Ala Leu Met Leu
 35 40 45

Leu Ser Ile Leu Leu Phe Leu Lys Ile Pro Ala Phe Phe Gly Ile Met
 50 55 60

Phe Asn Gln His His Tyr Glu Ile Asn
 65 70

<210> 2334

<211> 66

<212> PRT

<213> Homo sapiens

<400> 2334

Met Pro Arg Leu Gly Trp Leu Trp Ser Arg Ser Tyr Gly Pro Ser Ser
 5 10 15

Ser Glu Arg Gly Arg Asp Leu Lys Pro Leu Ala Gly Lys Ile Leu Thr

20 25 30
Leu Gly Val Asn Ile Ser Ser Leu Phe Thr Arg Val Leu Met Gly Leu
35 40 45
Ala Glu Leu Leu Gly Thr His Pro Tyr Cys Tyr Ser Trp Arg Gly Phe
50 55 60
Gly Tyr
65

<210> 2335
<211> 59
<212> PRT
<213> Homo sapiens

<400> 2335
Ala Leu Trp Ala Asp Leu Pro Leu Thr Tyr Tyr Ser Arg Ser Ala Val
5 10 15
Thr Ser Trp Asp Leu Pro Leu Pro Ala Ser Ile Pro Lys Ser Ser Pro
20 25 30
Ala Ile Thr Val Gly Met Ser Thr Gln Lys Leu Ser Gln Pro His Gln
35 40 45
Asp Ser Cys Glu Lys Arg Gly Tyr Val His Thr
50 55

<210> 2336
<211> 68
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(68)
<223> Xaa = Any amino acid

<400> 2336
Val Glu Asp Xaa Thr Pro Ile Pro Cys Arg Ser Ile Gly Arg Ser Lys
5 10 15
Val Ser Ser Met Gly Arg Ser Thr Pro Tyr Leu Leu Phe Gln Ile Cys
20 25 30
Ser His Phe Val Gly Ser Ala Pro Pro Cys Phe Asn Thr Gln Ile Leu
35 40 45
Ser Ser Tyr Asn Ser Arg Asp Glu Tyr Pro Lys Ala Gln Pro Ala Pro
50 55 60
Ser Gly Leu Leu
65

<210> 2337
<211> 58
<212> PRT
<213> Homo sapiens

```

<400> 2337
Ala Gln Leu Gly Ser Glu Cys Lys Lys Leu Ser Met Val Arg Glu Ala
      5                                10                                15
Cys Ala Leu Ile Gln Val Tyr Ser Thr Leu Ser Gly Asp Gln Asn Pro
      20                                25                                30
Leu Leu Ile Thr Pro Leu Gln Arg Gly Asp Trp Ala Leu Pro Leu Phe
      35                                40                                45
Asp Lys Pro Leu Thr Gln Val Leu Thr Pro
      50                                55

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<210> 2338
<211> 68
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> variant  
<222> (1)...(68)  
<223> Xaa = Any amino acid
```

```
<400> 2338  
Cys Xaa Ser Tyr Ser Asn Ala Val Gly Leu Ser Trp Leu Leu Pro Ser  
                    5                      10                      15  
  
Ser Trp Phe Trp Asn Pro Gln Phe Lys Val Ile Leu Arg Arg Glu Pro  
                20                      25                      30  
  
Gly Thr Asn Gly Cys Ala Ala Ile Gln Thr Val Ile Leu Gln Thr Ala  
            35                      40                      45  
  
Leu Lys Lys Lys Asp Gln Cys Ser Asn Tyr Phe Xaa Val Asn Pro Thr  
    50                      55                      60  
  
Arg Ser Pro Val  
    65
```

```
<210> 2339
<211> 143
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> variant  
<222> (1)...(143)  
<223> Xaa = Any amino acid
```

```

<400> 2339
Xaa Met Met Xaa Lys Leu Leu Lys Cys Ser Arg Leu Val Leu Ala Leu
      5                      10                      15

Ala Leu Ile Leu Val Leu Glu Ser Ser Val Gln Gly Tyr Pro Thr Gln
      20                      25                      30

Arg Ala Arg Tyr Gln Trp Val Arg Cys Asn Pro Asp Ser Asn Ser Ala
      35                      40                      45

Asn Cys Leu Glu Glu Lys Gly Pro Met Phe Glu Leu Leu Pro Xaa Glu
      50                      55                      60

```

Ser Asn Lys Ile Pro Arg Leu Arg Thr Asp Leu Phe Xaa Lys Thr Arg
65 70 75 80

Ile Gln Asp Leu Asn Arg Ile Phe Pro Leu Ser Glu Asp Tyr Ser Gly
85 90 95

Ser Gly Xaa Xaa Ser Gly Ser Gly Ser Gly Ser Xaa Ser Gly Ser Gly
100 105 110

Phe Leu Thr Glu Met Glu Gln Asp Tyr Gln Leu Xaa Asp Glu Ser Asp
115 120 125

Ala Phe His Asp Asn Leu Arg Ser Leu Asp Arg Asn Leu Pro Ser
130 135 140

<210> 2340
<211> 64
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(64)
<223> Xaa = Any amino acid

<400> 2340
Ser Ser Glu Ser Gly Lys Ile Arg Phe Lys Ser Trp Ile Leu Val Phe
5 10 15

Xaa Lys Arg Ser Val Leu Arg Arg Gly Ile Leu Leu Asp Ser Xaa Gly
20 25 30

Ser Ser Ser Asn Ile Gly Pro Phe Ser Ser Arg Gln Phe Ala Glu Leu
35 40 45

Leu Ser Gly Leu Gln Arg Thr His Trp Tyr Leu Ala Leu Cys Val Gly
50 55 60

<210> 2341
<211> 103
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(103)
<223> Xaa = Any amino acid

<400> 2341
Gly Cys His Gly Lys His His Phe Arg Xaa Leu Val Gly Asn Pro Val
5 10 15

Pro Phe Pro Leu Gly Ser His Ser Gln Ile Xaa Ile Gln Ser Arg Ser
20 25 30

Arg Xaa Xaa Ser Leu Ile Gln Ser Ser Pro Gln Lys Val Gly Arg Tyr
35 40 45

Asp Ser Ser Pro Gly Phe Ser Ser Leu Xaa Lys Gly Gln Ser Ser Asp
50 55 60

Gly Gly Ser Cys Trp Ile His Xaa Glu Val Val Arg Thr Leu Val Leu
65 70 75 80

Phe Leu Gln Gly Ser Leu Gln Asn Tyr Cys Leu Asp Cys Ser Ala Pro
85 90 95

Ile Gly Thr Trp Leu Ser Ala
100

<210> 2342
<211> 162
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(162)
<223> Xaa = Any amino acid

<400> 2342
Gln Met His Leu Trp Ala Gly Gly Asp Leu Gly Leu Cys Trp Asn Trp
5 10 15

Ile Ser Glu Leu Leu Leu His Leu Phe Ser Ser His Pro Gly Leu Phe
20 25 30

Arg Ala Ala Val Pro Ser Gly Ala Ser Thr Gly Ile Tyr Glu Ala Leu
35 40 45

Glu Leu Arg Asp Asn Asp Lys Thr Arg Tyr Met Gly Lys Gly Val Ser
50 55 60

Lys Ala Val Glu His Xaa Asn Lys Thr Ile Ala Pro Ala Leu Val Ser
65 70 75 80

Lys Lys Leu Asn Val Thr Glu Gln Glu Lys Ile Asp Lys Leu Met Ile
85 90 95

Glu Met Asp Gly Thr Glu Asn Lys Ser Lys Phe Gly Ala Asn Ala Ile
100 105 110

Leu Gly Val Ser Leu Ala Val Cys Lys Ala Gly Ala Val Glu Lys Gly
115 120 125

Val Pro Leu Tyr Arg His Ile Ala Asp Leu Ala Gly Asn Ser Glu Val
130 135 140

Ile Leu Pro Val Pro Ala Phe Asn Val Ile Asn Gly Xaa Ser His Ala
145 150 155 160

Gly Asn

<210> 2343
<211> 55
<212> PRT
<213> Homo sapiens

<400> 2343
Arg Lys Lys Gln Leu Pro Asn Asp Lys Cys Ile Cys Gly Arg Glu Gly

846

5 10 15
 Thr Trp Asp Cys Ala Gly Thr Gly Phe Leu Asn Cys Tyr Tyr Ile Phe
 20 25 30
 Phe Pro Leu Ile Gln Val Ser Ser Glu Leu Leu Cys Pro Val Val Leu
 35 40 45
 Gln Leu Val Ser Met Arg Pro
 50 55

<210> 2344
 <211> 66
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(66)
 <223> Xaa = Any amino acid

<400> 2344
 Ser Arg Trp Met Glu Gln Lys Ile Asn Leu Ser Leu Val Arg Thr Pro
 5 10 15
 Phe Trp Gly Cys Pro Leu Pro Ser Ala Lys Leu Val Pro Leu Arg Arg
 20 25 30
 Gly Ser Pro Cys Thr Ala Thr Ser Leu Thr Trp Leu Ala Thr Leu Lys
 35 40 45
 Ser Ser Cys Gln Ser Arg Arg Ser Met Ser Ser Met Ala Xaa Leu Met
 50 55 60
 Leu Ala
 65

<210> 2345
 <211> 98
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(98)
 <223> Xaa = Any amino acid

<400> 2345
 Val Ala Ser Met Arg Xaa Ala Ile Asp Asp Ile Glu Arg Arg Asp Trp
 5 10 15
 Gln Asp Asp Phe Arg Val Ala Ser Gln Val Ser Asp Val Ala Val Gln
 20 25 30
 Gly Asp Pro Leu Leu Asn Gly Thr Ser Phe Ala Asp Gly Lys Gly His
 35 40 45
 Pro Gln Asn Gly Val Arg Thr Lys Leu Arg Phe Ile Phe Cys Ser Ile
 50 55 60
 His Leu Asp His Gln Phe Val Asn Leu Leu Leu Phe Cys Asp Val Gln

Phe Leu Ala Asn Gln Gly Arg Arg Asn Ser Phe Ile Xaa Val Leu Asn

65 70 75 80

 85 90 95

Ser Leu

```
<210> 2346
<211> 100
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> variant
<222> (1)...(100)
<223> Xaa = Any amino acid
```

<400> 2346
Xaa Pro Pro Leu Met Thr Leu Asn Ala Gly Thr Gly Arg Met Thr Ser
 5 10 15

Glu Leu Pro Ala Lys Ser Ala Met Trp Arg Tyr Arg Gly Thr Pro Phe
20 25 30

Ser Thr Ala Pro Ala Leu Gln Thr Ala Arg Asp Thr Pro Arg Met Ala
35 40 45

Phe Ala Pro Asn Leu Asp Leu Phe Ser Val Pro Ser Ile Ser Ile Ile
50 55 60

Ser Leu Ser Ile Phe Ser Cys Ser Val Thr Phe Ser Phe Leu Leu Thr
65 70 75 80

Arg Ala Gly Ala Ile Val Leu Xaa Met Cys Ser Thr Ala Phe Glu Thr
85 90 95

Pro Phe Pro Ile
100

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<210> 2347
<211> 73
<212> PRT
<213> Homo sapiens
```

<400> 2347
Arg Met Leu Ser Tyr Ser Ser Met Leu Pro Pro Ser Gly Leu Met Leu
 5 10 15

His Tyr Thr Leu Leu Gly Ser Asn Leu Pro Leu Arg Leu Lys Ala Leu
20 25 30

Glu Gly Arg Val Phe Lys Met Leu Asp Leu Val Gln Ala Gln Ile Leu
35 40 45

Glu Leu Lys Ala Glu Gly Phe Leu Val Ala Glu Lys Lys Gln Asn Leu
50 55 60

Met Thr Phe Gly Thr Pro Val Leu Arg
65 70

<210> 2348
 <211> 52
 <212> PRT
 <213> Homo sapiens

<400> 2348
 Leu His Ala Ala Ala Glu Trp Leu Asp Ala Pro Leu His Pro Pro Trp
 5 10 15
 Ile Gln Pro Ser Ile Lys Ala Glu Gly Ser Arg Gly Gln Ser Ile Gln
 20 25 30
 Asp Val Arg Ser Gly Pro Ser Pro Asn Ser Arg Val Lys Ser Arg Gly
 35 40 45
 Val Leu Ser Gly
 50

<210> 2349
 <211> 64
 <212> PRT
 <213> Homo sapiens

<400> 2349
 Trp Lys Val Gly Ser Lys Glu Gly Val Met Glu His Gln Ala Thr Arg
 5 10 15
 Arg Gln His Gly Ala Ile Thr Lys His Pro Leu Gly Phe Cys Leu Ser
 20 25 30
 Arg His Leu Ala Leu Thr Leu Asp Leu Val Thr Val Val Trp Leu Ile
 35 40 45
 Pro Val Asn Ile Trp Arg Gln Ser Tyr Leu Ala Phe Ala Ser Arg Ala
 50 55 60

<210> 2350
 <211> 55
 <212> PRT
 <213> Homo sapiens

<400> 2350
 Leu Lys Thr Gly Val Pro Asn Val Ile Arg Phe Cys Phe Phe Ser Ala
 5 10 15
 Thr Lys Asn Pro Ser Ala Phe Asn Ser Arg Ile Trp Ala Trp Thr Arg
 20 25 30
 Ser Asn Ile Leu Asn Thr Leu Pro Ser Arg Ala Phe Ser Leu Asn Gly
 35 40 45
 Arg Leu Asp Pro Arg Arg Val
 50 55

<210> 2351
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 2351

Ile Leu Thr Leu Tyr Ser Glu Pro Ser Phe Asn Thr Met Val Ser Phe
5 10 15

Leu Arg Ala Ser Arg Ser Pro Val Arg Ser Met Val Ile Gly Pro Gly
20 25 30

Ala Leu Ser Gln Thr Arg Val Ser Arg Val Thr Thr Thr Leu Gly Ala
35 40 45

Phe Gly Ser Val Thr Thr Gly Pro Ser Pro Ser Ser Val Phe Leu Tyr
50 55 60

Leu Ile Arg Leu Ser Ser Ser Leu Ser Ile Ser Cys Ser Ser Phe Arg
65 70 75 80

Asp Phe Cys Gly Gly Gly Leu
85

<210> 2352

<211> 55

<212> PRT

<213> Homo sapiens

<400> 2352

His Asn Gly Phe Leu Phe Glu Gly Phe Gln Ile Ser Ser Lys Val His
5 10 15

Gly Asp Trp Ser Arg Gly Thr Leu Thr Asn Gln Gly Glu Pro Gly Asp
20 25 30

Asn Asp Ile Gly Gly Phe Arg Ile Cys His His Arg Thr Ile Ser Gln
35 40 45

Gln Arg Phe Leu Val Leu Asn
50 55

<210> 2353

<211> 50

<212> PRT

<213> Homo sapiens

<400> 2353

Thr Leu Ile Ile Phe Val His Phe Leu Gln Leu Phe Gln Gly Leu Leu
5 10 15

Trp Trp Arg Leu Ile Ile Glu Leu Ala Val Gln Leu Ile Ile Val Ile
20 25 30

Leu Leu His Met Trp Leu Trp Gly Phe Phe Ser His Ser Asp Leu Phe
35 40 45

Ile Gln
50

<210> 2354

<211> 123

<212> PRT

<213> Homo sapiens


```

<400> 2354
Ile Arg Met Thr Glu Lys Ala Pro Glu Pro His Val Glu Glu Asp Asp
                    5                                10                    15

Asp Asp Glu Leu Asp Ser Lys Leu Asn Tyr Lys Pro Pro Pro Gln Lys
                20                                25                    30

Ser Leu Lys Glu Leu Gln Glu Met Asp Lys Asp Asp Glu Ser Leu Ile
                35                                40                    45

Lys Tyr Lys Lys Thr Leu Leu Gly Asp Gly Pro Val Val Thr Asp Pro
                50                                55                    60

Lys Ala Pro Asn Val Val Val Thr Arg Leu Thr Leu Val Cys Glu Ser
                65                                70                    75                    80

Ala Pro Gly Pro Ile Thr Met Asp Leu Thr Gly Asp Leu Glu Ala Leu
                85                                90                    95

Lys Lys Glu Thr Ile Val Leu Lys Glu Gly Ser Glu Tyr Arg Val Lys
                100                               105                    110

Ile His Phe Lys Val Asn Arg Asp Ile Val Ser
                115                               120

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<210> 2355
<211> 69
<212> PRT
<213> Homo sapiens
```

```

<400> 2355
Lys Leu Leu Lys Cys Ser Arg Leu Val Leu Ala Leu Ala Leu Ile Leu
      5                      10                      15

Val Leu Glu Ser Ser Val Gln Gly Tyr Pro Thr Gln Arg Ala Arg Tyr
      20                      25                      30

Gln Trp Val Arg Cys Asn Pro Asp Ser Asn Ser Ala Asn Cys Leu Glu
      35                      40                      45

Glu Lys Gly Pro Met Phe Glu Leu Leu Pro Gly Glu Ser Asn Lys Ile
      50                      55                      60

Pro Arg Leu Arg Thr
      65

```

```
<210> 2356
<211> 66
<212> PRT
<213> Homo sapiens
```

```

<400> 2356
Ser Tyr Ser Asn Ala Val Gly Leu Ser Trp Leu Leu Pro Ser Ser Trp
          5                      10                      15

Phe Trp Asn Pro Gln Phe Lys Val Ile Leu Arg Arg Glu Pro Gly Thr
          20                      25                      30

Asn Gly Cys Ala Ala Ile Gln Thr Val Ile Leu Gln Thr Ala Leu Lys
          35                      40                      45

```

Lys Lys Asp Gln Cys Ser Asn Tyr Phe Gln Val Asn Pro Thr Arg Ser
 50 55 60

Pro Val
 65

<210> 2357
 <211> 156
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(156)
 <223> Xaa = Any amino acid

<400> 2357
 Gln Lys Leu Leu Lys Cys Xaa Arg Leu Val Leu Ala Leu Ala Leu Ile
 5 10 15

Leu Val Leu Glu Ser Ser Val Gln Gly Tyr Pro Thr Gln Arg Ala Arg
 20 25 30

Tyr Gln Trp Val Arg Cys Asn Pro Asp Ser Asn Ser Ala Asn Cys Leu
 35 40 45

Glu Glu Lys Gly Pro Met Phe Glu Leu Leu Pro Gly Glu Ser Asn Lys
 50 55 60

Ile Pro Arg Leu Arg Thr Asp Leu Phe Pro Lys Thr Arg Ile Gln Asp
 65 70 75 80

Leu Asn Arg Ile Phe Pro Leu Ser Glu Asp Tyr Ser Gly Ser Gly Phe
 85 90 95

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Phe Leu Thr
 100 105 110

Glu Met Glu Gln Asp Tyr Gln Leu Val Asp Glu Ser Asp Ala Phe His
 115 120 125

Asp Asn Leu Arg Ser Leu Asp Arg Asn Leu Pro Ser Asp Ser Gln Asp
 130 135 140

Leu Gly Gln His Gly Leu Glu Glu Asp Phe Met Leu
 145 150 155

<210> 2358
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(67)
 <223> Xaa = Any amino acid

<400> 2358
 Arg Ser Tyr Ser Asn Xaa Val Gly Leu Ser Trp Leu Leu Pro Ser Ser
 5 10 15

Trp Phe Trp Asn Pro Gln Phe Lys Val Ile Leu Arg Arg Glu Pro Gly
 20 25 30
 Thr Asn Gly Cys Ala Ala Ile Gln Thr Val Ile Leu Gln Thr Ala Leu
 35 40 45
 Lys Lys Lys Asp Gln Cys Ser Asn Tyr Phe Gln Val Asn Pro Thr Arg
 50 55 60
 Ser Pro Val
 65

<210> 2359
 <211> 64
 <212> PRT
 <213> Homo sapiens

<400> 2359
 Ser Ser Glu Ser Gly Lys Ile Arg Phe Lys Ser Trp Ile Leu Val Phe
 5 10 15
 Gly Lys Arg Ser Val Leu Arg Arg Gly Ile Leu Leu Asp Ser Pro Gly
 20 25 30
 Ser Ser Ser Asn Ile Gly Pro Phe Ser Ser Arg Gln Phe Ala Glu Leu
 35 40 45
 Leu Ser Gly Leu Gln Arg Thr His Trp Tyr Leu Ala Leu Cys Val Gly
 50 55 60

<210> 2360
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 2360
 Gly Cys His Gly Lys His His Phe Arg Leu Leu Val Gly Asn Pro Val
 5 10 15
 Pro Phe Pro Leu Gly Ser His Ser Gln Ile Leu Ile Gln Ser Arg Ser
 20 25 30
 Arg Ser Arg Ser Leu Ile Gln Ser Ser Pro Gln Lys Val Gly Arg Tyr
 35 40 45
 Asp Ser Ser Pro Gly Phe Ser Ser Leu Glu Lys Gly Gln Ser Ser Asp
 50 55 60
 Gly Gly Ser Cys Trp Ile His Leu Glu Val Val Arg Thr Leu Val Leu
 65 70 75 80
 Phe Leu Gln Gly Ser Leu Gln Asn Tyr Cys Leu Asp Cys Ser Ala Pro
 85 90 95
 Ile Gly Thr Trp Leu Ser Ala
 100

<210> 2361
 <211> 180
 <212> PRT

<213> Homo sapiens

<400> 2361

Gly Asn Asp Gly Ala Gln Arg Ser Phe Cys Gln Ser Cys Phe Asn Glu
5 10 15
Leu Asn Asp Leu Phe Lys Ala Ala Cys Leu Pro Leu Pro Gly Tyr Arg
20 25 30
Val Arg Glu Ile Thr Glu Asn Leu Met Ala Thr Gly Asp Leu Asp Gln
35 40 45
Asp Gly Arg Ile Ser Phe Asp Glu Phe Ile Lys Ile Phe His Gly Leu
50 55 60
Lys Ser Thr Asp Val Ala Lys Thr Phe Arg Lys Ala Ile Asn Lys Lys
65 70 75 80
Glu Gly Ile Cys Ala Ile Gly Gly Thr Ser Glu Gln Ser Ser Val Gly
85 90 95
Thr Gln His Ser Tyr Ser Glu Glu Glu Lys Tyr Ala Phe Val Asn Trp
100 105 110
Ile Asn Lys Ala Leu Glu Asn Asp Pro Asp Cys Arg His Val Ile Pro
115 120 125
Met Asn Pro Asn Thr Asn Asp Leu Phe Asn Ala Val Gly Asp Gly Ile
130 135 140
Val Leu Cys Lys Met Ile Asn Leu Ser Val Pro Asp Thr Ile Asp Glu
145 150 155 160
Arg Thr Ile Asn Lys Lys Lys Leu Thr Pro Phe Thr Ile Gln Glu Asn
165 170 175
Leu Asn Leu Ala
180

<210> 2362

<211> 72

<212> PRT

<213> Homo sapiens

<400> 2362

Met Val Lys Gly Val Ser Phe Phe Leu Leu Ile Val Leu Ser Ser Ile
5 10 15
Val Ser Gly Thr Asp Arg Leu Ile Ile Leu Gln Arg Thr Met Pro Ser
20 25 30
Pro Thr Ala Leu Lys Arg Ser Phe Val Phe Gly Phe Ile Gly Met Thr
35 40 45
Cys Arg Gln Ser Gly Ser Phe Ser Arg Ala Leu Phe Ile Gln Leu Thr
50 55 60
Lys Ala Tyr Phe Ser Ser Ser Glu
65 70

<210> 2363

```

<211> 94
<212> PRT
<213> Homo sapiens

<400> 2363
Glu Cys Trp Val Pro Thr Leu Asp Cys Ser Glu Val Pro Pro Ile Ala
      5                                10                                15

Gln Ile Pro Ser Phe Leu Leu Ile Ala Phe Leu Lys Val Leu Ala Thr
      20                                25                                30

Ser Val Leu Phe Arg Pro Trp Lys Ile Leu Ile Asn Ser Ser Lys Leu
      35                                40                                45

Ile Leu Pro Ser Trp Ser Arg Ser Pro Val Ala Ile Arg Phe Ser Val
      50                                55                                60

Ile Ser Arg Thr Leu Tyr Pro Gly Lys Gly Lys Gln Ala Ala Leu Asn
      65                                70                                75                                80

Lys Ser Phe Asn Ser Leu Lys Gln Leu Trp Gln Lys Leu Leu
      85                                90

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<210> 2364
<211> 50
<212> PRT
<213> Homo sapiens

<400> 2364
Gln Val Asp His Phe Thr Lys Asp Asn Ala Ile Ser Asn Ser Ile Lys
          5                                10                                15
Glu Ile Ile Arg Val Trp Val His Trp Asp Asp Met Pro Thr Ile Arg
          20                                25                                30
Ile Ile Phe Gln Gly Phe Val Tyr Pro Val Asp Lys Gly Ile Leu Phe
          35                                40                                45
Phe Leu
          50

```

```

<210> 2365
<211> 70
<212> PRT
<213> Homo sapiens

<400> 2365
Ala Met Glu Asn Leu Asp Lys Leu Ile Lys Ala Asp Pro Ser Ile Leu
          5                      10                      15

Val Gln Ile Thr Cys Ser His Gln Val Phe Cys Asn Phe Ser Tyr Ser
          20                      25                      30

Ile Pro Arg Gln Arg Gln Ala Ser Ser Leu Glu Gln Val Ile Gln Leu
          35                      40                      45

Ile Glu Ala Thr Leu Ala Lys Ala Ser Leu Ser Ser Ile Ile Ser Ser
          50                      55                      60

Ser Asp Thr Asp Pro Leu
          65                      70

```

<210> 2366
 <211> 54
 <212> PRT
 <213> Homo sapiens

<400> 2366
 Asn Pro Asp His His Pro Gly Ser His Leu His Gln His Pro Glu Glu
 5 10 15
 Gly Gly Leu Ala His Arg Glu Asp Ala Cys Ser Arg Phe His Cys Ile
 20 25 30
 Arg His Ala Trp Arg Tyr Gly Pro Lys Gly Thr Arg Arg Asp Tyr Glu
 35 40 45
 Gly Val Ser Phe Trp Leu
 50

<210> 2367
 <211> 187
 <212> PRT
 <213> Homo sapiens

<400> 2367
 Gln Met Glu Ala Pro His Ile Ile Val Gly Thr Pro Gly Arg Val Phe
 5 10 15
 Asp Met Leu Asn Arg Arg Tyr Leu Ser Pro Lys Tyr Ile Lys Met Phe
 20 25 30
 Val Leu Asp Glu Ala Asp Glu Met Leu Ser Arg Gly Phe Lys Asp Gln
 35 40 45
 Ile Tyr Asp Ile Phe Gln Lys Leu Asn Ser Asn Thr Gln Val Val Leu
 50 55 60
 Leu Ser Ala Thr Met Pro Ser Asp Val Leu Glu Val Thr Lys Lys Phe
 65 70 75 80
 Met Arg Asp Pro Ile Arg Ile Leu Val Lys Lys Glu Glu Leu Thr Leu
 85 90 95
 Glu Gly Ile Arg Gln Phe Tyr Ile Asn Val Glu Arg Glu Glu Trp Lys
 100 105 110
 Leu Asp Thr Leu Cys Asp Leu Tyr Glu Thr Leu Thr Ile Thr Gln Ala
 115 120 125
 Val Ile Phe Ile Asn Thr Arg Arg Lys Val Asp Trp Leu Thr Glu Lys
 130 135 140
 Met His Ala Arg Asp Phe Thr Val Ser Ala Met His Gly Asp Met Asp
 145 150 155 160
 Gln Lys Glu Arg Asp Val Ile Met Arg Glu Phe Arg Ser Gly Ser Ser
 165 170 175
 Arg Val Leu Ile Thr Thr Asp Leu Leu Asp Leu
 180 185

```
<210> 2368
<211> 71
<212> PRT
<213> Homo sapiens
```

```

<400> 2368
Gln Val Gln Gln Val Ser Gly Asn Gln Asn Ser Ala Arg Ala Arg Thr
      5                                10                                15

Lys Leu Pro His Asn His Val Ser Phe Leu Leu Val His Ile Ser Met
      20                                25                                30

His Gly Gly Tyr Ser Glu Ile Ser Ser Met His Leu Leu Gly Glu Pro
      35                                40                                45

Val His Leu Pro Pro Gly Val Asp Glu Asp Asp Cys Leu Gly Asp Gly
      50                                55                                60

Gln Gly Phe Ile Gln Val Thr
      65                                70

```

```
<210> 2369
<211> 84
<212> PRT
<213> Homo sapiens
```

```

<400> 2369
Arg Ser Ser Arg Ser Val Val Ile Lys Thr Leu Leu Glu Pro Glu Arg
      5                                10                                15
Asn Ser Leu Ile Ile Thr Ser Arg Ser Phe Trp Ser Ile Ser Pro Cys
      20                                25                                30
Met Ala Asp Thr Val Lys Ser Arg Ala Cys Ile Phe Ser Val Ser Gln
      35                                40                                45
Ser Thr Phe Leu Arg Val Leu Met Lys Met Thr Ala Trp Val Met Val
      50                                55                                60
Arg Val Ser Tyr Lys Ser His Ser Val Ser Ser Phe His Ser Ser Arg
      65                                70                                75                                80
Ser Thr Leu Met

```

```
<210> 2370
<211> 52
<212> PRT
<213> Homo sapiens
```

```

<400> 2370
Asn Trp Arg Ile Pro Ser Arg Val Asn Ser Ser Phe Leu Thr Arg Ile
          5                      10                      15

Arg Met Gly Ser Leu Met Asn Phe Leu Val Thr Ser Ser Thr Ser Glu
          20                      25                      30

Gly Ile Val Ala Asp Ser Lys Thr Thr Trp Val Leu Leu Leu Ser Phe
          35                      40                      45

```

Trp Asn Met Ser
50

<210> 2371
<211> 54
<212> PRT
<213> Homo sapiens

<400> 2371
Leu Trp Gln Glu Val Gln Ala Gly Val Leu His Leu Pro Gly Ala Pro
5 10 15
Gly Phe His Arg Arg Gly Asp Gln Ser Leu Pro Gly Val Gln Thr Gly
20 25 30
Arg Gly Gln Met Thr Gly Val Glu His Glu Glu Ile Ser Gly Val Ile
35 40 45
Ile Leu Ser Tyr Leu Gly
50

<210> 2372
<211> 161
<212> PRT
<213> Homo sapiens

<400> 2372
Gln Met Pro Ser Asp Lys Thr Ile Gly Gly Gly Asp Asp Ser Phe Asn
5 10 15
Thr Phe Phe Ser Glu Thr Gly Ala Gly Lys His Val Pro Arg Ala Val
20 25 30
Phe Val Asp Leu Glu Pro Thr Val Ile Asp Glu Val Arg Thr Gly Thr
35 40 45
Tyr Arg Gln Leu Phe His Pro Glu Gln Leu Ile Thr Gly Lys Glu Asp
50 55 60
Ala Ala Asn Asn Tyr Ala Arg Gly His Tyr Thr Ile Gly Lys Glu Ile
65 70 75 80
Ile Asp Leu Val Leu Asp Arg Ile Arg Lys Leu Ala Asp Gln Cys Thr
85 90 95
Gly Leu Gln Gly Phe Leu Val Phe His Ser Phe Gly Gly Gly Thr Gly
100 105 110
Ser Gly Phe Thr Ser Leu Leu Met Glu Arg Leu Ser Val Asp Tyr Gly
115 120 125
Lys Lys Ser Lys Leu Glu Phe Ser Ile Tyr Pro Ala Pro Gln Val Ser
130 135 140
Thr Gly Glu Glu Thr Arg Val Cys Leu Glu Cys Arg Leu Gly Gly Gly
145 150 155 160
Arg

<210> 2373
 <211> 132
 <212> PRT
 <213> Homo sapiens

<400> 2373
 Thr Trp Asn Pro Gln Ser Leu Met Lys Phe Ala Leu Ala Leu Thr Ala
 5 10 15
 Ser Ser Ser Thr Leu Ser Asn Ser Ser Gln Ala Arg Lys Met Leu Pro
 20 25 30
 Ile Thr Met Pro Glu Gly Thr Thr Pro Leu Ala Arg Arg Ser Leu Thr
 35 40 45
 Ser Cys Trp Thr Glu Phe Ala Ser Trp Leu Thr Ser Ala Pro Val Phe
 50 55 60
 Arg Ala Ser Trp Phe Ser Thr Ala Leu Val Gly Glu Leu Val Leu Gly
 65 70 75 80
 Ser Pro Arg Cys Ser Trp Asn Val Ser Gln Leu Ile Met Ala Arg Ser
 85 90 95
 Pro Ser Trp Ser Ser Pro Phe Thr Arg Arg Pro Arg Phe Pro Gln Glu
 100 105 110
 Arg Arg Pro Glu Ser Ala Trp Ser Ala Asp Trp Glu Gly Ala Asp Asp
 115 120 125
 Trp Gly Gly Ala
 130

<210> 2374
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 2374
 Glu Thr Phe His Glu Gln Arg Gly Glu Pro Arg Thr Ser Ser Pro Thr
 5 10 15
 Lys Ala Val Glu Asn Gln Glu Ala Leu Lys Thr Gly Ala Leu Val Ser
 20 25 30
 Gln Leu Ala Asn Ser Val Gln His Glu Val Asn Asp Leu Leu Ala Asn
 35 40 45
 Gly Val Val Pro Ser Gly Ile Val Ile Gly Ser Ile Phe Leu Ala Cys
 50 55 60
 Asp Glu Leu Leu Arg Val Glu Glu Leu Ala Val Ser Ala Ser Ala Asn
 65 70 75 80
 Phe Ile Asn Asp Cys Gly Phe Gln Val Tyr Lys His Cys Pro Gly Tyr
 85 90 95
 Met Leu Ala Ser Thr Arg Phe Thr Glu Glu Gly Val Glu Gly Ile Ile
 100 105 110
 Ser Ser Pro Asn Gly Leu Val Thr Trp His Leu
 115 120

```
<210> 2375
<211> 57
<212> PRT
<213> Homo sapiens
```

```

<400> 2375
Asp Arg Ile Ile Thr Pro Glu Ile Ser Ser Cys Ser Thr Pro Val Ile
      5                                10                                15

Cys Pro Leu Pro Val Cys Thr Pro Gly Arg Leu Trp Ser Pro Leu Leu
      20                                25                                30

Trp Lys Pro Gly Ala Pro Gly Lys Trp Arg Thr Pro Ala Trp Thr Ser
      35                                40                                45

Cys His Asn Gln Leu Arg Asp Val Pro
      50                                55

```

```
<210> 2376
<211> 53
<212> PRT
<213> Homo sapiens
```

```
<400> 2376
Ala Asn Thr Leu Ile Asn Gln Ser Pro Gly Lys Gln Leu Glu Cys Ile
      5                                10                        15

Ile Leu Trp Ser Ser Ile Leu Cys Ser Cys Ala Asp Ile Ser Leu Ser
      20                                25                        30

His Cys Val Ser Leu Ser Val Asp Thr Leu Lys Val Ala Leu Trp Lys
      35                                40                        45

Met Ser Lys Phe Phe
      50
```

```
<210> 2377
<211> 67
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> variant  
<222> (1)...(67)  
<223> Xaa = Any amino acid
```

```

<400> 2377
Lys Pro Pro Phe Phe Xaa Leu Leu Lys Arg Lys Gly Pro Gln Asp Thr
          5                      10                      15

Ile Phe Glu Trp Leu Met Val Phe Lys Xaa Phe Arg Glu Leu Pro Ala
          20                      25                      30

Phe Tyr Leu Glu Thr Glu Lys Ala Arg Lys Ile Leu Ser Phe Leu Ala
          35                      40                      45

Cys Ile Ser Arg Val Gly Ala Asn Asp Ser Lys Leu Val Ser Lys Pro
          50                      55                      60

```

Ile Pro Leu
65

<210> 2378
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(51)
<223> Xaa = Any amino acid

<400> 2378
Thr Asn Gln Ser Leu Leu Arg Asn Cys Tyr Ser Leu Asn Trp Ser Ile
 5 10 15

Lys Thr Ser His Gly Ser Gly Tyr Gly Val Ile Trp Cys Pro Cys Phe
 20 25 30

Ser Pro Xaa Gly His Leu Ile Xaa Glu Pro Pro Xaa Glu Phe Cys Gly
 35 40 45

Arg His Leu
 50

<210> 2379
<211> 60
<212> PRT
<213> Homo sapiens

<400> 2379
Asn Ser Val Met Met Val Phe Lys Asp Ser Arg Lys Gly Val Met Ser
 5 10 15

Gln Asn Leu Pro Glu Cys Pro Ser Ile Val Arg Arg Lys Arg Thr Ser
 20 25 30

Leu Val Asp Val His Val Leu Ile Pro Trp Arg Leu Gly His Gln Thr
 35 40 45

Met Arg Phe Gly Asn Ile Cys Tyr Gln Asp Glu Pro
 50 55 60

<210> 2380
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(51)
<223> Xaa = Any amino acid

<400> 2380
Asp Thr Phe Lys Trp Ala Gln Cys Gln Pro Thr Gly Leu Leu Thr Gly
 5 10 15

Thr Thr Ser Gln Met Pro Phe Ser Ala His Thr Leu Gln Ala Glu Ala
 20 25 30

Arg Gly Xaa His Pro Ser Gly Asp Gly Xaa Cys Xaa Cys Val Xaa Val
35 40 45

Cys Ser Ala
50

<210> 2381
<211> 59
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(59)
<223> Xaa = Any amino acid

<400> 2381
Pro Xaa Xaa Val Gln Met Ser Glu Thr Pro Ser Asn Gly Pro Ser Ala
5 10 15

Ser Gln Leu Gly Ser Ser Leu Ala Pro Arg Pro Arg Cys Pro Ser Leu
20 25 30

Pro Thr Pro Cys Arg Leu Arg Pro Glu Glu Xaa Thr Pro Pro Glu Met
35 40 45

Gly Xaa Val Xaa Val Cys Xaa Tyr Val Leu Xaa
50 55

<210> 2382
<211> 59
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(59)
<223> Xaa = Any amino acid

<400> 2382
Arg Arg Thr Tyr Xaa His Thr Xaa Thr Xaa Pro Ile Ser Gly Gly Val
5 10 15

Xaa Ser Ser Gly Leu Ser Leu Gln Gly Val Gly Arg Glu Gly His Leu
20 25 30

Gly Arg Gly Ala Ser Glu Glu Pro Ser Trp Leu Ala Leu Gly Pro Phe
35 40 45

Glu Gly Val Ser Asp Ile Trp Thr Xaa Xaa Gly
50 55

<210> 2383
<211> 58
<212> PRT
<213> Homo sapiens

<220>
<221> variant

<222> (1)...(58)

<223> Xaa = Any amino acid

<400> 2383

Ala Glu His Xaa His Thr His Xaa His Xaa Pro Ser Pro Glu Gly Xaa
 5 10 15

Pro Pro Leu Ala Ser Ala Cys Arg Val Trp Ala Glu Lys Gly Ile Trp
 20 25 30

Asp Val Val Pro Val Arg Ser Pro Val Gly Trp His Trp Ala His Leu
 35 40 45

Lys Val Ser Gln Thr Phe Gly Pro Xaa Xaa
 50 55

<210> 2384

<211> 135

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(135)

<223> Xaa = Any amino acid

<400> 2384

Xaa Arg Ser Ser Pro Lys Pro Val Leu Cys His Gln Ser Lys Glu Arg
 5 10 15

Lys Pro Ser Ala Glu Met Asn Arg Ile Thr Thr Lys Glu Ala Thr Ser
 20 25 30

Ser Cys Pro Pro Lys Ser Pro Leu Gly Glu Thr Arg Gln Lys Leu Trp
 35 40 45

Arg Ser Leu Lys Met Leu Pro Glu Arg Gly Gln Arg Val Arg Gln Gln
 50 55 60

Leu Lys Ser His Leu Ala Thr Val Asn Leu Ser Ser Leu Leu Asp Val
 65 70 75 80

Arg Arg Ser Thr Val Ile Ser Gly Pro Gly Thr Gly Lys Gly Ser Gln
 85 90 95

Asp His Ser Gly Asp Pro Thr Ser Gly Asp Arg Gly Tyr Thr Asp Pro
 100 105 110

Cys Ala Ala Thr Ser Xaa Lys Ser Pro Ser Gln Pro Gln Ala Pro Lys
 115 120 125

Xaa Xaa Lys Val Pro Thr Arg
 130 135

<210> 2385

<211> 50

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(50)

<223> Xaa = Any amino acid

<400> 2385

Ser Gln Ala Leu Gly Pro Glu Lys Ala Ala Lys Ile Thr Gln Gly Ile
 5 10 15
Pro Pro Arg Gly Thr Glu Ala Thr Arg Ile Pro Val Arg Pro His Xaa
 20 25 30
Xaa Lys Ala Pro His Ser Pro Arg His Gln Xaa Thr Xaa Arg Ser Pro
 35 40 45
Pro Gly
 50

<210> 2386

<211> 134

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(134)

<223> Xaa = Any amino acid

<400> 2386

Glu Val Leu Pro Lys Ala Ser Pro Val Ser Pro Ile Lys Gly Lys Glu
 5 10 15
Ala Val Ser Arg Asp Glu Gln Asn Asn His Gln Gly Ser His Phe Leu
 20 25 30
Leu Pro Pro Lys Ile Pro Ser Trp Arg Asp Pro Pro Glu Thr Leu Glu
 35 40 45
Glu Pro Gln Asn Ala Pro Arg Glu Arg Pro Glu Gly Pro Ala Ala Ala
 50 55 60
Lys Lys Pro Pro Arg His Cys Glu Leu Val Val Thr Leu Gly Cys Pro
 65 70 75 80
Glu Ile His Gly Asp Leu Arg Pro Trp Asp Arg Lys Arg Gln Pro Arg
 85 90 95
Ser Leu Arg Gly Ser His Leu Gly Gly Gln Arg Leu His Gly Ser Leu
 100 105 110
Cys Gly His Ile Xaa Xaa Lys Pro Leu Thr Ala Pro Gly Thr Lys Xaa
 115 120 125
Xaa Lys Gly Pro His Gln
 130

<210> 2387

<211> 84

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<400> 2387

Arg Gly Ala Phe

<210> 2388

<211> 50

<212> PRT

<213> Homo sapiens

<400> 2388

Thr Ser
50

<210> 2389

<211> 86

<212> PRT

<213> Homo sapiens

<400> 2389

Glu Glu Val Ala Ser Leu Val Val Ile Leu Phe Ile Ser Ala Asp Gly
65 70 75 80

Phe Leu Ser Phe Asp Trp
85

<210> 2390
<211> 78
<212> PRT
<213> Homo sapiens

<400> 2390
Pro Phe Pro His Val Lys Arg Val Val Leu Asp Asp Leu Gly Ile Gly
5 10 15

Thr Asn Gln Lys Gln Ser Leu Gln Gln Ser Arg Pro Leu Phe Ile Met
20 25 30

Glu Glu Pro Val Asp Thr Ser Glu Pro Leu Ser Ala Leu Pro Phe Thr
35 40 45

Gly Gln Gln Ser Phe Glu Pro Ser Gly Lys Phe Gly Gln Tyr Pro Ser
50 55 60

Met Gln Met Asn His Ile Gln Ala Leu Gly Lys Trp Arg Thr
65 70 75

<210> 2391
<211> 51
<212> PRT
<213> Homo sapiens

<400> 2391
Glu Pro Ile Arg Asn Asn Arg Phe Ser Asn Gln Asp His Cys Ser Ser
5 10 15

Trp Arg Asn Pro Trp Ile Pro Leu Ser Leu Tyr Leu His Tyr His Ser
20 25 30

Leu Gly Ser Ser Leu Leu Ser Gln Val Ala Asn Leu Asp Ser Ile His
35 40 45

Arg Cys Arg
50

<210> 2392
<211> 50
<212> PRT
<213> Homo sapiens

<400> 2392
Ala Ala Val Glu Ser Lys Ile Ser Gly Ala Val Thr Leu Ser Ser Cys
5 10 15

Lys Thr Ser Ser Leu Gly Arg Ser Gly His Arg Asn Gln Ser Glu Thr
20 25 30

Ile Ala Ser Ala Ile Lys Thr Ile Val His His Gly Gly Thr Arg Gly
35 40 45

Tyr Leu
50


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<210> 2393
<211> 82
<212> PRT
<213> Homo sapiens
```

```

<400> 2393
Ala Lys Trp Gln Ile Trp Thr Val Ser Ile Asp Ala Asp Glu Pro His
      5                                10                                15

Pro Gly Thr Gly Glu Val Glu Asp Ile Glu Gln Leu Asn Gln Cys Leu
      20                                25                                30

Ile Gln His Phe His Leu Ile Lys Thr Ser Leu Ile Phe Leu Cys Phe
      35                                40                                45

Leu Phe His Gly Ile His Glu Asn Leu Leu Thr Val Gly Val Ser Lys
      50                                55                                60

Glu Ala Tyr Leu Met Thr Ser Val Asn Gly Lys Asn Lys Thr Lys Met
      65                                70                                75                                80

Leu Tyr

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<210> 2394
<211> 78
<212> PRT
<213> Homo sapiens
```

```

<400> 2394
Lys Ala Lys Lys Asn Gln Thr Cys Leu Asn Glu Met Glu Val Leu Asp
          5                      10                      15

Gln Thr Leu Ile Glu Leu Phe Tyr Val Leu His Phe Pro Ser Ala Trp
          20                      25                      30

Met Trp Phe Ile Cys Ile Asp Gly Tyr Cys Pro Asn Leu Pro Leu Gly
          35                      40                      45

Ser Lys Asp Cys Cys Pro Val Asn Gly Asn Ala Asp Arg Gly Ser Glu
          50                      55                      60

Val Ser Thr Gly Ser Ser Met Met Asn Asn Gly Leu Asp Cys
          65                      70                      75

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<210> 2395
<211> 64
<212> PRT
<213> Homo sapiens
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```

<400> 2395
Lys Phe Ile Leu Phe Tyr Asn Thr Phe Arg Phe Ile Glu Lys Leu Gly
          5                      10                      15

Arg Trp Tyr Lys Glu Phe Pro Tyr Ile Pro Tyr Pro Val Ser Pro Asn
          20                      25                      30

Asn Ile Leu His Trp Tyr Ile Met Val Val Thr Ile Lys Trp Ala Asn
          35                      40                      45

```

Ile Asp Thr Leu Val Leu Thr Lys Val His Thr Leu Phe Arg Phe His
50 55 60

<210> 2396
<211> 57
<212> PRT
<213> Homo sapiens

<400> 2396
Asn Leu Asn Lys Val Trp Thr Leu Val Asn Thr Asn Val Ser Ile Leu
5 10 15

Ala His Leu Ile Val Thr Thr Ile Ile Tyr Gln Cys Lys Met Leu Leu
20 25 30

Gly Glu Thr Gly Tyr Gly Ile Tyr Gly Asn Ser Leu Tyr His Leu Pro
35 40 45

Asn Phe Ser Ile Asn Leu Lys Val Leu
50 55

<210> 2397
<211> 74
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(74)
<223> Xaa = Any amino acid

<400> 2397
Lys Ser Arg Arg Thr Ala Ala Ser Ile Gly Ser Gly Leu Lys Lys Lys
5 10 15

Ile Cys Ser Gln Ser Val Leu Glu Val Thr Ser Pro Thr Lys Leu Thr
20 25 30

Pro Tyr Ala Val Leu Arg Arg Trp Arg His Gln Ala Gln Lys Arg Lys
35 40 45

Phe Xaa Ile Ser His Trp Glu Ser Lys Val Pro Pro Ser Gln Asn Asp
50 55 60

Asn Cys Thr Val Ala Glu Gln Thr Pro Pro
65 70

<210> 2398
<211> 57
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(57)
<223> Xaa = Any amino acid

<400> 2398
Leu Lys Val Lys Lys Asp Ser Ser Lys His Arg Leu Arg Ile Lys Glu
5 10 15

Lys Asn Leu Leu Thr Val Cys Ser Gly Gly His Ile Thr Asn Lys Ala
20 25 30

His Ala Leu Cys Ser Ser Glu Lys Val Glu Ala Pro Gly Ser Lys Glu
35 40 45

Glu Ile Xaa Asn Phe Ser Leu Gly Glu
50 55

<210> 2399
<211> 58
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(58)
<223> Xaa = Any amino acid

<400> 2399
Leu Gln Gln Thr Gly Trp Gly Pro Pro Thr Leu Gly Trp Ser Leu Phe
5 10 15

Cys His Cys Ala Val Ile Ile Leu Gly Trp Gly Tyr Leu Thr Leu Pro
20 25 30

Met Arg Asn Xaa Lys Phe Pro Leu Leu Ser Leu Val Pro Pro Pro Ser
35 40 45

Gln Asn Cys Ile Gly Arg Glu Leu Cys Trp
50 55

<210> 2400
<211> 59
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(59)
<223> Xaa = Any amino acid

<400> 2400
Leu Gln Asp Ser Arg Glu Xaa Ala Asn Ile Gln Leu Ala Asp Asp Phe
5 10 15

Ala Gly Lys Gln Arg Lys Xaa Val Lys Ala Cys Leu Pro Ala Arg Lys
20 25 30

Leu Asp Thr Lys Xaa Arg Phe Gly Ala Arg Lys Gln Thr Gln Lys Ala
35 40 45

His Ser Lys Arg Arg Lys Lys Pro Gln Asn Leu
50 55

<210> 2401
<211> 50
<212> PRT
<213> Homo sapiens

<400> 2401
 Asp Leu Glu Leu Gly Asn Lys Pro Lys Arg Leu Thr Ala Ser Gly Glu
 5 10 15
 Lys Asn Pro Lys Ile Cys Asn Leu Tyr His Lys Ala Phe Ile Ser Phe
 20 25 30
 Arg Tyr Lys Glu Leu Leu Asp Ile Asn Lys Lys Asn Ala Asn Thr Pro
 35 40 45
 Glu Lys
 50

<210> 2402
 <211> 50
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(50)
 <223> Xaa = Any amino acid

<400> 2402
 Tyr Arg Leu Gln Ile Leu Gly Phe Phe Ser Pro Leu Ala Val Ser Leu
 5 10 15
 Leu Gly Leu Phe Pro Ser Ser Lys Ser Xaa Leu Gly Val Lys Phe Pro
 20 25 30
 Gly Trp Glu Thr Ser Phe Tyr Xaa Leu Pro Leu Leu Ala Ser Lys Val
 35 40 45
 Ile Cys
 50

<210> 2403
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 2403
 Leu His Leu Val His Val Gly Thr Pro Ser Pro Phe Gln Ser Thr Thr
 5 10 15
 Ser Ser Ser Asn Gln Tyr Phe Leu Glu Ser Leu Gly Asn Val Leu His
 20 25 30
 Ala Phe Lys Gln Ser Pro Phe Leu Glu Ile His Tyr Arg Val Thr Ile
 35 40 45
 Asn Ser Ala Thr Leu Arg Phe His His Tyr Gly Ser
 50 55 60

<210> 2404
 <211> 75
 <212> PRT
 <213> Homo sapiens

<400> 2404

Ser Ser His Leu Leu Ser Tyr Ile His Leu Gly Ile Pro Ile Ser Asn
5 10 15

Val Ser Leu Glu Ile Arg Ala Pro Gly Gly Gln Val Thr Glu Gly Gln
20 25 30

Lys Leu Ile Leu Leu Cys Ser Val Ala Gly Gly Thr Gly Asn Val Thr
35 40 45

Phe Ser Trp Tyr Arg Glu Ala Thr Gly Thr Ser Met Gly Lys Lys Thr
50 55 60

Gln Arg Ser Leu Ser Ala Glu Leu Glu Ile Pro
65 70 75

<210> 2405

<211> 63

<212> PRT

<213> Homo sapiens

<400> 2405

Asp Ile Gln Met Ser Leu Ser Thr Phe Leu Lys Asp Asn Cys Tyr Arg
5 10 15

Phe Pro Thr Ser Ile Gly Met Leu Ile Met Asp Tyr Leu Tyr Asn Leu
20 25 30

His Ile Pro Thr Phe Cys Ile Arg Glu Trp Asn Gln Ser Asn Pro Val
35 40 45

Pro Arg Val Ser Leu Arg Val Leu Thr Cys Cys Leu Ile Ser Ile
50 55 60

<210> 2406

<211> 68

<212> PRT

<213> Homo sapiens

<400> 2406

Gly Ile Ser Ser Ser Ala Asp Arg Glu Arg Trp Val Phe Phe Pro Ile
5 10 15

Leu Val Pro Val Ala Ser Leu Tyr Gln Glu Asn Val Thr Phe Pro Val
20 25 30

Pro Pro Ala Thr Glu Gln Ser Arg Ile Ser Phe Cys Pro Ser Val Thr
35 40 45

Cys Pro Pro Gly Ala Arg Ile Ser Lys Leu Thr Leu Glu Met Gly Ile
50 55 60

Pro Arg Trp Ile
65

<210> 2407

<211> 69

<212> PRT

<213> Homo sapiens

[illegible]

```
<210> 2408
<211> 50
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> variant  
<222> (1)...(50)  
<223> Xaa = Any amino acid
```

```

<400> 2408
Leu Trp Lys Arg Ala Pro Pro Gly Ala Xaa Gly Lys Asp Cys Phe Ser
      5                                10                                15

Leu Ser Ser Pro Ile Pro Gly Tyr Ser Arg Ala Asp Gln Gln Gly His
      20                                25                                30

Phe His Leu Thr Ser Cys Cys Ser Leu Met Phe Pro Trp Asp Lys Arg
      35                                40                                45

Gly Asn
      50

```

```
<210> 2409
<211> 59
<212> PRT
<213> Homo sapiens
```

```
<220>  
<221> variant  
<222> (1)...(59)  
<223> Xaa = Any amino acid
```

```

<400> 2409
Val Leu Leu Xaa His Pro Leu Pro Xaa Gly Ser Thr Arg Tyr Ala Thr
      5                      10                      15
Gly Ser Arg Asn Ile Asn Pro Arg Ile Leu Thr Leu Ser Gly Asn Thr
      20                      25                      30

```

Glu Cys Thr Pro Gly Met Leu Gly Glu Thr Arg Gly Ile Leu Leu Thr
35 40 45

Ile Asn Leu Gly Ser Lys Arg Pro Tyr Leu Ile
50 55

<210> 2410

<211> 68

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(68)

<223> Xaa = Any amino acid

<400> 2410

Gln Pro Gln Gln His Pro Leu Gly Leu Ser Leu Tyr Arg Met Pro Glu
5 10 15

Ala Cys Ala Ser Pro Arg Val Gly Arg Ser Cys Ala Ala Leu Arg Cys
20 25 30

Val His Ser Leu Ser Leu Leu Cys Leu Leu Lys Ser Phe Leu Xaa Thr
35 40 45

Leu Ser Leu Xaa Ala Leu Pro Gly Met Pro Arg Gly Ala Gly Ile Leu
50 55 60

Ile Leu Glu Ser
65

<210> 2411

<211> 54

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(54)

<223> Xaa = Any amino acid

<400> 2411

Leu Ser Val Ala Ile Gln Ser Val Leu Gln Gly Cys Trp Val Lys Pro
5 10 15

Gly Glu Phe Tyr Ser Pro Leu Thr Leu Gly Val Arg Gly His Thr Ser
20 25 30

Ser Glu Thr Leu Pro Ala Arg Ala Gly Arg Ser Lys Gly Xaa Phe Pro
35 40 45

Xaa Pro Leu Arg Xaa Tyr
50

<210> 2412

<211> 100

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(100)

<223> Xaa = Any amino acid

<400> 2412

```

Asn Ser Pro Gly Phe Thr Gln His Pro Trp Ser Thr Leu Cys Ile Ala
      5                      10                      15

Thr Glu Ser Gln Asp Ser Arg Ile Asn Ile Pro Ala Pro Arg Gly Ile
      20                      25                      30

Pro Gly Arg Ala Xaa Arg Glu Arg Val Xaa Lys Lys Asp Leu Ser Lys
      35                      40                      45

Gln Arg Arg Glu Arg Leu Cys Thr Gln Arg Arg Ala Ala Gln Leu Arg
      50                      55                      60

Pro Thr Leu Gly Asp Ala Gln Ala Ser Gly Met Arg Tyr Arg Asp Arg
      65                      70                      75                      80

Pro Ser Gly Cys Cys Cys Gly Cys His Leu Ile Ser Pro Leu Ile Pro
      85                      90                      95

Arg Glu His Gln
      100

```

<210> 2413

<211> 72

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(72)

<223> Xaa = Any amino acid

<400> 2413

```

Tyr Xaa Gly Ala Lys Xaa Gly Gly Xaa Gly Leu Leu Asn Gly Pro Pro
      5                      10                      15

Gly Gln Val Lys Phe Gln Met Arg Tyr Gly Leu Leu Leu Pro Arg Leu
      20                      25                      30

Met Val Ser Arg Ile Pro Arg Val Ser Pro Ser Ile Pro Gly Val His
      35                      40                      45

Ser Val Leu Pro Leu Arg Val Arg Ile Leu Gly Leu Ile Phe Leu Leu
      50                      55                      60

Pro Val Ala Tyr Leu Val Glu Xaa
      65                      70

```

<210> 2414

<211> 72

<212> PRT

<213> Homo sapiens

<400> 2414

```

Pro His Phe Thr Ile Lys Lys Leu Arg Leu Lys Arg Ile Lys Glu Phe
      5                      10                      15

```


Phe Arg Gly Glu Thr Ala Leu Pro Tyr Arg Arg Ile Pro Ser Asn Lys
 20 25 30
 Cys Glu Cys Ser Leu Ser Arg Arg Trp His Leu Ile Pro Leu Ser Trp
 35 40 45
 Ser Leu Thr Ser Leu Ser Asp Trp Leu Leu Met Asn Lys Met Gly Lys
 50 55 60
 Arg Lys Asn Ser Asn Ser Thr Val
 65 70

<210> 2415
 <211> 76
 <212> PRT
 <213> Homo sapiens

<400> 2415
 Glu Leu Leu Trp Phe Phe Ser Arg Pro Ala Pro Ser Leu Lys Cys Lys
 5 10 15
 Ala Val Pro Leu Met Gly Phe Trp His Ser Val Ser Arg Pro Pro Phe
 20 25 30
 Ser Ser Glu Gly Leu Ser Gly Glu Gln Arg Lys Asn Gln Pro Val Ser
 35 40 45
 Lys Leu Ala Arg Leu Arg Asp Trp Gly Pro Leu Pro Pro Val Lys Asp
 50 55 60
 Ala Asp Phe Thr Ala Leu Gln Tyr Ser Arg Val Lys
 65 70 75

<210> 2416
 <211> 52
 <212> PRT
 <213> Homo sapiens

<400> 2416
 Val Pro Pro Ser Gly Glu Gly Ala Phe Thr Phe Ile Thr Trp Asp Pro
 5 10 15
 Ser Val Arg Lys Ser Cys Phe Ser Ser Lys Lys Leu Phe Asn Pro Phe
 20 25 30
 Lys Pro Gln Phe Leu Asn Cys Glu Met Gly Leu Ile Pro Val Ser Asn
 35 40 45
 Gln Gly Ser Ser
 50

<210> 2417
 <211> 79
 <212> PRT
 <213> Homo sapiens

<400> 2417
 Arg Ser His Leu Thr Leu Leu Tyr Cys Ser Ala Val Lys Ser Ala Ser
 5 10 15

Pro Arg Thr Ser Ala Gly Ala Pro Leu Thr Ser Ile Phe Leu Leu Thr
 35 40 45

Thr Ser Ser Gly Gln Ser Arg Leu Phe Leu Ser Ser Ala His Cys Pro
 50 55 60

Ile Leu Ser Ile Pro Gln Ala Ile Ser Pro Phe Leu Gly Ile Cys Tyr
 65 70 75 80

Gly Ser Thr Pro Leu Pro Gly Thr Lys Thr Ser His Met Ile Met Thr
 85 90 95

Ala Pro His Cys Ser Gly Leu
 100

<210> 2421
 <211> 63
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(63)
 <223> Xaa = Any amino acid

<400> 2421
 Lys Lys Ile Lys Ile Tyr Xaa Val Tyr Xaa Leu Thr Ser Tyr Thr Gln
 5 10 15

Arg Ile Xaa Asp Phe Ser Leu Lys Ile Ile Ile Lys Pro Pro Ile Ser
 20 25 30

Pro Val Glu Lys Glu Ile Leu Arg Phe Xaa Cys Phe Phe Phe Gln His
 35 40 45

Asn Ser Val Thr Tyr Gly Trp Glu Lys Ile Cys Arg Glu Ile Ile
 50 55 60

<210> 2422
 <211> 52
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(52)
 <223> Xaa = Any amino acid

<400> 2422
 Cys Ser Arg Ala Ala Ala Xaa Xaa Xaa Xaa Lys Met Leu Thr Thr Ser
 5 10 15

Pro Xaa Ile Pro Ala Val Val Arg Pro Val Leu Phe Leu Glu Val Pro
 20 25 30

Val Thr Leu Ser Val Thr Thr Leu Leu Cys Trp Ala Pro Arg Pro Leu
 35 40 45

Ser Ser Leu Thr
 50

<210> 2423
<211> 90
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(90)
<223> Xaa = Any amino acid

<400> 2423
Gly Arg Xaa Xaa Xaa Leu Thr Leu Thr Arg Thr Val Thr Arg Cys Ser
 5 10 15
Ser Gly Arg Lys Ser Ser Trp Phe Pro Ser Gly Pro Gly Val Met Gln
 20 25 30
Gln Ser Ser Ser Xaa Tyr Xaa Xaa Xaa Asp Val Asp His Gln Pro Xaa
 35 40 45
Asp Ser Arg Ser Gly Lys Ala Cys Ser Val Pro Gly Ser Ser Cys Asn
 50 55 60
Ile Glu Cys His His Phe Thr Val Leu Gly Pro Gln Ala Ile Val Lys
 65 70 75 80
Pro His Met Ser Ser Phe Gln Asn Xaa Leu
 85 90

<210> 2424
<211> 56
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(56)
<223> Xaa = Any amino acid

<400> 2424
Ser Gly Asp Thr Gln Cys Tyr Arg Asn Phe Gln Glu Gln Asn Arg Pro
 5 10 15
Tyr His Cys Gly Asn Xaa Gly Ala Gly Gly Gln His Leu Xaa Xaa Xaa
 20 25 30
Xaa Cys Cys Cys Ser Ala Ala Leu Arg Gln Gly Pro Lys Glu Thr Arg
 35 40 45
Arg Thr Phe Cys His Trp Asn Ile
 50 55

<210> 2425
<211> 91
<212> PRT
<213> Homo sapiens

<220>
<221> variant

```
<210> 2426
<211> 78
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> variant
<222> (1)...(78)
<223> Xaa = Any amino acid
```

```

<400> 2426
Ser Pro Leu Arg Asn Pro Gly Asp Val Leu Gly Pro Gly Val Gly Ala
          5                               10                      15

Pro Cys His Trp Ile Arg Lys Pro Ala Ser Gln Gly Phe Asn Trp Glu
          20                               25                      30

Thr Gly Asp Ser Pro Ala Gly Pro Cys Ile Leu Val Arg Leu Arg Met
          35                               40                      45

Arg Thr Cys Glu Thr Lys Ala Ser Arg Tyr Gly Leu Gly Gln Xaa Lys
          50                               55                      60

Ser Ser Thr Ser Met Leu Leu Leu Pro Lys Gly Asn Phe Ala
          65                               70                      75

```

```
<210> 2427
<211> 64
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> variant
<222> (1)...(64)
<223> Xaa = Any amino acid
```

<400> 2427
Ser Gly Arg Phe Xaa Leu Pro Gln Thr Ile Ser Thr Gly Leu Cys Phe
 5 10 15

Thr Cys Pro His Ser Gln Ser Asp Gln Asn Ala Gly Pro Cys Trp Thr
 20 25 30
 Val Thr Cys Phe Pro Val Lys Ala Leu Thr Gly Arg Phe Ser Asn Pro
 35 40 45
 Val Ala Arg Cys Ser His Ser Arg Ala Gln His Ile Ser Trp Ile Pro
 50 55 60

<210> 2428
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(51)
 <223> Xaa = Any amino acid

<400> 2428
 Ala Lys Phe Pro Leu Gly Arg Ser Ser Ile Glu Val Glu Asp Leu Xaa
 5 10 15
 Cys Pro Arg Pro Tyr Leu Leu Ala Phe Val Ser His Val Leu Ile Leu
 20 25 30
 Ser Leu Thr Arg Met Gln Gly Pro Ala Gly Leu Ser Pro Val Ser Gln
 35 40 45
 Leu Lys Pro
 50

<210> 2429
 <211> 79
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(79)
 <223> Xaa = Any amino acid

<400> 2429
 Ile Xaa His Trp Gln Gly Ser Leu Gly Ala Ile Leu Gly Ser Cys Val
 5 10 15
 Asn Glu Gln Met Asn Ala Gln Asp Arg Ile Leu Ala Val Thr Met Met
 20 25 30
 Leu Glu Val Thr Tyr Pro Thr Val Leu Leu Ser Phe Ser Pro Asn Pro
 35 40 45
 Pro Leu Leu Pro Gly Lys Lys Pro Ser Ser Leu Cys Leu Ile Thr Phe
 50 55 60
 Ser Thr Gln His Leu Gln Gly Thr Tyr Ser Ala Val Gly Gln Cys
 65 70 75

<210> 2430

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<211> 67
<212> PRT
<213> Homo sapiens
```

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<400> 2430
Pro Arg Leu Ala Cys Ser Leu Phe Pro Ser Pro Gly Ile Gly Ser Leu
          5                      10                      15

Gly Leu Lys His Arg Ala Lys Phe Ser Arg Ile Asn Ile Pro Asp Ser
          20                      25                      30

Ser His Gly Leu Gly Leu Gly Ala Gly Met Lys Gly Glu Pro Gly Ser
          35                      40                      45

Ile Leu Asp Cys Leu Trp Leu Glu Gly Leu Gly Pro Trp His Gln Asp
          50                      55                      60

Leu His Phe
          65

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<210> 2431
<211> 70
<212> PRT
<213> Homo sapiens
```

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<400> 2431
Arg Ser Trp Cys Gln Gly Pro Arg Pro Ser Asn His Lys Gln Ser Arg
          5                      10                      15

Met Glu Pro Gly Ser Pro Phe Ile Pro Ala Pro Ser Pro Arg Pro Trp
          20                      25                      30

Glu Leu Ser Gly Met Leu Ile Leu Glu Asn Leu Ala Leu Cys Phe Arg
          35                      40                      45

Pro Lys Asp Pro Ile Pro Gly Leu Gly Lys Arg Glu Gln Ala Ser Arg
          50                      55                      60

Gly Tyr Leu Pro Pro Gly
          65          70

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<210> 2432
<211> 56
<212> PRT
<213> Homo sapiens
```

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<220>
<221> variant
<222> (1)...(56)
<223> Xaa = Any amino acid
```

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<400> 2432
Leu His Ile Cys Ser Asp Asp Lys Cys Leu Gln Pro Cys Pro Leu Gln
          5                      10                      15

Gly Cys Thr Gly Leu His Thr Gly Ser Cys Leu Arg Cys Leu Val Ser
          20                      25                      30

Ser Leu Lys Gly Trp Gly Ser Gly Val Ser Pro Val Tyr Leu Gly Lys
          35                      40                      45

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Xaa Leu Thr Leu Gly Xaa Met Lys
50 55

<210> 2433
<211> 50
<212> PRT
<213> Homo sapiens

<400> 2433
Lys Ser Gly Leu Gly Gly Asn Ala Phe Leu Leu Leu His Val Tyr Phe
5 10 15
Ser Cys Ile Ser Val Val Met Thr Asn Ala Ser Ser Leu Val Leu Cys
20 25 30
Lys Ala Ala Leu Gly Cys Ile Gln Ala Pro Val Ser Gly Val Trp Phe
35 40 45
Pro Pro
50

<210> 2434
<211> 58
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(58)
<223> Xaa = Any amino acid

<400> 2434
Phe His Xaa Ser Lys Cys Gln Xaa Leu Ala Gln Ile Asp Arg Ala Asp
5 10 15
Ser Ala Ala Pro Thr Phe Gln Gly Gly Asn Gln Thr Pro Glu Thr Gly
20 25 30
Ala Cys Met Gln Pro Ser Ala Ala Leu Gln Arg Thr Arg Leu Glu Ala
35 40 45
Phe Val Ile Thr Thr Asp Met Gln Leu Lys
50 55

<210> 2435
<211> 78
<212> PRT
<213> Homo sapiens

<400> 2435
Tyr Leu Pro Ala Ser Leu Ser Phe Thr Ala Gly Ile Ser Ser Ser Ala
5 10 15
Asp Arg Glu Arg Trp Val Phe Phe Pro Ile Leu Val Pro Val Ala Ser
20 25 30
Leu Tyr Gln Glu Asn Val Thr Phe Pro Val Pro Pro Ala Thr Glu Gln
35 40 45
Ser Arg Ile Ser Phe Cys Pro Ser Val Thr Cys Pro Pro Gly Ala Arg

50 55 60
Ile Ser Lys Leu Thr Leu Glu Met Gly Ile Pro Arg Trp Ile
65 70 75
<210> 2436
<211> 50
<212> PRT
<213> Homo sapiens
<400> 2436
Arg Thr Lys Thr Asp Pro Ala Leu Leu Ser Gly Trp Gly Tyr Arg Lys
5 10 15
Cys His Ile Leu Leu Val Gln Arg Gly His Arg Asn Gln Tyr Gly Lys
20 25 30
Glu Asn Pro Ala Phe Pro Val Ser Arg Ala Gly Asp Pro Ser Cys Glu
35 40 45
Arg Glu
50
<210> 2437
<211> 117
<212> PRT
<213> Homo sapiens
<400> 2437
Ser Ser His Leu Leu Ser Tyr Ile His Leu Gly Ile Pro Ile Ser Asn
5 10 15
Val Ser Leu Glu Ile Arg Ala Pro Gly Gly Gln Val Thr Glu Gly Gln
20 25 30
Lys Leu Ile Leu Leu Cys Ser Val Ala Gly Gly Thr Gly Asn Val Thr
35 40 45
Phe Ser Trp Tyr Arg Glu Ala Thr Gly Thr Ser Met Gly Lys Lys Thr
50 55 60
Gln Arg Ser Leu Ser Ala Glu Leu Glu Ile Pro Ala Val Lys Glu Ser
65 70 75 80
Asp Ala Gly Lys Tyr Tyr Cys Arg Ala Asp Asn Gly His Val Pro Ile
85 90 95
Gln Ser Lys Val Val Asn Ile Pro Val Arg Arg Pro Asp Gly Tyr Arg
100 105 110
Arg Asp Leu Met Thr
115
<210> 2438
<211> 54
<212> PRT
<213> Homo sapiens
<400> 2438
Tyr Leu Cys Thr Tyr Leu Asn Phe Gly Leu Phe Tyr Ser Ser Lys Thr

5 10 15
 Ile Thr Phe Leu Gly Phe His Lys Cys Ser Pro Phe Leu Ser Gln Phe
 20 25 30
 Gln Thr Met Tyr Ser Lys Gln Gly Lys Glu Ser Ser Gln Glu Phe Leu
 35 40 45
 Gly Gly Pro Ala Arg Ala
 50

<210> 2439
 <211> 58
 <212> PRT
 <213> Homo sapiens

<400> 2439
 Pro Asp Thr Asp Ile Cys Ala Leu Thr Leu Thr Leu Val Tyr Phe Ile
 5 10 15
 His Pro Lys Pro Leu His Phe Leu Val Phe Thr Asn Val Pro His Phe
 20 25 30
 Leu Ala Ser Ser Arg Gln Cys Ile Ala Ser Arg Gly Arg Lys Ala Val
 35 40 45
 Arg Ser Ser Trp Val Asp Leu Pro Gly Arg
 50 55

<210> 2440
 <211> 70
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(70)
 <223> Xaa = Any amino acid

<400> 2440
 Val Arg Gly Glu Gly Gly Xaa Thr Gly Leu Gly Ile Ser Ala Val Trp
 5 10 15
 Glu Met Arg Ser Ile Ser His His His His Leu Cys Tyr Xaa His Val
 20 25 30
 Ser Ala Cys Gln Arg Ala Thr Leu Ser Leu Pro Gln Val Gly Gly Phe
 35 40 45
 Ile Xaa Gln Ser Val Phe Phe Met Tyr Arg Ser Phe His Ser Ser Thr
 50 55 60
 Leu Xaa Leu Xaa Ser Leu
 65 70

<210> 2441
 <211> 111
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(111)
 <223> Xaa = Any amino acid

<400> 2441
 Phe Gly Glu Arg Val Val Xaa Gln Gly Leu Gly Tyr Arg Gln Cys Gly
 5 10 15
 Lys Cys Glu Ala Phe Leu Ile Ile Ile Ile Ser Ala Thr Xaa Met Phe
 20 25 30
 Leu His Val Ser Glu Arg His Cys Pro Cys Leu Arg Leu Glu Val Leu
 35 40 45
 Ser Xaa Lys Val Phe Phe Ser Cys Ile Val Arg Ser Ile His Pro Leu
 50 55 60
 Xaa Xaa Leu Xaa Ala Phe Glu Arg Leu Gly Cys Ser Gln Ala Ala Val
 65 70 75 80
 Leu Arg Asp Leu Lys Arg Asp Leu Val Ser Leu Gly Ala Glu Ser Ile
 85 90 95
 Tyr Leu Gly Thr Leu Phe Gln Glu Arg Pro Cys Leu His Phe His
 100 105 110

<210> 2442
 <211> 53
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(53)
 <223> Xaa = Any amino acid

<400> 2442
 Asp Asn Ala Ser Cys Val Cys Ser Gly Arg Ser Ser Lys Trp Asn Ala
 5 10 15
 Cys Cys Thr Xaa Pro Xaa Arg Val Xaa Ala Met Arg Pro Xaa Asp His
 20 25 30
 Thr Trp Gly Thr Asn His Xaa Leu Xaa His Xaa Ala Leu Glu Ser Pro
 35 40 45
 Leu Asp Arg Val Pro
 50

<210> 2443
 <211> 138
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(138)
 <223> Xaa = Any amino acid

<400> 2443

Ser Gly Arg Gly Trp Xaa His Arg Ala Trp Asp Ile Gly Ser Val Gly
 5 10 15
 Asn Ala Lys His Phe Ser Ser Ser Ser Ser Leu Leu Gln Xaa Cys Phe
 20 25 30
 Cys Met Ser Ala Ser Asp Thr Val Pro Ala Ser Gly Trp Arg Phe Tyr
 35 40 45
 Xaa Pro Lys Cys Phe Phe His Val Ser Phe Val Pro Phe Ile His Ser
 50 55 60
 Xaa Pro Xaa Gln Pro Leu Lys Gly Leu Val Ala Pro Arg Leu Leu Phe
 65 70 75 80
 Ser Gly Thr Leu Lys Gly Thr Trp Leu Val Leu Gly Gln Arg Val Ser
 85 90 95
 Thr Trp Ala Leu Ser Ser Lys Lys Asp Leu Val Ser Ile Phe Ile Arg
 100 105 110
 Thr Met Leu Leu Val Cys Val Leu Glu Asp Leu Leu Asn Gly Met Leu
 115 120 125
 Val Ala Leu Xaa Pro Xaa Glu Trp Xaa Pro
 130 135

<210> 2444
 <211> 101
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(101)
 <223> Xaa = Any amino acid

<400> 2444
 Gly Xaa Val Xaa Lys Xaa Met Ile Gly Pro Pro Ser Val Val Xaa Arg
 5 10 15
 Ser His Gly Xaa His Ser Xaa Gly Xaa Ser Ala Thr Ser Ile Pro Phe
 20 25 30
 Arg Arg Ser Ser Arg Thr His Thr Arg Ser Ile Val Leu Met Lys Met
 35 40 45
 Glu Thr Arg Ser Phe Leu Glu Glu Ser Ala Gln Val Asp Thr Leu Cys
 50 55 60
 Pro Lys Thr Asn Gln Val Pro Phe Lys Val Pro Glu Asn Ser Ser Leu
 65 70 75 80
 Gly Ala Thr Lys Pro Phe Lys Gly Xaa Gln Xaa Xaa Glu Trp Met Asn
 85 90 95
 Gly Thr Asn Asp Thr
 100

<210> 2445
 <211> 61

<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(61)
<223> Xaa = Any amino acid

<400> 2445
Met Glu Arg Thr Ile His Glu Lys Asn Thr Leu Xaa Asp Lys Thr Ser
 5 10 15

Asn Leu Arg Gln Gly Gln Cys Arg Ser Leu Thr Cys Arg Asn Met Xaa
 20 25 30

Val Ala Glu Met Met Met Met Arg Asn Ala Ser His Phe Pro His Cys
 35 40 45

Arg Tyr Pro Lys Pro Cys Xaa Thr Thr Leu Ser Pro Asn
 50 55 60

<210> 2446
<211> 196
<212> PRT
<213> Homo sapiens

<400> 2446
Asp Asn Val His Ser Pro Ile Leu Ser Thr Trp Ile Arg Val Thr Val
 5 10 15

Arg Ile Pro Val Ser His Pro Val Leu Thr Phe Arg Ala Pro Arg Ala
 20 25 30

His Thr Val Val Gly Asp Leu Leu Glu Leu His Cys Glu Ser Leu Arg
 35 40 45

Gly Ser Pro Pro Ile Leu Tyr Arg Phe Tyr His Glu Asp Val Thr Leu
 50 55 60

Gly Asn Ser Ser Ala Pro Ser Gly Gly Gly Ala Ser Phe Asn Leu Ser
 65 70 75 80

Leu Thr Ala Glu His Ser Gly Asn Tyr Ser Cys Asp Ala Asp Asn Gly
 85 90 95

Leu Gly Ala Gln His Ser His Gly Val Ser Leu Arg Val Thr Val Pro
 100 105 110

Val Ser Arg Pro Val Leu Thr Leu Arg Ala Pro Gly Ala Gln Ala Val
 115 120 125

Val Gly Asp Pro Leu Glu Leu His Cys Glu Ser Leu Arg Gly Ser Phe
 130 135 140

Pro Ile Leu Tyr Trp Phe Tyr His Glu Asp Asp Thr Leu Gly Asn Ile
 145 150 155 160

Ser Ala His Ser Gly Gly Gly Ala Ser Phe Asn Leu Ser Leu Thr Thr
 165 170 175

Glu His Ser Gly Asn Tyr Ser Cys Glu Ala Asp Asn Gly Leu Gly Pro
 180 185 190

Ser Thr Val Lys
195

<210> 2447
<211> 114
<212> PRT
<213> Homo sapiens

<400> 2447
Val Val Ser Arg Met Phe Cys Ser Gln Arg Glu Val Glu Gly Cys Pro
5 10 15
Ser Ser Arg Val Gly Arg Asp Val Pro Gln Gly Val Ile Leu Val Ile
20 25 30
Lys Pro Val Gln Asp Arg Glu Gly Ala Ser Gln Gly Leu Thr Val Lys
35 40 45
Leu Gln Arg Val Pro His His Ser Leu Gly Pro Gly Ser Pro Glu Gly
50 55 60
Glu Asp Gly Ala Arg His Arg Asn Cys Asp Pro Glu Thr His Ser Met
65 70 75 80
Thr Val Leu Gly Pro Gln Ala Ile Val Cys Ile Thr Gly Val Val Ser
85 90 95
Arg Met Phe Cys Ser Gln Arg Glu Val Glu Gly Gly Ser Ser Ser Arg
100 105 110
Gly Gly

<210> 2448
<211> 67
<212> PRT
<213> Homo sapiens

<400> 2448
Ala Val Pro Gln Gly Asp Ile Leu Met Ile Lys Ser Val Gln Asp Arg
5 10 15
Gly Arg Ala Ser Gln Gly Leu Thr Val Lys Leu Gln Gln Val Pro His
20 25 30
His Ser Val Gly Pro Gly Ser Pro Glu Gly Glu Asp Arg Val Arg Tyr
35 40 45
Arg Asn Ser His Gly Asp Ser Asn Pro Arg Ala Glu Asp Gly Ala Val
50 55 60
Asn Val Ile
65

<210> 2449
<211> 65
<212> PRT
<213> Homo sapiens

<400> 2449

Gln Ser Ala Gly Tyr Ile Ile Gly Thr Lys Gly Leu Phe Gln Phe Leu
5 10 15

Val Asn Pro Leu Gln Gln Ala Pro Pro Asp Asp Val Leu Ile Asp Ala
20 25 30

Leu Ser Gly Gln Ser Leu Ala Ala His Gly Lys Asp Ile Pro Leu Glu
35 40 45

Leu Arg Gln Leu Leu Phe Ala Ala Trp Leu Glu Leu Ala Gln His Lys
50 55 60

Arg
65

<210> 2450

<211> 50

<212> PRT

<213> Homo sapiens

<400> 2450

Lys Asp Ala Glu Thr Pro Ala Ser Asp Glu Pro Pro Leu Arg Gln Pro
5 10 15

Ala Val Arg Phe Glu Phe Leu Gln His Ala Pro Pro Asp Ser Leu Gln
20 25 30

Pro Leu Gly Ser Leu Val Thr Val Glu Gly Arg Arg Gln Thr Leu Val
35 40 45

Ser Gln
50

<210> 2451

<211> 85

<212> PRT

<213> Homo sapiens

<400> 2451

Met Pro Ser Val Val Arg Ala Trp Leu Pro Thr Ala Arg Thr Ser Pro
5 10 15

Ser Asn Ser Gly Ser Ser Phe Leu Gln Pro Gly Ser Ser Trp Leu Ser
20 25 30

Thr Lys Gly Lys Lys Met Gln Arg Pro Gln Pro Arg Met Asn Leu Leu
35 40 45

Cys Ala Asn Pro Leu Ser Asp Leu Asn Phe Phe Ser Thr Arg Pro Leu
50 55 60

Thr Leu Ser Ser Leu Trp Ala Ala Trp Ser Gln Leu Arg Ala Val Val
65 70 75 80

Arg His Trp Ser Ala
85

<210> 2452

<211> 116

<212> PRT

<213> Homo sapiens

<400> 2452

Leu Ala Asp Gln Cys Leu Thr Thr Ala Leu Asn Cys Asp Gln Ala Ala
5 10 15

Gln Arg Leu Glu Arg Val Arg Gly Arg Val Leu Lys Lys Phe Lys Ser
20 25 30

Asp Ser Gly Leu Ala Gln Arg Arg Phe Ile Arg Gly Trp Gly Leu Cys
35 40 45

Ile Phe Leu Pro Phe Val Leu Ser Gln Leu Glu Pro Gly Cys Lys Lys
50 55 60

Glu Leu Pro Glu Phe Glu Gly Asp Val Leu Ala Val Gly Ser Gln Ala
65 70 75 80

Leu Thr Thr Glu Gly Ile Tyr Glu Asp Val Ile Arg Gly Cys Leu Leu
85 90 95

Gln Arg Ile Asp Gln Glu Leu Lys Lys Thr Leu Gly Ala Asn Asp Val
100 105 110

Ser Cys Thr Leu
115

<210> 2453

<211> 54

<212> PRT

<213> Homo sapiens

<400> 2453

Pro Gly Cys Pro Glu Ala Gly Glu Ser Gln Gly Ala Arg Ala Glu Glu
5 10 15

Ile Gln Ile Gly Gln Arg Val Gly Ala Glu Glu Val His Pro Arg Leu
20 25 30

Gly Ser Leu His Leu Phe Thr Phe Cys Ala Glu Pro Thr Arg Ala Arg
35 40 45

Leu Gln Lys Gly Ala Ala
50

<210> 2454

<211> 50

<212> PRT

<213> Homo sapiens

<400> 2454

Ile Ser Lys Ser Ile Val Phe Glu Phe Val Cys Ser Ser Leu Ser Leu
5 10 15

Leu Val Ile Val Val Phe Cys Phe Leu Phe Cys Phe Gln Cys Lys Cys
20 25 30

Asp Val Ile Phe Leu Phe Ser Leu Asp Gln Ser Trp Thr Gly Asn Cys
35 40 45

Ile Val
50

<210> 2455
<211> 53
<212> PRT
<213> Homo sapiens

<400> 2455
Pro Leu Asp Gly Trp Gly Phe Thr Arg Glu Thr Asp Thr Pro Gly Ser
5 10 15
Ile Leu Lys Thr Leu Ser Gly Phe Pro Gly Gln Gln Ser Ser Leu Ile
20 25 30
Leu Ser Ser Ala Ser Glu Ala Asn Leu Thr Ser Met Cys Ser Ser Ser
35 40 45
Ser Glu Leu Val Arg
50

<210> 2456
<211> 81
<212> PRT
<213> Homo sapiens

<400> 2456
Thr Ile Phe Ser Ile Ser Thr Ala Phe Ser Ser Asn Ser Asn Cys Lys
5 10 15
Ser Arg Ile Arg Gly Pro Ile Phe Ser Arg Phe Ser Leu Ile Met Ala
20 25 30
Thr Asn Gly Met Thr Phe Phe Met Tyr Phe Phe Ser Ser Gly Ile Leu
35 40 45
Leu Ser Ser Leu Ala Met Thr Leu Leu Ser Gly Ser Phe Pro Leu Leu
50 55 60
Ala Ser Lys Cys Leu Arg Arg Thr Asp Arg Val Val Cys Cys Gln Gly
65 70 75 80
Gly

<210> 2457
<211> 50
<212> PRT
<213> Homo sapiens

<400> 2457
Leu Cys Cys Gln Ala Val Phe Arg Tyr Trp Pro Gln Ser Val Tyr Val
5 10 15
Glu Gln Thr Gly Trp Tyr Val Ala Lys Val Asp Ser Ser Leu Pro His
20 25 30
Arg Trp Cys Asn Val Arg Ala Ser Ala Gly Val Val Cys Gln Ser Ser
35 40 45

Ser Leu
50

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<210> 2458
<211> 193
<212> PRT
<213> Homo sapiens
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<220>
<221> variant
<222> (1)...(193)
<223> Xaa = Any amino acid
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<400> 2458																
Pro	Val	Ala	Gly	Pro	Val	Asn	Glu	Val	Leu	Ile	His	Ser	Xaa	Gln	Tyr	
5				10				15								
Leu	Met	Glu	Val	Thr	His	Asp	Leu	Arg	Leu	Arg	Leu	Lys	Asn	Tyr	Met	
20				25				30								
Met	Pro	Ala	Lys	Gly	Lys	Lys	Thr	Asp	Lys	Gln	Pro	Leu	Gln	Lys	Pro	
35				40				45								
Ser	His	Cys	Thr	Ile	Tyr	Val	Ala	Lys	Asn	Tyr	Pro	Pro	Trp	Gln	His	
50				55				60								
Thr	Thr	Leu	Ser	Val	Leu	Arg	Lys	His	Phe	Glu	Ala	Asn	Asn	Gly	Lys	
65				70				75				80				
Leu	Pro	Asp	Asn	Lys	Val	Ile	Ala	Ser	Glu	Leu	Ser	Ser	Met	Pro	Glu	
85				90				95								
Leu	Lys	Lys	Tyr	Met	Lys	Lys	Val	Met	Pro	Phe	Val	Ala	Met	Ile	Lys	
100				105				110								
Glu	Asn	Leu	Glu	Lys	Met	Gly	Pro	Arg	Ile	Leu	Asp	Leu	Gln	Leu	Glu	
115				120				125								
Phe	Asp	Glu	Lys	Ala	Val	Leu	Met	Glu	Asn	Ile	Val	Tyr	Leu	Thr	Asn	
130				135				140								
Ser	Leu	Glu	Leu	Glu	His	Ile	Glu	Val	Lys	Phe	Ala	Ser	Glu	Ala	Glu	
145				150				155				160				
Asp	Lys	Ile	Arg	Glu	Asp	Cys	Cys	Pro	Gly	Lys	Pro	Leu	Asn	Val	Phe	
165				170				175								
Arg	Ile	Glu	Pro	Gly	Val	Ser	Val	Ser	Leu	Val	Asn	Pro	Gln	Pro	Ser	
180				185				190								

Asn

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<210> 2459
<211> 58
<212> PRT
<213> Homo sapiens
```

<400> 2459
Cys Gln Leu Lys Gly Arg Arg Leu Thr Asn Asn Pro Cys Arg Ser Pro
 5 10 15

His Ile Ala Pro Ser Met Trp Gln Arg Thr Ile His Leu Gly Asn Ile
 20 25 30

Pro Pro Cys Leu Phe Tyr Val Asn Thr Leu Arg Pro Ile Thr Glu Asn
 35 40 45

Cys Leu Thr Thr Lys Ser Leu Leu Val Asn
 50 55

<210> 2460
 <211> 109
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(109)
 <223> Xaa = Any amino acid

<400> 2460
 Asn Gly Val Ala Ala Lys Val Ala Ser Phe Ser Phe Phe Gln Asn Ala
 5 10 15

Gln Met His Gln Phe Leu Asn Ile His Val Lys Phe Glu Asn Cys Thr
 20 25 30

Phe Gly Glu Ile Lys Phe Tyr Ile Gln Leu Ala Ile Val Gln Leu Cys
 35 40 45

Cys Ser Phe Ser Ile Lys Ala Lys Val Phe Asn Met Arg Lys Cys Asp
 50 55 60

Thr Phe Asp Thr Val Trp Gly Gly Ser Gly Trp Ala Ala Leu Gly Gly
 65 70 75 80

Thr Gly Pro Xaa Thr Arg Leu Cys Pro Pro Arg Ile His Ala Gly Arg
 85 90 95

Arg Glu Ala Glu Val Ser Asn Xaa Thr Ser His Gln Ala
 100 105

<210> 2461
 <211> 51
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(51)
 <223> Xaa = Any amino acid

<400> 2461
 Pro Leu Gly Glu Arg Xaa Gly Leu Ile Pro Leu Pro Pro Ser Cys Gln
 5 10 15

His Gly Phe Trp Val Asp Thr Ala Leu Xaa Lys Val Gln Tyr His Gln
 20 25 30

Glu Leu Pro Ile His Ser His Pro Thr Leu Tyr Gln Met Tyr His Ile
 35 40 45

Phe Ser Cys
50

<210> 2462
<211> 51
<212> PRT
<213> Homo sapiens

<400> 2462
Leu Tyr Ile Lys Phe Asn Leu Thr Glu Cys Thr Val Phe Lys Phe His
5 10 15
Val Tyr Ile Lys Glu Leu Met His Leu Ser Ile Leu Lys Glu Arg Lys
20 25 30
Arg Ser Tyr Phe Ser Cys His Pro Ile Leu Glu Lys Ser Leu Ile Phe
35 40 45
Lys Leu Phe
50

<210> 2463
<211> 67
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(67)
<223> Xaa = Any amino acid

<400> 2463
Glu Xaa Trp Phe Asp Thr Ser Ala Ser Leu Leu Pro Ala Trp Ile Leu
5 10 15
Gly Gly His Ser Leu Val Xaa Gly Pro Val Pro Pro Arg Ala Ala His
20 25 30
Pro Leu Pro Pro His Thr Val Ser Asn Val Ser His Phe Leu Met Leu
35 40 45
Asn Thr Leu Ala Leu Ile Glu Asn Glu Gln Gln Ser Trp Thr Ile Ala
50 55 60
Ser Cys Ile
65

<210> 2464
<211> 82
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(82)
<223> Xaa = Any amino acid

<400> 2464
Ala Asp Ser Gln Asn Thr Phe Xaa Ile Pro Glu Ile Arg Lys Ile Asn

5 10 15
 Asp Lys Ile Ser Val Ser Gln Ala Thr Asn Arg Cys Lys Ile Met Lys
 20 25 30
 Gly Val Val Gly Cys Ala Lys Phe Gly Lys Val Val Thr Ala Ser Glu
 35 40 45
 Lys Glu Ala Val Arg Leu Asn Ser Trp Trp Leu Pro Ser Val Thr Ser
 50 55 60
 Arg Gly Ser Leu Gln His Arg Pro Arg Ala Arg Arg Asn Thr Val Ala
 65 70 75 80
 Pro Met

<210> 2465
 <211> 65
 <212> PRT
 <213> Homo sapiens

<400> 2465
 Phe Leu Ala Phe Leu Ser Ala Leu Leu Pro Ser Gln Glu Pro Gly Asp
 5 10 15
 Ala Lys His Pro Glu Cys Asp Gly Thr Arg Trp Gly Gln Gly Pro His
 20 25 30
 Leu Pro Ala Glu Val Arg Pro Gly Leu Leu Val Pro Gly Gln Ser Pro
 35 40 45
 Glu Pro Leu Cys Leu Val Glu Gln Ala Pro Val Cys Arg Ile Pro Thr
 50 55 60
 Val
 65

<210> 2466
 <211> 81
 <212> PRT
 <213> Homo sapiens

<400> 2466
 His Leu Cys Arg Lys Cys Val Glu Phe Ser Val Phe Phe Leu Cys Asp
 5 10 15
 Phe Trp Pro Phe Tyr Gln His Phe Ser Pro Pro Arg Ser Leu Gly Met
 20 25 30
 Pro Asn Ile Gln Asn Val Met Gly Gln Asp Gly Gly Arg Gly Leu Thr
 35 40 45
 Ser Leu Gln Arg Ser Gly Gln Val Ser Leu Ser Leu Asp Asn Leu Leu
 50 55 60
 Ser Leu Ser Ala Trp Trp Ser Arg His Leu Cys Ala Glu Phe Pro Leu
 65 70 75 80
 Trp

<210> 2467
<211> 79
<212> PRT
<213> Homo sapiens

<400> 2467
Pro Gln Trp Glu Phe Cys Thr Gln Val Pro Ala Pro Pro Ser Arg Glu
 5 10 15
Ala Gln Glu Ile Val Gln Gly Gln Gly Asp Leu Ala Gly Pro Leu Gln
 20 25 30
Gly Gly Glu Ala Pro Ala Pro Ile Leu Ser His His Ile Leu Asp Val
 35 40 45
Trp His Pro Gln Ala Pro Gly Arg Gly Glu Val Leu Ile Lys Arg Pro
 50 55 60
Lys Ile Thr Gln Lys Glu Asp Arg Lys Leu His Ala Leu Pro Thr
 65 70 75

<210> 2468
<211> 50
<212> PRT
<213> Homo sapiens

<400> 2468
Val Leu Pro Tyr Ser Tyr Glu His Gly Ala Cys Val Glu Asp Ser Leu
 5 10 15
Trp Lys Leu Gln Lys Glu Ala Thr Lys Ser Ser Ala Ser Gln Pro Leu
 20 25 30
Ser Gln Met Gln Ser Pro Leu Tyr Gln Thr Trp His Ile Gln Pro Leu
 35 40 45
Leu Ser
 50

<210> 2469
<211> 59
<212> PRT
<213> Homo sapiens

<400> 2469
His Ser Gly Asn Ser Ala His Arg Cys Leu Leu His Gln Ala Glu Arg
 5 10 15
Leu Arg Arg Leu Ser Arg Asp Lys Glu Thr Trp Pro Asp Leu Cys Arg
 20 25 30
Glu Val Arg Pro Leu Pro Pro Ser Cys Pro Ile Thr Phe Trp Met Phe
 35 40 45
Gly Ile Pro Arg Leu Leu Gly Gly Glu Lys Cys
 50 55

<210> 2470

<211> 107
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(107)
 <223> Xaa = Any amino acid

<400> 2470
 Lys Gly Gln Lys Ser His Arg Lys Lys Thr Glu Asn Ser Thr His Phe
 5 10 15
 Leu His Arg Cys Tyr Arg Ile Pro Thr Ser Thr Gly Pro Val Leu Lys
 20 25 30
 Thr Pro Ser Gly Ser Tyr Arg Arg Lys Pro Pro Arg Val Gln Pro His
 35 40 45
 Ser Leu Phe Leu Arg Cys Ser His His Phe Thr Lys Leu Gly Thr Ser
 50 55 60
 Asn His Ser Phe His Asn Phe Thr Pro Val Cys Gly Leu Ala Asp Arg
 65 70 75 80
 Tyr Phe Val Ile Asp Leu Ser Asn Phe Arg Asp Xaa Lys Cys Val Leu
 85 90 95
 Arg Ile Cys Ser Ala Leu Arg Asp Ser Val Phe
 100 105

<210> 2471
 <211> 57
 <212> PRT
 <213> Homo sapiens

<400> 2471
 Gly Pro Cys Pro His Leu Val Pro Ser His Ser Gly Cys Leu Ala Ser
 5 10 15
 Pro Gly Ser Trp Glu Gly Arg Ser Ala Asp Lys Lys Ala Lys Asn His
 20 25 30
 Thr Glu Arg Arg Gln Lys Thr Pro Arg Thr Ser Tyr Ile Gly Ala Thr
 35 40 45
 Val Phe Leu Arg Ala Arg Gly Leu Cys
 50 55

<210> 2472
 <211> 64
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(64)
 <223> Xaa = Any amino acid

<400> 2472
 Arg Leu Pro Leu Glu Val Thr Glu Gly Ser His Gln Glu Phe Ser Leu

5 10 15
 Thr Ala Ser Phe Ser Asp Ala Val Thr Thr Leu Pro Asn Leu Ala His
 20 25 30
 Pro Thr Thr Pro Phe Ile Ile Leu His Leu Phe Val Ala Trp Leu Thr
 35 40 45
 Asp Ile Leu Ser Leu Ile Phe Leu Ile Ser Gly Ile Xaa Asn Val Phe
 50 55 60

<210> 2473
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 2473
 Val Arg Arg Ser Ser Ser Val Ala Gln Val Lys Ala Met Ile Glu Thr
 5 10 15
 Lys Thr Gly Ile Ile Pro Glu Thr Gln Ile Val Thr Cys Asn Gly Lys
 20 25 30
 Arg Leu Glu Asp Gly Lys Met Met Ala Asp Tyr Gly Ile Arg Lys Gly
 35 40 45
 Asn Leu Leu Phe Leu Ala Cys Tyr Cys Ile Gly Gly
 50 55 60

<210> 2474
 <211> 74
 <212> PRT
 <213> Homo sapiens

<400> 2474
 Asp Pro Asp Cys Asp Leu Gln Trp Lys Glu Thr Gly Arg Trp Glu Asp
 5 10 15
 Asp Gly Arg Leu Arg His Gln Lys Gly Gln Leu Thr Leu Pro Gly Met
 20 25 30
 Leu Leu Tyr Trp Arg Val Thr Thr Leu Gly Met Gly Cys Trp Gln Gly
 35 40 45
 Ser Lys Ser Leu Phe Leu Leu Ile Ser Tyr Ser Thr Asn Thr Ser Ser
 50 55 60
 Asp Asp Phe Pro Lys Leu Met Arg Met Arg
 65 70

<210> 2475
 <211> 74
 <212> PRT
 <213> Homo sapiens

<400> 2475
 Leu Ile Val Leu Glu Ser Lys Lys His Arg Val Gly Gln Tyr Thr Ser
 5 10 15
 Ser Tyr Pro Ser His Pro Asn Leu Thr Leu Leu Ile Ser Phe Ser Leu

20 25 30
 Ile Leu Gly Asn His Gln Lys Met Cys Ser Leu Ser Lys Arg Leu Lys
 35 40 45
 Glu Ile Ser Phe Leu Ile Pro Ala Asn Thr Pro Cys Pro Gly Trp Ser
 50 55 60
 Pro Ser Asn Thr Ile Thr Cys Gln Glu Glu
 65 70

<210> 2476
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 2476
 Leu Leu Trp Pro Cys Pro Glu Thr Thr Pro Asn Ser Trp Leu Val Met
 5 10 15
 Arg Gly Gly Glu Tyr Ser Ala Gly Leu Gln Met Gly Arg Lys Arg Glu
 20 25 30
 Ala Ala Glu Ala Leu Ala Gln Gln Cys Gln Ala Glu Gly Gly Arg Gly
 35 40 45
 Asp Trp Gly Leu Ser Ser Ala Tyr Arg Arg Asn Pro
 50 55 60

<210> 2477
 <211> 126
 <212> PRT
 <213> Homo sapiens

<400> 2477
 Ser Ile Thr Thr Ala Trp Gly Pro Glu Gly Ala Ile Thr Cys Cys Cys
 5 10 15
 Leu Met Glu Gly Pro Ala Trp Asp Thr Ser Gln Ile Ile Ile Thr Gly
 20 25 30
 Ser Gln Asp Gly Met Val Arg Val Trp Lys Thr Glu Asp Val Lys Met
 35 40 45
 Ser Val Pro Gly Arg Pro Ala Gly Glu Glu Pro Leu Ala Gln Pro Pro
 50 55 60
 Ser Pro Arg Gly His Lys Trp Glu Lys Asn Leu Ala Leu Ser Arg Glu
 65 70 75 80
 Leu Asp Val Ser Ile Ala Leu Thr Gly Lys Pro Ser Lys Thr Ser Pro
 85 90 95
 Ala Val Thr Ala Leu Ala Val Ser Arg Asn His Thr Lys Leu Leu Val
 100 105 110
 Gly Asp Glu Arg Gly Arg Ile Phe Cys Trp Ser Ala Asp Gly
 115 120 125

<210> 2478

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<211> 97
<212> PRT
<213> Homo sapiens
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<400> 2478
Gly Gly Phe Phe Cys Arg Gln Ser Ser Gly Pro Ser His Leu Cys His
      5              10              15
Pro Gln Pro Gly Thr Val Val Pro Glu Pro Leu Leu Pro Leu Ser Ser
      20              25              30
Tyr Pro Ser Ala Asp Gln Gln Asn Ile Leu Pro Leu Ser Ser Pro Thr
      35              40              45
Arg Ser Leu Val Trp Phe Leu Asp Thr Ala Arg Ala Val Thr Ala Gly
      50              55              60
Leu Val Leu Leu Gly Phe Pro Val Lys Ala Met Leu Thr Ser Ser Ser
      65              70              75              80
Arg Leu Lys Ala Arg Phe Phe Ser His Leu Trp Pro Leu Gly Leu Gly
      85              90              95
Gly

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<210> 2479
<211> 75
<212> PRT
<213> Homo sapiens
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<400> 2479
Gly Val Ser Ser Val Gly Arg Ala Gln Ala Pro Val Thr Ser Ala Thr
      5                      10                      15

Leu Ser Leu Ala Leu Leu Cys Gln Ser Leu Cys Cys Leu Ser Leu Pro
      20                      25                      30

Thr His Leu Gln Thr Ser Arg Ile Phe Ser Pro Ser His His Gln Pro
      35                      40                      45

Gly Val Trp Cys Gly Phe Trp Thr Arg Pro Glu Gln Ser Leu Arg Gly
      50                      55                      60

Trp Phe Cys Trp Ala Ser Leu Ser Lys Gln Cys
      65                      70                      75

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<210> 2480
<211> 52
<212> PRT
<213> Homo sapiens
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<400> 2480
Arg Pro Ala Leu Asp Ser Arg Pro Gly Ser Ser Pro Thr Cys Gly Leu
          5              10              15

Leu Gly Leu Glu Ala Glu Pro Gly Ala Pro Leu Leu Leu Ala Val Gln
          20              25              30

Glu Gln Thr Ser Ser His Pro Gln Ser Ser Lys Pro Gly Pro Cys Arg
          35              40              45

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Leu Asp Ser Arg
50

<210> 2481
<211> 153
<212> PRT
<213> Homo sapiens

<400> 2481
Ala Glu Leu Arg Pro Gln Ser Pro Leu Pro Pro Ser Ala Trp His Cys
5 10 15
Cys Ala Arg Ala Ser Ala Ala Ser Leu Phe Leu Pro Ile Cys Arg Pro
20 25 30
Ala Glu Tyr Ser Pro Pro Leu Ile Thr Asn Gln Glu Phe Gly Val Val
35 40 45
Ser Gly His Gly Gln Ser Ser His Cys Gly Ala Gly Phe Ala Gly Leu
50 55 60
Pro Cys Gln Ser Asn Ala Asn Val Gln Leu Ser Thr Gln Gly Gln Val
65 70 75 80
Leu Leu Pro Leu Val Ala Ser Trp Ala Trp Arg Leu Ser Gln Gly Leu
85 90 95
Leu Ser Cys Trp Pro Ser Arg Asn Arg His Leu His Ile Leu Ser Leu
100 105 110
Pro Asn Pro Asp His Ala Val Leu Thr Pro Gly Asp Asp Asp Leu Ala
115 120 125
Cys Val Pro Cys Trp Ala Leu His Gln Ala Ala Thr Gly Tyr Gly Ser
130 135 140
Phe Trp Ala Pro Gly Cys Gly Asp Ala
145 150

<210> 2482
<211> 63
<212> PRT
<213> Homo sapiens

<400> 2482
Tyr Cys Lys Gly Pro Leu Glu Phe Leu Lys Trp Leu His Arg Ile Glu
5 10 15
Ile Ile Ser Asn Asn Cys Lys Gly Thr Glu Asn Leu His Arg Asp Glu
20 25 30
Val Gly Phe Pro Leu Gly Ala Leu Lys Phe Asp Asn Lys Ser Ser Thr
35 40 45
Ser Thr Gly Gln Tyr Ile Asp Phe Gly Cys Leu Arg Pro Gln Asp
50 55 60

<210> 2483
<211> 87

<212> PRT

<213> Homo sapiens

<400> 2483

Thr Leu Lys Tyr Phe Ile Ile Gly Gly Asn Leu Trp Arg Leu Val Ala
5 10 15

Ser Asn Leu Gly Ala Ser Asp Thr Gln Asn Leu Tyr Ile Asp Gln Trp
20 25 30

Lys Leu Met Ile Cys Tyr Gln Ile Ser Lys His Leu Met Glu Thr Pro
35 40 45

Leu His Leu Cys Glu Asp Phe Gln Phe Leu Tyr Ser Tyr Leu Lys Leu
50 55 60

Phe Gln Phe Cys Gly Ala Thr Ser Glu Thr Pro Met Gly Leu Cys Asn
65 70 75 80

Ile Lys Met Trp Arg Met His
85

<210> 2484

<211> 65

<212> PRT

<213> Homo sapiens

<400> 2484

Met Leu Gln Tyr Leu Asn Met Leu Cys Gln Thr Ile Pro Leu Cys Asn
5 10 15

Arg Leu His Ile Val Phe Met Ile Leu Ile Lys Leu Tyr Val Glu Thr
20 25 30

Glu Cys Glu Val Lys Ser Glu His Lys Lys Ile Met His Asp Glu Ile
35 40 45

Ala Tyr His Phe Ile Gly Tyr Leu Leu Cys Ile Tyr Thr Leu Arg Pro
50 55 60

Leu
65

<210> 2485

<211> 64

<212> PRT

<213> Homo sapiens

<400> 2485

Leu Thr His Leu Phe Leu Leu Lys Arg Tyr Cys Pro Leu Gly Gly Glu
5 10 15

Trp Glu Ser Leu Leu His Cys Cys Ser His Ser Glu Arg Thr Phe Pro
20 25 30

Cys Thr Tyr Leu Ser Thr Cys Phe Asn Leu Ile Asn Ala Thr Phe Cys
35 40 45

Ile Phe Gln Thr Ser Ile Asn Ser Ala Ile Lys Arg Cys Ser Phe Phe
50 55 60

<210> 2486
 <211> 74
 <212> PRT
 <213> Homo sapiens

<400> 2486
 Ile Tyr Asp Ser Leu Ala Tyr Trp Asn Trp Ser Ala Ser Lys Thr Gly
 5 10 15
 Trp Leu His Arg Arg Thr Arg Gln Ser Arg Leu Phe Leu Cys Thr Asp
 20 25 30
 Ser Glu Thr Val Leu Ser Gly Arg Ser Ser Gly Leu Pro Gly Pro Asp
 35 40 45
 Thr Cys Pro Arg Glu Ser Pro Glu Ala Trp Thr Val Leu Leu Cys Phe
 50 55 60
 His Arg Ser Gly Arg Gly Glu Ser Pro Trp
 65 70

<210> 2487
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 2487
 Lys Thr Ile Tyr Arg Gln Phe Phe Thr Ser Leu Ile Phe Thr Asp Ser
 5 10 15
 Thr Ser Tyr Gly Met Ala Tyr Gly Leu Pro Pro Lys Tyr Thr Ile Leu
 20 25 30
 Trp His Ile Gly Ile Gly Gln Pro Gln Arg Pro Ala Gly Tyr Ile Val
 35 40 45
 Ala Arg Asp Ser Pro Ala Tyr Ser Ser Ala Arg Thr Arg Arg Arg Ser
 50 55 60
 Ser Ala Gly Gly Ala Gln Val Ser Leu Gly Gln Thr Arg Ala Pro Glu
 65 70 75 80
 Ser Pro Gln Lys His Gly Gln Phe Cys Ser Val Ser Ile Ala Gln Ala
 85 90 95
 Gly Glu Arg Val Arg
 100

<210> 2488
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 2488
 Lys Gln Ser Thr Gly Ser Ser Leu Gln Val Ser Tyr Leu Gln Ile Ala
 5 10 15
 Gln Ala Met Ala Trp Arg Met Ala Ser Leu Leu Asn Ile Arg Phe Phe
 20 25 30

Gly Ile Leu Glu Leu Val Ser Leu Lys Asp Arg Leu Ala Thr Ser Ser
35 40 45
His Glu Thr Val Pro Leu Ile Pro Leu His Gly Leu Gly Asp Gly Pro
50 55 60
Gln Arg Glu Glu Leu Arg Ser Pro Trp Ala Arg His Val Pro Gln Arg
65 70 75 80
Val Pro Arg Ser Met Asp Ser Ser Ala Leu Phe Pro Ser Leu Arg Gln
85 90 95
Gly Arg Glu Ser Val
100

<210> 2489
<211> 74
<212> PRT
<213> Homo sapiens

<400> 2489
His Gly Leu Ser Pro Leu Pro Glu Arg Trp Lys Gln Ser Arg Thr Val
5 10 15
His Ala Ser Gly Asp Ser Leu Gly His Val Ser Gly Pro Gly Arg Pro
20 25 30
Glu Leu Leu Pro Leu Arg Thr Val Ser Glu Ser Val Gln Arg Asn Lys
35 40 45
Arg Asp Cys Leu Val Arg Arg Cys Ser Gln Pro Val Phe Glu Ala Asp
50 55 60
Gln Phe Gln Tyr Ala Lys Glu Ser Tyr Ile
65 70

<210> 2490
<211> 64
<212> PRT
<213> Homo sapiens

<400> 2490
Gly Pro Ser Pro Ser Pro Cys Arg Gly Ile Ser Gly Thr Val Ser Cys
5 10 15
Asp Asp Val Ala Ser Arg Ser Leu Arg Leu Thr Asn Ser Asn Met Pro
20 25 30
Lys Asn Arg Ile Phe Arg Arg Glu Ala Ile Arg His Ala Ile Ala Cys
35 40 45
Ala Ile Cys Lys Tyr Glu Thr Cys Lys Glu Leu Pro Val Asp Cys Phe
50 55 60

<210> 2491
<211> 136
<212> PRT
<213> Homo sapiens

<400> 2491

Tyr	Leu	Lys	Val	Ile	Val	Ala	Leu	Gly	Met	Pro	Gly	Gln	Glu	Asp	Glu
				5				10						15	
Gly	Ala	Leu	Trp	Thr	Gln	Gln	Ser	Ala	Glu	Phe	Arg	Ser	Gly	Lys	Pro
			20					25					30		
Met	Val	Ala	Gly	Thr	Pro	Cys	Phe	Leu	Pro	Leu	Leu	Ser	Ala	Cys	Val
		35					40					45			
Thr	His	Ile	Asn	Gly	Asn	Asn	Phe	Phe	Gln	Leu	Leu	Ala	Glu	Val	Gly
	50					55					60				
Glu	Ala	Gly	Ser	Leu	His	Arg	Glu	Gly	Leu	Ser	Ser	Leu	Leu	Leu	Pro
65					70					75					80
Ala	Ser	Phe	Cys	Phe	Gly	Cys	Arg	Glu	Trp	Phe	Ile	His	Thr	Leu	Ile
				85					90					95	
Pro	Ser	Pro	Pro	Leu	Val	Asp	Gly	Gly	Leu	Ala	Phe	Ser	Ile	Pro	Val
			100					105					110		
Phe	Trp	Cys	Leu	Pro	Leu	Ser	Ala	Thr	Leu	Asn	His	Leu	Pro	Trp	Ser
	115						120					125			
Cys	Cys	Val	Met	Gly	Thr	Cys	Leu								
	130					135									

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<210> 2492
<211> 79
<212> PRT
<213> Homo sapiens
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<400> 2492
Thr Arg Pro Thr Lys Ala Arg Ser Met Ser Pro Gln Val Ser Ser Gln
          5                      10                      15

Ser Arg Leu Thr Leu Ser Ser Gly Arg Val Tyr Ile Ala Val Phe Asn
          20                      25                      30

Thr Ser Arg Ser Leu Trp Leu Trp Gly Cys Arg Gly Arg Arg Thr Arg
          35                      40                      45

Val Arg Cys Gly His Ser Ser Pro Arg Asn Ser Val Leu Gly Ser Gln
          50                      55                      60

Trp Ser Pro Ala Pro Leu Ala Ser Ser Leu Cys Cys Leu Pro Val
          65                      70                      75

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<210> 2493
<211> 73
<212> PRT
<213> Homo sapiens
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<400> 2493
His Thr Ser Met Ala Ile Thr Ser Ser Asn Ser Ser Gln Lys Trp Glu
          5                      10                      15
Arg Pro Ala Ala Cys Thr Glu Arg Gly Phe Pro Leu Ser Cys Ser Pro
          20                      25                      30
Leu Arg Ser Val Leu Ala Ala Glu Ser Gly Ser Ser Ile Leu Ser Phe

```

35 40 45
 Pro Arg Leu Pro Leu Trp Thr Gly Val Leu Pro Phe Gln Phe Leu Cys
 50 55 60

Phe Gly Val Phe Pro Tyr Leu Leu Pro
 65 70

<210> 2494
 <211> 57
 <212> PRT
 <213> Homo sapiens

<400> 2494
 Leu Tyr Leu Ile Pro Gln Gly His Cys Gly Ser Gly Asp Ala Gly Ala
 5 10 15

Gly Gly Arg Gly Cys Ala Val Asp Thr Ala Val Arg Gly Ile Pro Phe
 20 25 30

Trp Glu Ala Asn Gly Arg Arg His Pro Leu Leu Pro Pro Ser Val Val
 35 40 45

Cys Leu Cys Asp Thr His Gln Trp Gln
 50 55

<210> 2495
 <211> 89
 <212> PRT
 <213> Homo sapiens

<400> 2495
 Leu Leu Pro Thr Pro Arg Arg Ser Gly Arg Gly Arg Gln Pro Ala Pro
 5 10 15

Arg Gly Ala Phe Leu Ser Leu Ala Pro Arg Phe Val Leu Phe Trp Leu
 20 25 30

Gln Arg Val Val His Pro Tyr Ser His Ser Leu Ala Ser Pro Cys Gly
 35 40 45

Arg Gly Ser Cys Leu Phe Asn Ser Cys Val Leu Val Ser Ser Leu Ile
 50 55 60

Cys Tyr Pro Glu Ser Pro Ala Leu Val Leu Leu Cys Asp Gly Asn Met
 65 70 75 80

Leu Val Asn Cys Val Thr Asn Leu Leu
 85

<210> 2496
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 2496
 Lys Gly Lys Thr Pro Val His Lys Gly Arg Arg Gly Asn Glu Ser Met
 5 10 15

Asp Glu Pro Leu Ser Ala Ala Lys Thr Glu Arg Ser Gly Glu Gln Glu

20	25	30
Arg Gly Lys Pro Leu Ser Val Gln Ala Ala Gly Leu Ser His Phe Cys		
35	40	45
Glu Glu Leu Glu Glu Val Ile Ala Ile Asp Val Cys His Thr Gly Arg		
50	55	60
Gln Gln Arg Glu Glu Ala Arg Gly Ala Gly Asp His Trp Leu Pro Arg		
65	70	75
Thr Glu Phe Arg Gly Leu Leu Cys Pro Gln Arg Thr Leu Val Leu Leu		
85	90	95
Pro Arg His Pro Gln Ser His Asn Asp Leu Glu Val Leu Asn Thr Ala		
100	105	110
Ile Tyr Thr Arg Pro Glu Leu Arg Val Asn Leu Asp		
115	120	

<210> 2497

<211> 123

<212> PRT

<213> Homo sapiens

<400> 2497

Phe Arg Val Ala Asp Lys Gly Arg His Gln Asn Thr Gly Ile Glu Lys		
5	10	15
Ala Arg Pro Pro Ser Thr Arg Gly Gly Glu Gly Met Arg Val Trp Met		
20	25	30
Asn His Ser Leu Gln Pro Lys Gln Asn Glu Ala Gly Ser Lys Arg Glu		
35	40	45
Glu Ser Pro Ser Arg Cys Arg Leu Pro Ala Ser Pro Thr Ser Ala Arg		
50	55	60
Ser Trp Lys Lys Leu Leu Pro Leu Met Cys Val Thr Gln Ala Asp Asn		
65	70	75
Arg Gly Arg Lys Gln Gly Val Pro Ala Thr Ile Gly Phe Pro Glu Arg		
85	90	95
Asn Ser Ala Asp Cys Cys Val His Ser Ala Pro Ser Ser Ser Cys Pro		
100	105	110
Gly Ile Pro Arg Ala Thr Met Thr Leu Arg Tyr		
115	120	

<210> 2498

<211> 58

<212> PRT

<213> Homo sapiens

<400> 2498

Cys Pro Ser Ala Ile Thr Ile Gln Gln Leu Gln Ala Gly Leu Ala Asp		
5	10	15
Arg Glu Tyr Gly Arg Arg Thr Arg Ser Asp Glu Asn Met His Ala Thr		
20	25	30

Ile Phe Thr Thr Glu His Thr Val Phe Cys Asp Arg Asn Cys Arg Pro
35 40 45

Cys Trp Gly Thr Arg Tyr Ser Arg Pro His
50 55

<210> 2499

<211> 71

<212> PRT

<213> Homo sapiens

<400> 2499

Lys Ser Arg Pro Thr Cys Ser His Trp Thr Asp Val Gln Val Gln Ser
5 10 15

Pro Tyr Ser Ser Tyr Arg Gln Gly Trp Leu Ile Gly Ser Met Gly Glu
20 25 30

Gly His Ala Gln Met Lys Thr Cys Met Gln Arg Phe Ser Pro Leu Asn
35 40 45

Thr Leu Phe Ser Val Ile Glu Thr Val Gly Pro Ala Gly Gly Gln Asp
50 55 60

Ile His Gly Leu Thr Ser Gln
65 70

<210> 2500

<211> 73

<212> PRT

<213> Homo sapiens

<400> 2500

Gly Arg Glu Tyr Leu Val Pro Gln Gln Gly Arg Gln Phe Leu Ser Gln
5 10 15

Lys Thr Val Cys Ser Val Val Lys Ile Val Ala Cys Met Phe Ser Ser
20 25 30

Glu Arg Val Leu Leu Pro Tyr Ser Leu Ser Ala Ser Pro Ala Cys Ser
35 40 45

Cys Cys Met Val Ile Ala Leu Gly His Gln Ser Asn Asp Cys Lys Ser
50 55 60

Ala Trp Ile Phe Thr Cys Arg Gly Tyr
65 70

<210> 2501

<211> 88

<212> PRT

<213> Homo sapiens

<400> 2501

Ser Arg Leu Leu Glu Gln Leu Ala Trp Ala Gly Phe Ser His Pro Gly
5 10 15

Cys Pro Leu Asp Cys Ser Thr Gln Ala Phe Pro Trp Gly Leu Gly Ser
20 25 30

```

Leu His Lys Val Arg Cys Leu Leu Pro Tyr Gly Pro Ser Leu Ala Gly
      35                      40                      45

Asn Lys Gly Ala Ser Gly Ala Gly Arg Pro Gly Gly Ile Ser Leu Ala
      50                      55                      60

Ser Glu Ala Val Asn Ile Leu Ser Pro Ser Arg Ala Asp Ser Phe Tyr
      65                      70                      75                      80

His Arg Lys Gln Cys Val Gln Trp
      85

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<210> 2502
<211> 59
<212> PRT
<213> Homo sapiens
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<400> 2502
Ser Glu Val Cys Ser Ser Gly Leu Ser Ser Pro Leu Leu Glu Gln His
          5                               10                      15

Lys Thr Asn Leu Ile Phe Tyr Ala Ser Gly Asp Ile Cys Ser Ala Asn
          20                               25                      30

Gly Lys Ser Gly Phe Asn Gln Pro Leu Pro Phe Leu Lys Thr Phe Cys
          35                               40                      45

Cys Thr His Arg Ile Leu Ser Cys Thr Tyr Leu
          50                               55

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<210> 2503
<211> 171
<212> PRT
<213> Homo sapiens
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```
<400> 2503  
Leu Leu Asp Ser Ile Trp His Gln Pro Ile Phe Asn Leu Leu Ser Ile  
          5                      10                      15  
  
Gly Gln Ser Leu Tyr Ala Lys Ala Lys Glu Leu Asp Arg Val Lys Glu  
        20                      25                      30  
  
Ile Gln Glu Gln Leu Phe His Ile Lys Lys Leu Leu Lys Thr Cys Arg  
      35                     40                     45  
  
Phe Ala Asn Ser Ala Leu Lys Glu Phe Val Gly Gln Val Pro Gly His  
    50                    55                    60  
  
Leu Thr Asp Glu Leu His Leu Phe Ser Leu Glu Asp Leu Val Arg Ile  
   65                70                75                80  
  
Lys Lys Gly Leu Leu Ala Pro Leu Leu Lys Asp Ile Leu Lys Ala Ser  
            85                  90                  95  
  
Leu Ala His Val Ala Gly Cys Glu Leu Cys Gln Gly Lys Gly Phe Ile  
       100                 105                 110  
  
Cys Glu Phe Cys Gln Asn Thr Thr Val Ile Phe Pro Phe Gln Thr Ala  
     115                   120                   125
```

Thr Cys Arg Arg Cys Ser Ala Cys Arg Ala Cys Phe His Lys Gln Cys
 130 135 140

Phe Gln Ser Ser Glu Cys Pro Arg Cys Ala Arg Ile Thr Ala Arg Arg
 145 150 155 160

Lys Leu Leu Glu Ser Val Ala Ser Ala Ala Thr
 165 170

<210> 2504
 <211> 100
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(100)
 <223> Xaa = Any amino acid

<400> 2504
 Lys Leu Pro Leu His Met Trp Leu Ala Val Ser Cys Val Lys Glu Arg
 5 10 15

Ala Leu Phe Val Asn Phe Ala Arg Ile Arg Leu Ser Ser Ser His Phe
 20 25 30

Arg Gln Gln His Val Glu Asp Val Gln Arg Ala Gly Leu Ala Phe Thr
 35 40 45

Asn Ser Ala Ser Ser Pro Pro Ser Ala Pro Gly Val Arg Gly Ser Gln
 50 55 60

Arg Gly Glu Asn Phe Trp Lys Val Trp Pro Leu Gln Gln His Asp Ala
 65 70 75 80

Pro Glu Tyr Xaa Glu Lys Asp Cys Ser Thr Cys Leu Met Ile Thr Pro
 85 90 95

Ile Xaa Val Tyr
 100

<210> 2505
 <211> 55
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(55)
 <223> Xaa = Any amino acid

<400> 2505
 Lys Met Phe Ser Val Gln Gly Leu Leu Ser Gln Thr Val Leu Pro Val
 5 10 15

Leu Arg Val Pro Pro Val Cys Glu Asp His Ser Glu Glu Lys Thr Ser
 20 25 30

Gly Lys Cys Gly Leu Cys Ser Asn Met Met Pro Leu Ser Thr Xaa Lys
 35 40 45

Lys Thr Val Gln His Ala Leu
50 55

<210> 2506
<211> 72
<212> PRT
<213> Homo sapiens

<400> 2506
His Ser Ser Gln Pro Ala Thr Cys Ala Arg Glu Ala Phe Arg Met Ser
5 10 15

Leu Ser Lys Gly Ala Ser Ser Pro Phe Leu Ile Leu Thr Arg Ser Ser
20 25 30

Arg Glu Asn Arg Trp Ser Ser Ser Val Lys Cys Pro Gly Thr Cys Pro
35 40 45

Thr Asn Ser Phe Asn Ala Leu Leu Ala Asn Leu Gln Val Phe Asn Ser
50 55 60

Phe Leu Ile Trp Lys Ser Cys Ser
65 70

<210> 2507
<211> 58
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(58)
<223> Xaa = Any amino acid

<400> 2507
Xaa Gln Ile Gly Val Ile Ile Arg His Val Glu Gln Ser Phe Xaa Gln
5 10 15

Tyr Ser Gly Ala Ser Cys Cys Cys Arg Gly His Thr Phe Gln Lys Phe
20 25 30

Ser Pro Arg Cys Asp Pro Arg Thr Pro Gly Ala Leu Gly Gly Leu Glu
35 40 45

Ala Leu Phe Val Lys Ala Ser Pro Ala Arg
50 55

<210> 2508
<211> 53
<212> PRT
<213> Homo sapiens

<400> 2508
Cys Thr Val Ser Lys Pro Thr Gly Leu Gln Gln Leu Leu Asp Met Glu
5 10 15

Glu Leu Leu Leu Asn Phe Leu His Ser Val Gln Leu Leu Gly Phe Arg
20 25 30

Ile Gln Ala Leu Ala Asp Ala Gln Gln Ile Glu Asn Gly Leu Val Pro

35 40 45

Tyr Ala Val Glu Gln
50

<210> 2509
<211> 52
<212> PRT
<213> Homo sapiens

<400> 2509
Arg Thr Ile Gly Gly Cys Arg His Val Leu Leu Glu Gln Leu Pro Arg
5 10 15
Thr Thr Leu Leu Arg Ser Gly Phe Gln Arg Pro Pro Asn Phe Val Ser
20 25 30
Phe Asn Ser Phe Arg Pro Asp Leu Leu Phe Gly Ser Val Thr Gly Arg
35 40 45
Gln Val Ser Thr
50

<210> 2510
<211> 115
<212> PRT
<213> Homo sapiens

<400> 2510
His Met Pro Asp Trp Leu Phe Ala Thr His Leu Lys Asp Thr Thr Gln
5 10 15
Ser Met Glu Ala Phe Asn Arg Thr Ala Leu Pro Ile Ser Gly Leu Leu
20 25 30
Ala Asp Ala Asp Met Phe Tyr Ser Ser Ser Tyr Gln Gly Pro Leu Tyr
35 40 45
Cys Asp Gln Asp Ser Asn Asp His Leu Ile Ser Tyr Leu Ser Thr Leu
50 55 60
Phe Asp Arg Thr Ser Tyr Ser Glu Ala Leu Gln Glu Asp Arg Ser Gln
65 70 75 80
Leu Arg Asp Gln Ile Thr Leu Ser Thr Leu Trp Asp Arg Cys Asn Leu
85 90 95
Ala Leu Gln Gly Ser Ala Pro Ile Thr Ser Arg Pro Ala Asn Thr Asp
100 105 110
Leu Glu Val
115

<210> 2511
<211> 52
<212> PRT
<213> Homo sapiens

<400> 2511
Val Glu Thr Cys Leu Pro Val Thr Leu Pro Asn Lys Arg Ser Gly Arg

5 10 15
 Lys Glu Leu Lys Asp Thr Lys Leu Gly Gly Arg Trp Asn Pro Asp Arg
 20 25 30
 Ser Lys Val Val Leu Gly Asn Cys Ser Ser Arg Thr Cys Leu His Pro
 35 40 45
 Pro Ile Val Arg
 50

<210> 2512
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 2512
 Asn Met Ser Ala Ser Ala Asn Ser Pro Leu Ile Gly Arg Ala Val Arg
 5 10 15
 Leu Lys Ala Ser Ile Asp Trp Val Val Ser Phe Lys Trp Val Ala Lys
 20 25 30
 Ser Gln Ser Gly Ile Cys His Glu Gly Phe Ser Asp Arg Leu Met Val
 35 40 45
 Cys Cys Leu Thr Ser Leu Gly Lys
 50 55

<210> 2513
 <211> 57
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(57)
 <223> Xaa = Any amino acid

<400> 2513
 Ala Thr Phe Ile Asn Thr Asp Ile Leu Glu Leu Phe Thr Phe Leu Leu
 5 10 15
 Phe Ile Phe Glu Phe Ser Val Xaa Tyr Leu Val Leu Ile His Cys Cys
 20 25 30
 Ile Xaa Asn Cys Thr Leu Ile Ser Ser Ser Ile Lys Ser Ile Xaa Leu
 35 40 45
 Gln Phe Xaa Gly Ile Ile Ile Asn Leu
 50 55

<210> 2514
 <211> 75
 <212> PRT
 <213> Homo sapiens

<220>
 <221> variant
 <222> (1)...(75)

<223> Xaa = Any amino acid

<400> 2514

Leu Ile Pro Pro Pro Val Xaa His Val Tyr Ser Arg Leu Ala Asp Lys
5 10 15

Ala Leu Phe Gly Gly Pro Ala Ser Val Gly Ser Gln Lys Pro Asn Tyr
20 25 30

Cys Gly Leu Gln Arg Ile Ser Arg Ser Phe Thr Lys Gln Thr Ser Leu
35 40 45

His Pro Asp Cys Xaa Phe Ala Xaa Ser Gly Ser Gln Xaa Met Ser Xaa
50 55 60

Gly Ala Gly Ser Phe Trp Leu Leu Glu Lys Pro
65 70 75

<210> 2515

<211> 64

<212> PRT

<213> Homo sapiens

<220>

<221> variant

<222> (1)...(64)

<223> Xaa = Any amino acid

<400> 2515

Leu Asn Ile Leu Asn Xaa Ala Leu Leu Ser Val Glu Leu Leu Tyr Phe
5 10 15

Thr Phe Ser Ala Phe Gly Asp His Tyr Leu Ile Glu Phe Val Glu Ile
20 25 30

Asp Phe Pro Asp Arg Ser Leu Phe Phe Asn Glu Gln Met Ile Arg Asn
35 40 45

Asn Leu Thr Pro Tyr Met Thr Met Glu Leu Asn Lys Leu Thr Leu Ile
50 55 60

<210> 2516

<211> 100

<212> PRT

<213> Homo sapiens

<400> 2516

Leu Asn Lys Arg Gly Thr Asn Phe Gln Phe Val Lys Leu Gln Ser Arg
5 10 15

Lys Tyr Trp Cys Leu Leu Pro Cys Glu Phe Phe Leu Arg His Ala Glu
20 25 30

Lys Met Tyr Ala Arg Asp Gln Lys Asp Gly Ser Lys Leu Cys His Val
35 40 45

Thr Cys Asn Lys Ile Phe Ser Ser Arg Phe Phe Leu Cys Trp Gln Ile
50 55 60

Ile Ser Pro Cys Ser Phe His Ser Leu Ile Leu Ala Phe Arg Val Thr
65 70 75 80

Met Ile Ile Leu Pro Met Trp Phe Leu Arg Lys Lys Asp Gln Phe Phe.
85 90 95

Val Cys Ser Arg
100

<210> 2517
<211> 52
<212> PRT
<213> Homo sapiens

<400> 2517
Asn Ser Lys Ala Glu Ser Ile Gly Ala Cys Tyr Leu Val Asn Ser Ser
5 10 15

Leu Asp Met Gln Arg Lys Cys Met Gln Glu Thr Lys Lys Met Ala Pro
20 25 30

Ser Tyr Val Met Leu Pro Val Ile Lys Ser Phe Leu Leu Asp Ser Phe
35 40 45

Tyr Val Gly Arg
50

<210> 2518
<211> 50
<212> PRT
<213> Homo sapiens

<400> 2518
Asp Arg Tyr Trp Tyr Ser Phe Ile Ile Glu Thr Lys Arg Ser Ala Leu
5 10 15

Leu Asp Phe Pro Leu Phe Val Leu Lys Gly Ile Lys Asp Cys Arg Phe
20 25 30

Pro Ala Leu Ser Ser Arg Gly His Tyr Glu Gln Ile Lys Trp Lys Asp
35 40 45

Lys Phe
50

<210> 2519
<211> 51
<212> PRT
<213> Homo sapiens

<400> 2519
Trp Pro Arg Glu Asp Arg Ala Gly Asn Leu Gln Ser Leu Ile Pro Phe
5 10 15

Arg Thr Lys Ser Gly Lys Ser Ser Lys Ala Asp Leu Leu Val Ser Ile
20 25 30

Ile Lys Glu Tyr Gln Tyr Arg Ser Gln Lys Arg Ser Val Ser Leu Gln
35 40 45

Gly Tyr Phe
50

<210> 2520
<211> 87
<212> PRT
<213> Homo sapiens

<400> 2520
Ile Leu Thr Leu Tyr Ser Glu Pro Ser Phe Asn Thr Met Val Ser Phe
5 10 15
Leu Arg Ala Ser Arg Ser Pro Val Arg Ser Met Val Ile Gly Pro Gly
20 25 30
Ala Leu Ser Gln Thr Arg Val Ser Arg Val Thr Thr Thr Leu Gly Ala
35 40 45
Phe Gly Ser Val Thr Thr Gly Pro Ser Pro Ser Ser Val Phe Leu Tyr
50 55 60
Leu Ile Arg Leu Ser Ser Leu Ser Ile Ser Cys Ser Ser Phe Arg
65 70 75 80
Asp Phe Cys Gly Gly Gly Leu
85

<210> 2521
<211> 55
<212> PRT
<213> Homo sapiens

<400> 2521
His Asn Gly Phe Leu Phe Glu Gly Phe Gln Ile Ser Ser Lys Val His
5 10 15
Gly Asp Trp Ser Arg Gly Thr Leu Thr Asn Gln Gly Glu Pro Gly Asp
20 25 30
Asn Asp Ile Gly Gly Phe Arg Ile Cys His His Arg Thr Ile Ser Gln
35 40 45
Gln Arg Phe Leu Val Leu Asn
50 55

<210> 2522
<211> 120
<212> PRT
<213> Homo sapiens

<400> 2522
Leu Lys Lys Pro Gln Ser Pro His Val Glu Glu Asp Asp Asp Asp Glu
5 10 15
Leu Asp Ser Lys Leu Asn Tyr Lys Pro Pro Pro Gln Lys Ser Leu Lys
20 25 30
Glu Leu Gln Glu Met Asp Lys Asp Asp Glu Ser Leu Ile Lys Tyr Lys
35 40 45
Lys Thr Leu Leu Gly Asp Gly Pro Val Val Thr Asp Pro Lys Ala Pro
50 55 60

Asn Val Val Val Thr Arg Leu Thr Leu Val Cys Glu Ser Ala Pro Gly
 65 70 75 80
 Pro Ile Thr Met Asp Leu Thr Gly Asp Leu Glu Ala Leu Lys Lys Glu
 85 90 95
 Thr Ile Val Leu Lys Glu Gly Ser Glu Tyr Arg Val Lys Ile His Phe
 100 105 110
 Lys Val Asn Arg Asp Ile Val Ser
 115 120

<210> 2523
 <211> 75
 <212> PRT
 <213> Homo sapiens

<400> 2523
 Glu Leu Gln Glu Glu Ser Gly Leu Glu Asp Ser Gln Arg Asn Lys Ser
 5 10 15
 Arg Leu Asn Cys Ile Arg Tyr Ile Pro Ala Cys Trp Gln Leu His Lys
 20 25 30
 Asn Ile Ser Asp Phe Asn Pro Asn Leu Ala Asn Glu Thr Gly Phe Leu
 35 40 45
 Phe Phe Met Leu Cys Val Thr Glu Leu Lys Thr Gln Phe Pro Asn Pro
 50 55 60
 Gln Phe Met Gln Pro Pro Ser Gly Ile Leu Ser
 65 70 75

<210> 2524
 <211> 59
 <212> PRT
 <213> Homo sapiens

<400> 2524
 Val Phe Ser Ser Val Thr His Asn Ile Lys Asn Lys Asn Pro Val Ser
 5 10 15
 Leu Ala Lys Phe Gly Leu Lys Ser Glu Met Phe Leu Trp Ser Cys Gln
 20 25 30
 Gln Ala Gly Met Tyr Leu Ile Gln Phe Asn Leu Leu Leu Phe Leu Trp
 35 40 45
 Leu Ser Ser Lys Pro Leu Ser Ser Cys Asn Ser
 50 55

<210> 2525
 <211> 51
 <212> PRT
 <213> Homo sapiens

<400> 2525
 Tyr Ser Leu Ile Cys Phe Tyr Phe Phe Gly Cys Leu Pro Asn His Phe
 5 10 15

Leu Pro Val Ile Leu Lys Leu Ala Ser Pro Pro Ser Ser Glu Lys Leu
20 25 30

Pro Leu Arg Ile Phe Leu Ile Val Arg Val Tyr Phe Arg Ile Glu Glu
35 40 45

Ser Phe Gly
50

<210> 2526
<211> 72
<212> PRT
<213> Homo sapiens

<400> 2526
Gln Met Gln Lys Asn Lys Asn Lys Asn Thr Thr Gln Asn Ala Thr Cys
5 10 15

Lys Trp Trp Ser Met Tyr Leu Tyr Ile Thr Ser Pro His Thr Tyr Ile
20 25 30

His Ser Lys Gln Tyr Tyr Ile Ile Phe Leu Cys Glu His Thr Met Ser
35 40 45

Phe Trp Lys Asn Ile Gln Lys Leu Val Thr Val Ala Asn Phe Arg Gly
50 55 60

Glu Ser Leu Ile Arg Val Gly Arg
65 70

<210> 2527
<211> 52
<212> PRT
<213> Homo sapiens

<400> 2527
Lys Asp Phe Ser Pro Phe Cys Lys Val Gly Ser Thr Tyr Leu Gln Lys
5 10 15

Glu Cys Ile Ser Val Leu Cys Val Asn Ile Pro Leu Ile Ser Lys Arg
20 25 30

Phe His Glu Lys Ile Phe Glu Glu Leu His Lys His Pro Leu Leu Cys
35 40 45

Arg Gln Arg Trp
50

<210> 2528
<211> 75
<212> PRT
<213> Homo sapiens

<400> 2528
Leu Leu Leu Pro Val Phe Val Cys Ser Ser Arg Arg Thr Leu Tyr Val
5 10 15

His Ile Glu Lys Leu Tyr Ser Ile Val Leu Ser Val Cys Met Tyr Val
20 25 30

Gly Met Leu Cys Ile Asn Thr Tyr Ser Thr Ile Tyr Met Trp His Phe
35 40 45

Val Leu Cys Phe Cys Phe Cys Phe Phe Ala Phe Ala Ile Phe Ile Cys
50 55 60

Cys Ser Phe Lys Leu Cys Ser Val Glu Leu Glu
65 70 75

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<210> 2529 .
<211> 93
<212> PRT
<213> Homo sapiens
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<400> 2529
Gly Phe Val Pro Ser His His Leu Cys Leu His Ser Lys Gly Cys Leu
      5                                10                                15
Cys Asn Ser Ser Lys Ile Phe Ser Trp Asn Leu Leu Glu Ile Asn Gly
      20                                25                                30
Ile Phe Thr His Asn Thr Glu Ile His Ser Phe Cys Lys Tyr Val Leu
      35                                40                                45
Pro Thr Leu Gln Lys Gly Leu Lys Ser Phe His Leu Pro Thr Leu Ile
      50                                55                                60
Lys Asp Ser Pro Leu Lys Leu Ala Thr Val Thr Ser Phe Cys Met Phe
      65                                70                                75                                80
Phe Gln Lys Asp Ile Val Cys Ser His Arg Lys Ile Ile
      85                                90

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<210> 2530
<211> 53
<212> PRT
<213> Homo sapiens
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<400> 2530
Phe Phe Phe Leu His Arg Ile Gly Arg Gly Gly Arg Phe Gly Arg Lys
      5                      10                      15
Gly Val Ala Ile Asn Phe Val Thr Glu Glu Asp Lys Arg Ile Leu Arg
      20                      25                      30
Asp Ile Glu Thr Phe Tyr Asn Thr Thr Val Glu Glu Met Pro Met Asn
      35                      40                      45
Val Thr Asp Leu Ile
      50

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<210> 2531
<211> 58
<212> PRT
<213> Homo sapiens
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<400> 2531
Lys Val Ser Met Ser Arg Arg Ile Leu Leu Ser Ser Ser Val Thr Lys
 5 10 15

Phe Ile Ala Thr Pro Phe Leu Pro Asn Arg Pro Pro Leu Pro Ile Leu
20 25 30

Cys Lys Lys Lys Asn Gln Asn Val Thr Ser His Ile Met Tyr Lys Leu
35 40 45

Leu Asn Met Thr Ile His Leu Leu Thr Thr
50 55

<210> 2532
<211> 67
<212> PRT
<213> Homo sapiens

<220>
<221> variant
<222> (1)...(67)
<223> Xaa = Any amino acid

<400> 2532
Xaa Pro Ile Xaa Gln Gln Arg Ala Leu His Arg Lys Leu Ser Ser Gln
5 10 15

Glu Leu Asn Lys Val Ser His Ile His Gly His Leu Leu His Cys Ser
20 25 30

Ile Val Glu Ser Leu Asn Val Thr Lys Asn Pro Leu Val Phe Phe Ser
35 40 45

Asn Lys Val Tyr Ser His Thr Phe Pro Pro Lys Ser Thr Pro Ser Ala
50 55 60

Asn Ser Val
65